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November 4, 2000, 13:30:39; Search time 4075.18 Seconds (without alignments) 439.418 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AF051838 Zea mays AF037030 Zea mays AF037037 Zea mays AF051837 Zea mays AF0518900 Arabidops AF007029 Zea mays AF007029 Zea mays AF007020 Zea mays AF007020 Zea mays AF007020 Zea mays AF007020 Zea mays AF037029 Z
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gb_htg4:* gb_htg5:* gb_htg6:*

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(bases 1 to 634)
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1 (bases 1 to 1686)
Redinbaugh,M.G. and Campbell, W.H.
Nitrate regulation of the oxidative pentose phosphate pathway in maize (Zea mays L.) root plastids; induction of 6-phosphogluconate dehydrogenesse activity, protein and transcript levels plant Sci. 134 (2), 129-140 (1998)

2 (bases 1 to 1686)
Redinbaugh,M.G. and Bailey-Serres, J.
Characterization of cubas encoding cytosolic and a putative plastidic 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                            AF061838 1686 bp mRNA PLN 08\text{-JUN-}2000 2ea mays strain W64A x A182E putative cytosolic 6-phosphogluconate dehydrogenase (pdh2) mRNA, complete cds.
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AE001620 Chlamydia
AP002546 Chlamydop
AL008609 Mycobacte
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D31631 Bacillus li
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U14465 Escherichia
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AE002301 Chlamydia
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AC073566 Leishmani
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AE001213 Treponema
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                      D89161 Schizosacch
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                                                                            AL113362 Botrytis
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/db_xref="taxon:4577"
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SC6PGDEHY
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TBGNDG
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SPBC660
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Bukaryota; Diliopsida; Poales; Poaceae; Zea.

I chases 1 to 634)

Padegimas, L. S. and Reichert, N.A.
Isolation of genes and regulatory sequences implicated in hypersensitive response from Zea mays nematode-resistant line MP307 Unpublished
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KVAAQVPDSGPCVTYICKGGSGNFVKMVHNGIEYGDMOLISEAYDVLKFVGKLTNSEL
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KICSYAQGMNIIKAKSAEKGWOLNLGELARIFWGGGIIRAIFLDRIKKAYDRNPGLAS
LLVDPPERAQEIMDIKAAARKRVVCLAINNGVSTPGMSASLAYFDSYRRDRLPANLVQAO
RDYFGAHTYERVDMPGSFHTEWFKIARNISNN*
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rakaegnlpvygfhdpasfyksiqkprvyimlvkagaPvdqiiatlaahleqgdciid
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             /gene="pdh2"
/note="NADPH producing dehydrogenase of the oxidative
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                                                                                                                    /protein_id="AAC27703.1"
/db_xref="GI:3342802"
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/translation="MALTRIGLAGLAVMGONIALNIAEKGFPISVYNRTTSKVDETVO
RAKABGNLPVYGFHDPASFVNSIOKPRVVIMLVKAGAPVDQTIATLAAHLEQGBCIID
GGNERYENTERREKAMEERGLLYLGMGVSGGGEGARNGPSLMPGGSFDAYKYVEDIVL
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                                                                                                                                                                                                   /product="6-phosphogluconate dehydrogenase isoenzyme B"
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              Direct Submission
Submitted (06-DEC-1997) Department of Plant and Soil Sciences,
Mississippi State University, Box 9555, Mississippi State, MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 gtacaacaggacaactcccaaggtggacgagaccgtgcagcgtgccaaggcagaaggaaa 130
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AP001552
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome, 6, PAC
clone:P0029D06
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98.2%; Pred. No. 2.8e-70;
Live 0; Mismatches 7; Indels
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 Padegimas, L.S. and Reichert, N.A.
                                                                                                                                     /db_xref="taxon:4577"
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join(13886. .13953,14703. .14914,14920. .15114,15144. .15314,
15374. .15492)
   Sasaki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
Submitted (29-MAR-2000) to the DDBJ/EMBL/GenBank databases. Takuji
Sasaki, National Institute of Agrobiological Resources, Rice Genome
(E-mail:tsasaki@abr.affrc.go.jp,
URL:http://www.dna.affrc.go.jp,
Fax:81-298-38-7468)
                                                                                                                                                                                                                                                                                           Genes were predicted from the integrated results of the following:GENSCANI.0, BLASTX2.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against the non- redundant database NRP (PIR, SWISSPROT, GENPEPT, PDB) from MAFF DNA bank and the cDNA sequence database at RGP. Protein similarities of the coding regions were searched against NRP with BLASTP2.0. ESTS represent the identified cDNA sequences using BLASTN2.0 with the corresponding DDBJ accession no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MIKAPTAVTVIGRSRCLEGLAAGGKRGDCEANRVSGLCPVADVE
RKVVEVAAGIEGSWRCRLGAEGVLSCSWRKACLAWRPAAGGGRLARHEEA"
join(2761. 3848,5363. 5544,5878. 5959,6846. 7125)
/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TKLPALSFIMSVLGAQGSSLGTQSRQRVDSNARTLRRRCAGPDRDTVKRLCLAYRKDV
PMECRYADEFIALAAASSLGIFINCPKNLRNDDAGPWSLHLPPAATACLSMESCWYSVR
PPHVHGPGASALKSLTFKDSFWVLHPGYLQDTAFPSLEELHISGCTLSGSIEITSATM
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APTSVELLRSAGSAGEEVELAGSGGPSLLTGKSEEVAVAHEEGARGHRIRQAAVSSAA
TPGPDGHRVRPPPADVTTRRGIRREEAPASGPTDVVCAAMRRRGLMVAAAVPPPPPRP
TPHRRHLPTSTFNHRHRYYPCWLRRSREGKRAAARAEVEEQRAAETPLPASEVRENK
SSDARGAHGRLRRRGRGGVVPRAGEHFTMAVTVEGH"
                                                                                                                                                                                                                                                                   The orientation of the sequence is from SP6 to T7 of the PAC clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRLKHLRIADVSVVSLGTAAAIAVLADELTTLEVSCHDGGKDDPPSSHEMLCVETLFR
ASFTEYSYFRLRAPKLRVFDWRCCYAKEVRVDAVGRHLSDVYIELFAGRLPRCYNEAK
RFLQMEDCDKLMNDILGGIMFGRWKYVQSLPYRRARNKVRWGEQDDREEEEVGQWHPR
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RPADRARRERMRPGGQRRGRRGNEAVTGWARRRRAERYSIVTAGGSTSARLRRPDAAR
TSGSAHEDEPDDEGGGAGAEEEEGAGSFSYKFKQN"
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/db_xref="G1:7363270"
/translation="MVDKRPAVEPVLARRPASRCRRLDRRYAEQLLPPERKGGAPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MARRKGKDLISQLPDDILLHILSMVRYKEAVRTAAVSRRWKHLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MNLKQVHPKGTKGVANGSDDKGILDGSDETNLFETSSTEKDFNS
GAGKREQD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and RGP clone ID.
This sequence of this clone has an overlap with P0541H01 clone, DDBJ:AP001389 at the 3' end,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone ends at the position 26,826 of P0541H01. Detailed information on overlap and assembly quality together with annotation of this entry at athetp://www.dna.affrc.go.jp:82/genomicdata/GenomeFinished.html. Location/Qualifiers 1.150120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(1887. .2096,2316. .2390))
/note="hypothetical protein"
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/note="hypothetical protein"
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/note="hypothetical protein"
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/db_xref="GI:7363268"
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/db_xref="G1:7363269"
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/protein_id="BAA93015.1"
/db_xref="G1:7363271"
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/db_xref="taxon:4530"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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AUTHORS
TITLE
                                                                 JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(29217. 30334,31321. 31609,31701. 31862))
/note="hypothetical protein"
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VKPRLLOSAGNKETYYGLITARLNIPSTSHLLLCSKSSIFYWOGTNSWSEHPFGGERI
LQIVLFKGEFFAMDFHRLHTMRFAPQLSWGEVGVVWGEENEVGVHFRFWIVISGDML
LMLDLSYGIHHSYGFPGTFQVFRLDFSAQTAKWMKMEKLENSALFVSLDRRNPTFSCT
NPERWGGKSNCIYVAKPSEDSDEPWTAVELGQPIPGATHCVPYSHPLLHTEGHCSQLE
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/translation="MQSPSKVSEASGSAPPATSVIEGWAELPEGLLHSIVALLGSFLD
LLAFTGTCHSWRAAFSSYPSKSNFRTILPPLLVRPNVRVRAPYSSNGHRKLRSCEVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LANRNTPLRCQIPOETLORMHFAGSSHGOLICCRRGYCLYVDVFTGAEVSPPRLPFSE
NCDEFYYCGILTAPITSPNSHLISTQSSLFDWPVGSDSWSELKLPVNRVDQIVEFNG
QLIAVIEYSLYTLQLAPILRLEKIKTLWWDNMNECPYMRPWFVVCGDMLLIVDHYISF
SFGABVLYRPYRLDMSTKPARWVEVKKLENWALFIGGDARSPPFSFKNPERWGGRSNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(34717. .34935,35401. .35912,36242. .36363,36470. .36542,36626. .36754,36936. .37247,37336. .38617,38724. .392921)
//note="Similar to Arabidopsis thaliana DNA chrmosome V, BAC clone TM021B04; N. tabacum membrane-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYRTILHIIDMYDTIREVLITIGKDPTQREDWPIIHAMVLAFESFEFVFNAHLMLVIL
GYTNEPSNSIGKRDQDIVNAMSLVGLAKKKNQOMRPRGWEGFLGKVTSFCIKYSIDIP
AMDAKVYPRGSHRFYPYQTIDDHYRREVIGVIERIHQELENRFDEVSMELLLCMSA
FNPTDSFASPDAQKILRLASFYPKDIEGSNLMKLELQLDTYINDMREDHRFKGLNKIG
OLSIKLVETKKHDLYDLLYLLLKLVLILPVATASVERVFSAMNLVKTKVRNSMSDKLL
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RRPLRRCRRAQCGPKSKVGLDWLGLPWIITSLTHPPPRLASTPIGRAAAAAVATAGL
VSSPAHPGKLRVSKRSWTGAAGSGSGEDHGRRRRRPSPRQRSSPLSAKGLMDSWLHQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MEKSSIALLEQKHEAKKNACDLPIPHVDEGSSIPAVNDAPIDED IVVDEGVCEETEEDTVVDDAPPPDVVVDEVSIETKEESLPIYDVDDLEHDPGLRVPIS SFDANDQDAARRGYILKGPCHLWAFNFPSRKIYGKDRRFSVIWFHKYPWIEYSVDKDA
                                                                                                                           /translation="MNPEADQPDSPADPTPSRPPLPGADVSKRGGTDMRAPLVSGSRE
                                                                                                                                                                                                                         ELQDTLREEMREVRGREGYHGEREPWPTAAAMBGLTGTRRTTAFDGGIRWRRGRRAAA
SGGRRSGKGGGGRNDRGHGRRWKEEKGGEECGEAL"
join(19096. .19172,20123. .20329,20389. .20395)
/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="paa93017.1"
/db_xref="GI:7363273"
/translation="MQIEFTMHQCLVQWQGDKIEIVPANRPQSCSRRRLGTAAPTRRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TECEVOYLEGKESGKEVTGGWHNWNVGAKALDKHVGGTSSDHNFAQEKYNLFVKKGCL
RYLLRQGLAFRGHDETEESNNRGNFLELLKWLAGNNENANKVVLNNAPGNCILTSPRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QKQVIRCCSMETTSCILKELGDEHYAILADESSDISHKEQLVVCLRYVDKLGGVCERF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAVVHVAGTSSLQLKTAIQSLLTSHHLTLTQIHGQGYDGASNMKGEVKGKCWLPNLFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OVSRILINIVGVSCTRHDMLRDVRAQKLKKALNLGEIASGSGLNQEMALARPGDTRWGS
                                                                                                                                                                   RGRDAGTWAPLAVAQGGRGCGWQAGPTGHGSKREGAASAGLGSAPSRPAGERRRQAAT
                                                                                                                                                                                                DGGDRREDGDSRRRGRRHIAATRMRGAAARARGREGEGVLTGVRPATREETTTNGDAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(21843. .22489,22572. .23072,23168. .24293)
/note="Similar to Arabidopsis thaliana DNA chromosome 4,
BAC clone F17A8; putative protein. (AL049482)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIPLPSPPESRRPTLPAASAAAPSRQPPRPASGQRHSISGSGSALRLSGLRI"
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/note="hypothetical protein"
/note="hypothetical protein"
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/db_xref="G1:7363275"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="BAA93018.1"
/db_xref="G1:7363274"
                                                             /protein_id="BAA93016.1"
                                                                                                     /db xref="GI:7363272
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/note="3' LTR"
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LTR CDS

CDS

LTR

CDS

CDS

CDS

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complement(join(40023. 40413.40774. .40971,41292. .41464,
41783. .42027,42111. .42288,42719. .42901,43197. .43301,
44137. .44274,44361. .45353))
/note="ESTS C74776(E51022),C26123(C116681) correspond to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPPVAAQGRRRRSSESVDSAPQNEGFSDDDDSCSVSQESAHNFHGQRGGRTAAQEGRR
AQVVTFGVTEDSRYESK EENEDVSEQYVAVTKREKRGRTCSRCGKRKWESKESCIVCDA
RFCSYCVLRAMGSWPEGRKCITCIGQPIDESKRSKLGKGSRILSRLLSPLEVRQILKA
EKECQANQLRPEQLIINGFPLNPDEMASLLSCQRPPQKLKRGRYWYDKESGLWGKEGE
                                                                                                                                                                                                                                                                                                                                                                                                           IYDRMISSGIPRSMOTFNIMISYYGGGKLEKAYEMFSAAQEIGLPIDEKTYTMMLSF
YGKACLHNEAEIIRQEMQKNNHVPDSHTYLALIRAYTEGKCYSKAEEAIQMMLRSNMT
PSCTHFNHLISAFLKEGQIDEAQRMYNQMEEAGIPADLACCRTWMRMHLDHGYVDDGI
                                                                                          /translation="WAAAIAGAAASTAVSITCSSYSYEDDGAATSWSLSSGTSSSSS
SORORPYRRLLHDEAORLRRERRGOGSGAHTPRWVRRTPDQWARYVEDDRAGHVYGRH
VVAAVRAARATASCSSPSSADMREAMASFVAKLTFREMCFVLHELRGWRQARDFFAWM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LFFETACRLLKPDSFILSAAFHLYEHSGRESEAGDVLDAINMSGASFLRNLKVGSKLE
QIQPKWWSIVKSGPLFPQKAHGVPLKYKQRSPWCCSVEQVVAREGEVDAAQRFGSRDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVSYELPRIDPVDLPAIPTAQPVSGPLVPGRSNGVVAPVVRPVFMPPVHRKQDAHRAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MAGAGAVGGSNWEEMVRRMLPPGTTIPEAPANLDYSIALEYDGP
                                                                                                                                                                     KLQLCYEPSVVAYTILLRLYGQVGKVKLAEVTFLEMLQAGCEPDAVACGTLLCAYARW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50782 GAGAGGAGGAAAAGGCAATGGAGCGTGGCCTCCTCTATCTTGGGATGGGTTTCC 50841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 cttcccgtctacggcttccatgaccccgcgtcctttgtgaagtccattcagaagccacgg 191
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Similar to Arabidopsis thaliana cultivar Landsberg
extra-large G-protein (AF060942)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="BAA93022.1"
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Zea mays 6-phosphogluconate dehydrogenase isoenzyme A gene, partial
                                                                                                                                                                   Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Zea. [ tbases 1 to 2392)
Padegimas, L.S. and Reichert, N.A. Isolation of genes and regulatory sequences implicated in hypersensitive response from Zea mays nematode-resistant line MP307 (pubblished)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MALTRIGIAGLAVMGONLALNIAEKGFPISVYNRTTSKVDETVO
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GGNEWYENTERREKAMEERGLLYLGMGVSGGEEGARNGPSLMPGGSFEAYKYIEDILL
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                                                                                                                                                                                                                                                                                                                                      Submitted (06-DEC-1997) Department of Plant and Soil Sciences, Mississippi State University, Box 9555, Mississippi State, MS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2250 cGGAGGAGGAGGTGCCCGCAATGGCCCGTCCTTGATG 2289
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                                                                                                                                                                                                                                                                                                      Padegimas, L.S. and Reichert, N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Zea mays"
/db_xref="taxon:4577"
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                                       DNA
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/note="6pgdh(A)"
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                                                                                                      GI:3925238
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DYRGAHTYERVDMPVLSTPRLEFTISALTRYEKV"
                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
1 (bases 1 to 1818)
                                                                                                                                                                                                                                                                                                        Redinbaugh, M.G. and Campbell, W.H.
Nitrate regulation of the oxidative pentose phosphate pathway in maize (Zea mays L.) root plastids: induction of 6-phosphogluconate maize (Zea mays L.) root plastids: induction of 6-phosphogluconate plant Sci. 134 (2), 129-140 (1998)
2 (bases I to 1818)
Redinbaugh, M.G. and Bailey-Serres, J.
Characterization of cDNAs encoding cytosolic and a putative plastidic 6-phosphogluconate dehydrogenase
                                                                  Zea mays strain W64A x A182E putative cytosolic 6-phosphogluconate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (28-APR-1998) USDA, ARS/Dept. Plant Path., OARDC/OSU,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="pdh1"
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                                                          08-JUN-2000
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Redinbaugh, M.G., Campbell, W.H. and Balley-Serres, J.
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                                                                                              dehydrogenase (pdh1) mRNA, complete cds.
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RAKVEGNLPVFGFHDPASFVSSIOKPRVVIMLVKAGAPVDQTIATLAAHLDQGDCIVD
GGNEWYENTERREKAMEERGLLYLGMGVSGGEBGARDGPSLMPGGSFEAYKYIEDILL
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401 GGAGAGGAGGAAAGGCGATGGAGGAGGGGGGGCTCCTTTATCTTGGCATGGCGTCTC 460
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                                                         341 GCCGCACCTTGATCAGGGGGACTGTATCGTCGATGGTGGCAACGAGTGGTATGAGAACAC 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (06-DEC-1997) Department of Plant and Soil Sciences, Mississippi State University, Box 9555, Mississippi State, MS
                                                                                                                                                                                                                                                                            26-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolation of genes and regulatory sequences implicated in hypersensitive response from Zea mays line MP307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 319; DB 7; Length 645;
Pred. No. 7e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
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                                                                                                                                                                           461 cGGAGGAGAGGGTGCCCGCAATGGCCCGTCCTTGATG 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tch 77.8%; Score 319; DB al Similarity 87.2%; Pred. No. 7e-56 349; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 645)
Padegimas, L.S. and Reichert, N.A.
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Padegimas, L.S. and Reichert, N.A.
Direct Submission
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/note="6pgdh(A)"
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AF037029.1 GI:3925222
                                                                                                                                                                                                                                                                                 645 bp
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Budicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 9620, Town, C.D., Benito, M., Creasy, T.H., Ronning, C.M., Koo, H., Fujii, C.Y., Utterback, T., Barnstead, M.E., Bowman, C.L., White, O., Nierman, W.C. and Fraser, C.M.
Arabidopsis thaliana 'IGF' BAC 'Filhl2' genomic sequence near marker 'mi74'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (11-MAY 2000) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA, xiin@tigr.org
on Jun 2, 2000 this sequence version replaced gi:7769972.

* NOTE: This is a 'working draft' sequence. It currently
consists of I' contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
as soon as it is available and the accession number will

* be preserved.
                                                                                                                  311 ggagaggagagaaggccatggagagagcgcggcctnctgtatcttggcatgggtgtctc 370
chromosome III clone IGF-F11A12, ***
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contig of 3914 bp in length
gap of unknown length
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41731: contig of 4247 bp in length
41781: gap of unknown length
43856: contig of 2075 bp in length
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46860: contig of 2954 bp in length
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                                                                                                                                                                                                                                                                                 46910: gap of
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Lin,X. and Kaul,S.
Direct Submission
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50874:

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ELGSVESEWINGCELLSFLIETTADIFCIKDDKGDGYLVDKVLDKTGRKGTGKRTVOOA
AELSTAAPTEASLIDARFLSGLKEERVEAAKVFKSGGIGDIVTDGHVDKQKLIDDVRK
ALYAAKICSYAGGMILIRAKSIEKGMUNLKLGELARTIWKGGCITRAIFENDRIRQAYERN
PULANLLVDPEFAREIIDYQSAWRRVVCLAIRSGISFPGMSASLAYFDTYRRERLPAN
LVQAQRDYFGAHTYERVDIEGSYHTEWFKLAKOSKKLDYCISANQDFPNKCNIFCSDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MAOPSTGIGLAGLAVMGONLALNIAEKGFPISVYNRTTSKVDET
VERAKQEGNLPVYGYHDPEAFVHSIQKPRVIIMLVKAGAPVDQTIKTLSAYMEKGDCI
IDGGNEWYENTERREKEVAELGLLYLGLGVSGGEEGARNGPSLMPGGSFEAFKYIEDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLKVAAQVPDSGPCVTYIGKGSGNFVKMIHNGIEYGDMQLIAEAYDVLKSVGKLSNE
                                                                                                                                                                                   Molecular cloning of 6-phosphogluconate dehydrogenase full length cDNA from soybean soybean Published Only in DataBase (1997) In press Location/Qualifiers
                    Katsurada, Tezukayama Gakuin College, Deprt. of Nutrition; 4-2-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 tacaacaggacaactccaaggtggacgagaccgtgcagcgtgccaaggcagaaggaaac 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 cttocogtotacogottocatgacocogogtoctttgtgaagtocattoagaagocacog 191
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                                              Harumidai, Sakai, Osaka 590-11, Japan
(E-mail:LDD00547@niftyserve.or.jp, Tel:+81-722-96-1331,
Fax:+81-722-92-2135)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.1%; Score 230; DB 7; Length 1667; 73.4%; Pred. No. 9.2e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="6-phosphogluconate dehydrogenase"
/protein_id="BAA22812.1"
/db_xref="GI:2529229"
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                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="root nodules"
55. .1590
                                                                                                                                                                                                                                                                                                                           /organism="Glycine max"
/db_xref="taxon:3847"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /EC_number="1.1.1.44"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                               2 (bases 1 to 1667)
Katsurada, A.
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55. .1590
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euphyllophytes: Spermatophyta; Magnollophyta; eudicotyledons;
Rosidae: Fabales; Fabaceae; Papillonoideae; Glycine.
1 (bases 1 to 1667)
Katsurada, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 13068 GCTGTGATGGGTCAGAACCTAGCTCTCAACATTGCAGAAAGGCTTCCCAATCTCTGTT 13127
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63.9%; Score 262; DB 56; Length 96240;
Best Local Similarity 78.4%; Pred. No. 1e-44;
Matches 313; Conservative 0; Mismatches 86; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   846 others
                                                                                                                                                                                                                                                                          4 83051: contig of 4208 bp.in length
2 83101: gap of unknown length
2 96240: contig of 13139 bp in length
Location/Qualifiers
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bp in length
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    96240
    /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"

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contig of 5839 b: gap of unknown 1: contig of 4470 b: gap of unknown 1: contig of 5574 b: gap of unknown 1: contig of 6612 b): gap of unknown 1: contig of 6522 b): gap of unknown 1: gap of unk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IGF-F11A12"
18610 c 20275 g 28013 t
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                       56763:
61235:
61285:
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56713:
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VERAKQEGNLPLYGFHDPEAFVNSIEKPRVIIMLVKAGAPVEQTTKTLSAYLEKGDCI
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LLKVAAQVPDSGPCYTYIGNGSGGNEVKMIHMGIEYGDMQLIAEAZVDVLKSVGKKTIND
ELQSAFTEMNKGELLSFLIEITADIFGIKDDKGDGYLVDKVLDKTGMKGTGKWTVQQA
ABLSVPAPTIEASLDARELSGLMDERVEAAKVFKSGGFGILLDQQVVRKOLIDDVRK
ALVAAKICSYAQGMNLIRKSABKGWDLALGELARIWKGGIIITAJFLDDYRK
PNLANLLVDPEPRAEIIERQTAMRRVYSLSVNSGISLGGMSSLAFFDSYRRERLPAN
LVQAQRDYFGAHTYERVDIEGSYHTEWFKLAKQSRI"
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                                                                                                                                                             Medicago sativa subsp. sativa
Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
Magnoliophyta; eudicotyledons, core eudicots, Rosidae, eurosids I;
Fabales, Fabaceae, Papilionoideae, Medicago.
                                                                                                                                                                                                                                                                                    Stress responses in alfalfa (Medicago sativa L.) XIX.
Transcriptional activation of oxidative pentose phosphate pathway
genes at the onset of the isoflavonoid phytoalexin response
Plant Mol. Biol. 28 (5), 885-900 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (06-DEC-1994) Theo Fahrendorf, Samuel Roberts Noble Foundation, Plant Biology Division, 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
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                30-JAN-1997
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/protein_id="AAB41553.1"
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/cultivar="Apollo"
                                                                                                                                                                                                                                                         1 (bases 1 to 1618)
Fahrendorf,T., Ni,W., Shorrosh,B.S. and Dixon,R.A.
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284 c 405 g 46
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/clone="019"
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Fahrendorf, T.
                    1618 bp
                                                                                                      U18239.1 GI:603220
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IISKCAAQVUGEPCTTYLGSIGSGNYYKWYHNIEYGDMQLIAEVYDVLKHVAGLTNDE
LSATFTDWNQGELQSFLIEITAVIFSRKDDLTSSGHVVDKILDKTGMKGTGRWTVQEA
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RDFFGAHTYERVDKESYFHCLWDDTHKEIATSPAHGGRTLIGSLPNLFRPLCMGCLNW
SSTVVSVAYCGMKYXIGSLSFT
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TVARAKEEGNLPLRGFKDPKSFVDSLSKPRKIVLLVQAGAAVDATIATLSELLEEGDI
LVDGGNEWFPNSQRRAKELEPKKIMFVGMGVSGGEEGARNGFSLMPGGPREAYDALSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moulin, P., Crepineau, F., Kloareg, B. and Boyen, C.
Isolation and characterization of six cDNAs involved in carbohyrate
biosynthesis in Laminaria digitata (Phaeophyta) - Utilization of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-NOV-1998) Boyen C., Laboratoire de Biologie
Moleculaire et Cellulaire des Algues, Station Biologique - CNRS UPR
9042, BP 74, 29682 Roscoff cedex, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Crepineau, F., Roscoe, T., Kaas, R., Kloareg, B. and Boyen, C. Alternation of generations in laminaria digitata: a comparison of the gametophyte and sporophyte physiology by an EST strategy
                                                                                                          Gaps
                              305 gaacacggaggaggaggagagaggccatggaggagcgcctnctgtatcttggcatggg 364
245 gctcgcagctcacttggagcagggcgactgcatcatcgatggggggaacgagtggtacga 304
                                                                                                                                                                                                                                                                                                                                     17-NOV-1999
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Laminaria digitata mRNA 6-phosphogluconate dehydrogenase.
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/protein_id="CAB61332.1"
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67.2%; Pred. No. 1.1e-30;
tive 0; Mismatches 134;
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/db_xref="taxon:80365"
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Laminaria digitata
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FEATURES COMMENT

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Arabidopsis thallana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shina, P., Khan, S., Brocks, S., Buehler, E., Chao, Q., Dunn, P., Kim, C., Walker, M., Altafi, H., Araujo, R., Conn, L., Conway, A. B., Gonzalez, A., Hansen, N.F., Huizer, L., Kremenetskiala, I., Lenz, C., Li, J., Liu, S., Luros, S., Rowley, D., Schwartz, J., Toriumi, M., Vysotskala, V., Yu, G., Davis, R.W., Federspiel, N.A., Theologis, A. and Ecker, J. R., Genomic sequence for Arabidopsis thaliana BAC F22C12 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chao, Q., Brooks, S., Buehler, E., Johnson-Hopson, C., Khan, S., Kim, C., Shinn, P., Altafi, H., Bei, B., Chin, C., Chiou, J., Choi, E., Conn, L., Conzalez, A., Hansen, N., Howing, B., Koo, T., Iam, B., Lee, J., Lenz, C., Li, J., Liu, J., Liu, J., Liu, S., Wukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Traveri, A., Toriumi, M., Vaysberg, M., Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (09-JUN-1999) Arabidopsis thaliana Genome Center, obstruent of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA (bases I to 111222)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-JUL-1999) Arabidopsis thaliana Genome Center, pepartment of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
                                              100 CTATGGCTTGGCGTCATGGGACAGAACTTCGCGCTCAACATGGCGAGCCACGGCTTCTC 159
                                                                                                                                                 160 ceretrereaceaceerceerceacaagerreaceraceraceercecececeaaga 219
                                                                                                                                                                                                                                      220 GGAGGGCAACCTCCCCTTGAGGGCTTCAAGGACCCCAAGAGCTTCGTGGACTCCTCTC 279
                                                                                                  62 catototgtgtacaacaggacaacotoccaaggtggacgagaccgtgcagcgtgccaaggc 121
                                                                                                                                                                                                     122 agaaggaaaccttcccgtctacggcttccatgaccccgcgtcctttgtgaagtccattca 181
                                                                                                                                                                                                                                                                                                                                         340 CACGCTTTCCGAGCTCTTGGAGGAAGGAGACATCCTCGTCGACGGTGGCAACGAGGTGGTT 399
                                                                                                                                                                                                                                                                                                                   gaagccacgggtggtgatcatgctcgtcaaggccggcggccagttgaccagaccatcgc 241
                                                                                                                                                                                                                                                                                                                                                                                                                 302 cgagaacacggaggaggaggaggaaggccatggaggagcgcgctnctgtatcttggcat 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        400 CCCCAACTCGCAGCGCCGCGCGAAGGAGCTGGAGCCGAAGAAGATCATGTTCGTCGGCAT 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC007764 111222 bp DNA PLN 28-JUN-2000 Genomic sequence for Arabidopsis thaliana BAC F22C12 from
     ccacgegtccgcggtcatggggcagaaccttgccctcaacattgcagaaagggttccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome I, complete sequence.
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Direct Submission Submitted (12-JAN-2000) Arabidopsis thallana Genome Center,

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ODSYMEFEADEFERVIRIHPTOSFTELKKWYTERIGYELOTSDVRIAKNEAIKRVFGD
CDOSFEDLPKLMAAIHSSNGLLVDWRYDLFPNPKFASFRGVFWAFSQSIBGFHHCRPL
I VDTKNLLNCKYQWKLMIAASAVDAADNFFLLARAFTFELSTDSWRWFLSGIRRRYTQR
KGLCLISSPDPDLLAVINESGSQWQEWARYNRFCLRHLLSQFSGIFRDYYLEDLVKRA
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FNVSHLDNHYLTGYYLRLFDELRHSFDEFFOFSGRRKCGNYTEPYTEKLAESRKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAF24584.1"
/db_xref="G1:6692119"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYWNGRIEYGSNGVYDRSTPRMIKVKRKTELSILLDQLYLLTGLDVNDRRSKVRIFGR
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VVNLTQDNNISLKDLNQDSSSGVSKPCLSSLWLDDHDLRVGLCFKDIDGLKKAVDWCS
FRGQRSCVMREAEKDEYMFECARWKCKWTLEAARMEKHGLIEIIKYTCPHTCSCAIEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTYDVMPLDNNAFQVTAPQENDEWTVQLSDCSCTGGERGSCKFPCLHALAVCKLLKING
ELEVYDDCYTLERLXRYTYATESPPPEREJSAWPERSGVFRLEPPVIPLEPPPPPEPPPINAV
LITYCSAATLGSPLKKYENQAKTDRKLKPTVPFFFFFT ISFELLISLIKLLPFLKNPS
LISTPSWTVVLMAMETLREHVMLLCYTNACIKYGSDGVYYEGSSPKKIRVRRYTERPT
LINGLYP IFGLARQRST SIFGRYPALSPDLTKHPSTLHPPVINSTEFFMLEVPSRYPS
ILNGLYP IFGRAVQRST SIFGRYPALSPDLTKHPSTLHPPVINSTEFFMLEVPSRYPS
IKKUPETYLEVKSTSEGYIDPAGACSSPLENGSSLKROFTGSRYPS
IKKUPETYLEVKSTSEGYIDPAGACSSPLENGSSLKROFTGSRYPS
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IKKUPETYLEVKSTSEGYIDPAGAGGGSTHGYTGSRYPS
IKKUPETYLEVKSTSGYUDBAGAGGGGTHGYVNANGSSCHOVOTLTANNAESN
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HYVPQDDYLKNLVYBAGSTSEKEEFDSYMNEIEKKNSBARKWLDOFPOYOWAOAHDSG
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YTKPVMDQLEKLMTDSIPHVVMPLEKGLFQVTEPLQEDEMIVQLSEWSCTGGEFQLKK
                                                                                                                   Cheuk R., Shinn, P., Brooks, S., Buehler, E., Chao, O.,
Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C.,
Chiou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N.,
Howing, B., Koo, T., Lan, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J.,
Schwartz, J., Southwick, A., Thaveri, A., Torium, P., Sakano, H.,
Yu, G., Davis, Federspiel, N., Theologis, A. and Ecker, J.
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EITKCNTPHTCCPIGPDNYDVEFAADEIECLIRVQPTLTIEELRNWWFENFGDMLATS
EMQAAKQEVIKKVFGDWDQSFRVLPNLMAAFHSSNGLVVDWQYKLFPNPEFASFRSVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement join (979. 3122,3735. 5930,6862. 6892,6983. 7068,7655. 9286,9346. 10019,10228. 10279,10673. 100673. 101047. 13429,13585. 13835,14366. 14645))
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RLVNVPVFCCWNGCIKDGINGIYYEGSNYRMTIVKGKTKFNELLDHLYQVTGLDRKRS
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OWQEPWAYHRFSLNHFYSQFSRVFPSFCLGARIRRAGSTSQKDEFVSYMNDIKEKNPE
ARKWLDQFPQNRWALAHDNGRRYGIMEINTKALFAVCNAFEQAGHVVTGSVLLLFDEL
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Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA 5 (bases 1 to 111222)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (28-JUN-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA On Jul 16, 1999 this sequence version replaced 91:5030434. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"/db_xref="taxon:3702"
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/note="similar to vacuolar ATPase gi|3600058"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MESAALSRIGLACLAVMGONLALNIAEKGFPISVYNRTTSKVDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MASKRIIKELKDLQKDPPTSCSAVAEDMFHWQATIMGPSDSPYSGGVELVTIHPPDYPFKPKYAFRTKVFHPWNNSUSICLDILKEQWSPALTISKVLLSIGLELDPHPDDPLVPETHAHWKTDRAKYESTARSHTQKYAMG" complement(join(18031, 18617, 18685, 119861)) /note="putative receptor kinase emb|CAA23040.1"
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DFPSDFTNLKSLTHYLQHNHLSGPLLAIFSELKNLKYLDLGNNGFNGSIFFSLSGLS
SLQVLNLANNSFSGEIPNLHLPFLSQINLSNNKLIGTIPKSLQRFGSSAFSGNNLTFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EAEKKITROEYEKKEKOVDVRKITDYSMQLNASTIKVLQAQDDIVNAMKEEAAKQLLK
SOROFFNHHHHYVKHLLKDLYQCLLERLKEPAVLLRCREEDLDIVESMLDDASEBYC
VRAKVHAPETIVDKDITELPPARSDDDPHALSCAGGVVLASRGKIYOENTLDARLEVA
FRNKLPEFCSKGSFLEMCVDPKVALRQGWCSLMSDSNFITKEKLRDAKSMNPTGRRCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WTSRDDNTEEGGKIIFFGGRNHLFDLDDLLSSSAEVLGKGAFGTTYKVTMEDMSTVVV
KRLKEVVVGRREFEQQMEIIGMIRHENVAELKAYYSKDDKLAVYSYYNHGSLFEILH
GNRGRYHRVPLDWDARLRIATGAARGLAKIHEGKFIHGNIKSSNIFLDSQCYGCIGDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPTGGENMDLASWIRSVVAKEWTGEVFDMEILSQSGGFEEEMVEMLQIGLACVALKQQ
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                             KGECIVQLSDCSCTCGDFQRYKFPCLHALAVCKKLKFNPLQYVDDCYTLERLKRTYAT
IFSHVPEMSAWPEASGVPRLLPPVIPPSPPPSPPTYVSVREKVMVLCHLNGYIKYGAD
                                                                                                 GVYYEGSIIKKITIIMRKTALSRLLDRLYQLFGLDKQKSEFKIFGKYPVDVSPDLFTYV
HFPVLNDSSLETMLEVPRNHPSVNNLEFYLEAQPTSDAVVPVTCSSPLESPDSSSKR
QRITQQEIVDNNSGSAGILVKVVNSGALKPCLLPRLMIDDDHDMHLGLCFKDRDELKK
                                                                                                                                                                                                          AVDUMO TRRRRNCIVRETEKEMYTFECVRWKCKWSLRAARMEEHGLVEITKYTGPHTC
SHEYDNDESESFAADEIERVYRIQPILSIAELKKWKERGYSELGYSKRUGKKLEVIK
RVFGDEDGSERVWRKLISAEHSSNGLIVDWOYDLFPRPDFASFRGYFRSFSOSIEGFO
HCRPLIVVDTKSLNGKYQLKLMIASGVDAANKFFPLAFAVTKEVSTDSWRWFFTKIRE
                                                                                                                                                                                                                                                                                                                                                                                                                                ALFÄVCRGFPYCTVAMTGGVMLMFDELRSSFDKSLSSIYSSLNRGVYTTEPFMDKLEE
FMTDSIPYVITQLERDSFRVSESSEKEEMIVQLNVSTCTCRKFQSYKFPCLHALAVFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKORKTPFGLSQLAFLLILSAACVLCVSGLSFIMITCFGKTRISGKLRKRDSSSPPGN
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                                                                                                                                                                                                                                                                                                                                                                                          LVEQAGSTNQKEEFDSYMNDIKEKNPEAWKWLDQIPRHKWALAHDSGLRYGIIEIDRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLKINPLQYVDECYTVEQYCKTYAATFSPVPDVAAWPEDCRVPTLFPPSQQLSPNT"
complement(join(15674. .15817,15904. .16008,16075. .16196,
17033. .17102))
RSKFDKSFSCSRSSLNCGDVYTEPVMDKLEEFRTTFVTYSYIVTPLDNNAFQVATALD
                                                                                                                                                                                                                                                                                                                                                        KVTQRKDLCLISSPLRDIVAVVNEPGSLWQEPWAHHKFCLNHLRSQFLGVFRDYNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to ublquitin-conjugating enzyme E2-17 Kd sp|P35135; similar TO ESTs gb|R84048, gb|R45251, gb|A1100555, gb|R71055, gb|T21697, emb|229145, gb|T20867".
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/product="F22C12.2"
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/db_xref="GI:6692095"
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CDS

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ELAEIFTEWNSGELESFLVEITSDIFRVKDEFGDGELVDKILDKTGMKGTGKWTVQQA
AELSVAAPTTAASLDCKTLSGIKDREKRENAKVLFERGALKEETGSASSGIDKKRLVDDV
RQALYASKICSYAQGMNLLRAKSLEKSWNLNFGELARIWKGGCIIRAVFLDRIKKAYD
RNPDLASLVVDPEFREEMVORQAARRRVVGIANSAGISTPGWCASLAYFDTYRRARLP
ANLVQAQRDLFGGAHTYERTDRPGAYHTEWTKLARKNH"
COMPLEMENT (101n(25806. 26028, 26204. 26373, 26722. 28161,
28379. 28489, 28868. 29224))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; coreeudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
ILEKVAAQVEDGPCVTYIGEGGSGNFVKMVHNGIEYGDMQLĮSEAYDVEKNVGGLSNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (sites)
Sato,S., Kotani,H., Nakamura,Y., Kaneko,T., Asamizu,E., Fukami,M.,
Miyajima,N. and Tabata,S.
Structural analysis of Arabidopsis thaliana chromosome 5. I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24103 ATCTCTCATCATCCTCGTCAAAGCTGGAGCTCCCGTTGACCAAACAATCGACGCCTTCTC 24162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24163 CGAATACATGGAGCCAGGAGATTGCATCGACGGTGGAAACGAATGGTATCAGAACAC 24222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24223 AGAGCGACGGATCTCCGAAGCTGAGCAAAAGGATTGCTCTATTTAGGTATGGGAGTCTC 24282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone: MBK23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23983 CTACAATCGAACCACTTCCAAAGTCGACGAAACCCTAGATCGAGCCGCCGTCGAAGGAAA 24042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 23923 CGCCGTGATGGGCCAAAACCTCGCCTTAAACATCGCCGAGAAAGGTTTCCCAATCTCAGT 23982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24043 CCTCCCAGTCTCCGGCCAATACTCTCCCCGGGATTCGTCCTCTCGATCCAACGGCCTAG 24102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 ggagaggaggagaaggccatggaggaggggggcctnctgtatcttggcatgggtgtctc 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 gtacaacaggacaacctccaaggtggacgagaccgtgcagcgtgccaaggcagaaggaaa 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 octtocogtotacggottccatgaccccgcgtcctttgtgaagtccattcagaagccacg 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191 ggtggtgatcatgctcatcaaggccggcgccagttgaccagaccatcgcgacgctcgc 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                251 agctcacttggagcagggcgactgcatcatcgatgggggaacgagtggtacgagaacac 310
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                                                                                                                                                                                                                                                                                                                                                                                                             .;
                                                                                                                                                                                                                                                                                                                                                    Score 183; DB 7; Length 111222;
Pred. No. 1.5e-28;
0; Mismatches 136; Indels 0;
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                                                                                                                                                                                                                                                                      /evidence=not_experimental
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DNA Res. 4 (3), 215-230 (1997)
97471969
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Nakamura, Y.
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                                                                                                                                                                                                                                                                                                                                                                   Query Match
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JOURNAL
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KEYWORDS
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2 (bases 1 to 38587)
Myler, P.J., Sisk, E., Cawthra, J., Handley, F., Vogt, C., Robertson, L., McDonagh, P., Stuart, K. and Ivens, A.
Direct Submission
Submitted (28-APR-2000) Seattle Biomedical Research Institution, 4 Nickerson Street, Seattle, WA 98109-1651, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myler,P.J., Sisk,E., Cawthra,J., Handley,F., Vogt,C., Robertson,L.,
McDonagh,P. and Stuart,K.
                                                                                                                                                                                                                                                                                                                                                                                                                           61964 CTACAATCGAACCACTTCCAAAGTCGACGAACCTTAGATCGTGCCTCCAACGAAGGAAA 61905
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61844 ATCGTTATCATCCTTGTCAAAGCCGGTGCTCCCGTTGACCAAACCATCTCTGTCTCTC 61785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yasukazu Nakamura, Kazusa DNA Research Institute, Laboratory of
Gene Structure 2; 1532-3, Yana, Kisarazu, Chiba 292, Japan
(E-mail:ynakamu@kazusa.or.jp, Tel:+81-438-52-3935,
Fax:+81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 gtacaacaggacaactccaaggtggacgagaccgtgcagcgtgccaaggcagaaggaaa 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agctcacttggagcagggcgactgcatcatcgatggggggaacgagtggtacgagaacac 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 cettecegtetacggettecatgacecegegteetttgtgaagteeatteagaageeacg 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 egeggicatgggggaagcttgcctcaacattgcagagaaagggttccccatctctgt 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 ggtggtgatcatgctcgtcaaggccggcgccagttgaccagaccatcgcgacgctcgc
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                                                                                                                                                                                                                                                                                                                              Length 79837;
                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 141; Indels
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                                                                                                                     /organism="Arabidopsis thaliana"
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/chromosome="5"
/clone="MBK23"
                                                                                                                                                                                                                                                                                                                            Score 175; DB 7;
Pred. No. 6.9e-27;
                                                                                                                                                                                                                        /clone_lib="Mitsui P1"
14362 c 13908 g 25590 t
                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC011913.2 GI:7658329
                                                                                                                                                                                                                                                                                                                      Best Local Similarity 64.8%;
Matches 259; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leishmania.
1 (bases 1 to 38587)
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/translation="MQLDDWDTYRETLLYARELAVLLPSSWSELSSEQSATKSSSSLS
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ESAAPCRRANAGAEVGYSFAVPSSPSGNAAAASKSNSVDVQAVFTELQQLFPSYLVP
VKALMTYVPBAEDQOVRARVLDALRSPOHRAMITHEHPAHCASHSTSADBRELTHVL
EHGYVQLRLNPAAGDDVAAAPNPQSPNTRAAGHEVQPYEWYRVARVLPTTATELLFSG
ELQEQATLLLPPGRAAAPNQSPNTRAAGHEVQPYEWYRVARVLPTTATELLFSG
CVKYDATPPPSILCASVYVRFRLEERRVVPDMAGAREESILRELETLTABRAASSLAPV
SRQRRRKKKLQRQLATLRNPTPYFDERVLAQHILFDLLPLRDGVHQSALLGSLPOPAVQ
3 (bases 1 to 38587)
Myler,P.J., Sisk,E., Cawthra,J., Handley,F., Vogt,C., Robertson,L.,
McDonagh,P., Ivens,A., Nguyen,D., Munden,H. and Stuart,K.
Direct Submission
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LRSDPQEGTTISRSLPRLPRLVRERLFTMQDIIAEVLLLYPDKVEVLADRSPSISSLS
LSSSPHTSEADERALRELRTVRGRRDFLVPFRFVGEWQAKLTEKYTKQQTKDAVKSMR
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                                                                                      Submitted (14-MAY-2000) Seattle Biomedical Research Institution, Mickerson Street, Seattle, MA 98109-1651, USA
On Apr 28, 2000 this sequence version replaced gi:6056180.
NOTE: This Sequence is still preliminary and may contain some errors, such as substitutions and frameshifts. Please regard all should be available within a few weeks.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="L4407.1; predicted using Glimmer, Testcode, and CodonUsage; CodonUsage marginal; Glimmer predicts start
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="L4407.2; predicted using Glimmer, Testcode and CodonUsage; ORF starts at 6990, Testcode and CodonUsage predict 2nd ATG used as start codon"
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                                                                                                                                                                                                                                                                                    1. .38587
/organism="Leishmania major"
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                                                                                                                                                                                                                                                                                                                            /strain="Friedlin"
/db_xref="taxon:5664"
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/product="L354.4"
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predict 2nd ATG
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/gene="L354.3"
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/gene="L354.4"
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/gene="L354.4"
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IETRQEYAGDIANQSDLLADVLVFLEWWRLKARGASTADFVAKLQLKEDRLEHVRGLI
TYLRVQISDYAFVDDLEDEATLSAVMQSIKSNASIFTFFEAVALARRLFFVRDAGSIN
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TALMVTDVDTALVYLTSÓRGMGPFTHLVLPNLTRMNPLVSYFLWGLRERVYRÓSAILD
TAAPPLHVIVSVSGAMTERMQOFFAKQTVATPTTFPMQPLVEFSYDEANALAĞMDVLD
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VONKSEGFMASSASEWASKMDVEERRQLPGTKYPGCYIALYPPAADVVLPTTEAPQPT
VYEVEDALLQCSRAQLPIQRANQEMVCPVEAESIEQVQHSLSEKCLIANLSDFSLTFT
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WNHAIRYLQVLRTAKKPLSRHKFNFMLKEEDRHFDLEELRAEVQRELQNLVTEIEVAE
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SHQPESDPAVVYAKLKQLIASQDAYFHGGNAAAADVVSDEVLGLKEVASHQVVLLQRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /traislation="MALDFDVDDAPTFPELVRDARLDVWKGRTWTACWVELADOHTVF
RDIAKEGRRAGELIGAVLAAVOGICOALQRVELINEBVRAPEPACTALFSSPAOGAVG
RTPGRWLEERQTLAQVSRAVYSLYCSTPIPTCAQWVRSLQVVFPQPLNAVSTAANGA
SASRRDDDAGAVPATPEASSTLCRYLTKLRQSYDDVAQELPDSRVDGKDGSFAEEKLKE
LVVCCMTVGRRVARPTMLPPLDAILVREMVKVLQDFVGNSTLEW"
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PLSLPKGLELLAQVALERNKPLLFISDIRSGSVALPNFEDHVAENMRAQECWTNILHG
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YLRPIRPELKTAKTGELRKEVLRVAHSITAHLGITFEDAIRRRDALMINHAKKSQNKA
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                           VCLPLSLSLFRANASAVDITVRYDHQQQCSFGYNNTGAFRYEASPGDVWQTGCVTDVP
FRVDKHLKAPVYVYYGLENFYQNHRRFSNSKSDAQLAGQRVSAAAIASATSPLTYPGE
                                                                                        LRHTADQGINLLGTELHYSDFYYYPAGLIPWSMFNDTFTLYRITHHEAAAVTAPSLRL
ICNGSAFSRFTNEPLDGAGRCHKKGIAWTSDVEFKYKKPHFPPPSSFRPWFSAPKWAY
                                                                                                                                                     EAADGDVNPNPPSRMPSDNAYFNEGWYADEPCHRIPVTTDEDLMVWARVASLPKFRKL
YRVIDEDLVPGTYLMRIQEHFNAASYGGTKSFSLATLSWLGGRNTFMAMMYFTIGAVS
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/translation="MGSGYLKRKRORQELLNDFYSALSLSSFDTTSGQFSKLVTRTVY
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IVYAGAAPGTHLAFLDEMFSCRHTWELIDPGQFDRAVLEPRANFRLRNEFFTNATAYG
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/translation-"MPVAPAAVVQRPSIWALFKQQRLPAWQPILTPQHSALCLIAVAV
                                                                                                                                                                                                                                                                                         /gene="L354.5"
/note="L4407.4; predicted using Glimmer, Testcode and
CodonUsage; scores for Testcode and CodonUsage are rather
low in the middle of the ORF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        //octe-"Blastp similarity to hypothetical proteins from several organisms"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="L354.6"
/note="L4407.5; predicted using Glimmer, Testcode and
CodonUsage"
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/db_xref="G1:7801408"
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/db_xref="GI:7801406"
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/gene="L354.6"
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ERDRYLNFLNAVDGIJSTLMPMAPGIFKDTFLEVLPLLADSFOWVVNATSHSRVQAS
IAPDASDGAGTLSRLTNEAAQSVTNADGEASNAVAVSVPPVAHNADAAAVFGEDLEHI
RFCVRVVAAYIHKYMDSLTLAMASGATSDSVRRDLTRLLQPTIVMLYSPIFPKDVLNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VGLLVASILTVVRTCDAWLLAFVCAALRDDVAQCTGGAARLLGAETSTDSVPELQESGT
AGALSLAHLFAQADVALRIVSAANPREAAQADGGSGAKALHDVFSHLTPNGCFALLKG
ILAHTSAPIRGDWASLGLLRPLPWTSLSATGAENAPSNVSHGTVVAYDIILQAAQQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IAGCSCOGETAEYVMRRGIIEPLARATTEKGYVGYSSNYSEAVNISHITAHFVAPLYK
ODPACLRAILTAVAASLOGASYGOSSLPGTLAAPEYERVEOGYVETVARARGYGYDIT
PYLAPGSTTLRVLEEGSRSLNYEVRNTALCLCVLGARKIQAVQPWQLRRVEEYIIFNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APSSALAAKVVRTTDAALOELLOLSLTPEQOLHAİSKMTGAİREIPKSRLAATLTEPT
GELHSWSRTLALEAVVPLLLDCRVRYLHRALMTLLRTLLPAPDAAAEATVREMYVARI
LHSAKSWEADTATAMRPVAALGARSDTSEAAAAVYFPSSSEDRGTTIPAARSIYDCSA
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HQASFTTHGVHCLAPKQVAGVVDGVDASDVDVSRKFHDGDLWASSFASKTDTPATWAA
ATSITANHVPTTAQSSALTFPMNAASIDDDKDDEVEVWGELYFRWNGPIIDDDE"
                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAR70126.1"
/db_xref="G1:7801409"
/translation="MAEQSANATLTRRRQRRPDLQSTFDVPEDVRQPLEQVARALEVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNVVQEPETRFMAIQTVDSVVRHVSSVLTIAVKALAQSAKNEGAAALTKLASSQCSLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FIAALQRHYGYPNAAADAVSAFSRTLLTGASNHKIGNVAGDVFAHLARGIAKAPPGSA
                                                                             /wore="14407.7; predicted using Glimmer, Testcode and Codombage; Glimmer predicts 2nd ATG at 22877 is used as start codon."
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                                                                                                                                                                                                                                                                                   /note="Blastp similarity to hypothetical proteins from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 gtacaacaggacaacctccaaggtggacgagac---cgtgcagcgtgccaaggcagaagg 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30318 CTTCAACCGCACCTACGCGAAGACGACGTCGTTTCTCAAGGAGCATGAGAGGAGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 aaaccttcccgtctacggcttccatgaccccgcgtcctttgtgaagtccattcagaagcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30378 TGCCGCCAACCTGAATGGATACGAGACCATGAAGGAGTTCGCTGCGTCCCTCAAGAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 acgggtggtgatcatgctcgtcaaggccggcgcgccagttgaccagaccatcgcgacgct
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/gene="L354.8"
                                                                    19922, .26827
/gene="L354.8"
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AC073566.1 GI:8698748
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Best Local Similarity 57.1%;
Matches 228; Conservative
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Myler, P.J., Sisk, E., Cawthra, J., Handley, F., Vogt, C., Robertson, L., McDonagh, P., Ivens, A., Nguyen, D., Munden, H. and Stuart, K. Direct Submission
                                                                                                                                                Submitted (24-JUN-2000) Seattle Biomedical Research Institution, 4 Nickerson Street, Seattle, WA 98109-1651, USA.
* NOTE: This is a "working draft" sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7469 TITGCCGCCAACCTGAATGGATACGAGACCATGAAGGAGTTCGCTGCGTCCCTCAAGAAG 7410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 ggaaaccttcccgtctacggcttccatgaccccgcgtcctttgtgaagtccattcagaag 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 gigiacaacaggacaacticcaaggiggacgag---accgigcagcgigccaaggeagaa 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.9%; Score 110.4; DB 57; Length 42000;
                                                 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                      1990: contig of 1990 bp in length 2023: gap of unknown length 3694: contig of 1641 bp in length 3697: gap of unknown length 6805: contig of 3108 bp in length 10632: contig of 3794 bp in length 1064: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1.3e-13;
0; Mismatches 172; Indels
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of 5771 bp in length
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gap of unknown length
contig of 9050 bp in length.
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of 3687
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contig of 3597
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/chromosome="35"
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11999 c 118
                                                                                 (bases 1 to 42000)
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              Leishmania major
                                     Leishmania major
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                                                                   Leishmania.
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Matches
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Direct Submission
Submitted (15-NOV-1996) to the DDBJ/EMBL/GenBank databases. Sachiyo
Yoshioka, Tsukita Cell Axis Project ERATO JST, Kyoto Research Park;
17 Chudouji Minamimachi, Shimokyo-ku, Kyoto, Kyoto 600, Japan
(E-mail:syoshi@cell.tsukita.jst.go.jp, Tel:+81-75-315-7913,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /traislation-*PTHNOTFINHTTKRIMSQKEVADFGLIGLAVWGONLILNGADK
GFTVCCVRTTSRVDBFLANRAKGKSIVGAHSLEEPYSKLKKPRVCILLVKAGKPVDY
LIEGLAPLLEKGDIIVDGGNSHYDPTRREEELSKKGILFVSGSGSVGGGEBGARXGPSL
MPGGNPAAWPRIKPITFOTLAAKAGNNEPCCDWVGEGGAGHYVKMVHNGIEYGDMGLIC
ETYDIMKRGLGMSCDESTDVFEKWNTGKLDSFLIEITRDVLRYKADDGKPLVEKILDA
RQGNGTGWNTADNALEMGTPYSLITEAYFARCLISSLKSERYRASKKLTGPWTKFTGDK
KQLIDDLEDALYASIISYAGGFMLAREAAKEYGWKLNNAGIALMHGGCIIRSVFLK
DITEAFREDPNLESILEHPFFNGVEKAQAGRRRVVAQAAMGIPVPATSTGLISFVDG
YRSAVLPANLLQAQRDYFGAHTFRVLPEAADKSLHINWTGHGGNISATTYDA
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Yoshioka,S., Kato,K., Nakai,K., Okayama,H. and Nojima,H.
Identification of open reading frames in Schizosaccharomyces pombe
                                               7289 GACCACGACAAGCGCGCGCGCTCAGTTGGAGAGCCAGGGTCTCCGCTTCCTCGGCATGGGC 7230
306 aacacggaggaggaggaggagaggccatggaggagcgcctnctgtatcttggcatgggt 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 cGGTTTGGCCGTCATGGGTCAAAACTTGATTCTCAACGGTGCCGACAAGGCCTTTACCGT 145
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                                                                                                                                                                                                                                                                     13-MAR-1998
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                                                                                                                                                                                                                                                                     D89161 1683 bp mRNA PLN 13-MAR-1999
Schizosaccharomyces pombe mRNA, partial cds, clone: SY 0651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to Saccharomyces cerevisiae
6-phosphogluconate dehydrogenase(decarboxylating),
SWISS-PROT Accession Number P38720"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 9
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                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces pombe (strain:PR745) cDNA to mRNA, clone_lib:library of H. Nojima clone:SY 0651. Schizosaccharomyces pombe
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                                                                                         /clone_lib="library of H. Nojima"
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/db_xref="G1:1749530"
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QQ		199
QY	agtccattcagaa	184
QD	_	259
Qy	categegae	244
qq	260 GCCTCGTGTTTGTTTTTGCTTGTTAAGGCTGGTAAGCCTGTTGATTACCTTATTGAGGG 319	319
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QY	305 gaacacggagagagagagagagagccatggaggagcgcgccinctgtatcttggcatggg 3	364
qa	380 TGATACCAGCGTTGCGAGGAGTTGGCCAAGAGGGCATTCTTTTGTTGGTTCCGG 439	139
QY	365 tgtctctggaaggaaaggaggtgcccgcaacggcccgtccttgatg 410	
qq	440 TGTTTCTGGTGGTGAGGGTGCTCGTTACGGTCCCTCTTTGATG 485	

Search completed: November 4, 2000, 13:32:00 Job time: 16969 sec

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November 4, 2000, 13:40:13 ; Search time 4075.18 Seconds (without alignments) 321.525 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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58: em_htg5:* 59: em_htg5:* 61: em_htg6:** 62: em_htg6:** 63: gb_htg18:* 64: gb_htg18:* 65: gb_htg18:* 66: em_htg1:** 67: em_htg1:** 70: em_htg1:** 71: em_htg1:** 72: em_htg1:** 73: em_htg1:** 74: em_htg1:** 75: em_htg1:** 77: em_htg1:** 77: em_htg1:** 77: em_htg1:** 77: em_htg1:** 77: em_htg2:** 80: em_htg2:** 81: em_htg2:** 82: gb_pt7:** 84: gb_pt7:** 84: gb_pt7:** 85: gb_htg2:** 86: gb_htg2:** 86: gb_htg2:** 87: em_htg2:** 88: gb_htg2:** 88: gb_htg2:** 89: gb_btg2:** 89: gb_htg2:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

em_pat:*
em_ph:*
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		Description		ACCOUSED Spinacia	ALTONOM ALADIACES	ALCOURT ATTRIBUTED	P1377 Guerra	Pool 2 Symechocyst	DAUGIST SYNECHOCYST	AEUU1224 Treponema	AL3652/0 Homo sapi	AL353604 Homo sapi	AE002356 Chlamydia	AC023104 Homo sani	AC019951 Drosophil	
		B ID	45 SOJ00265	7 AF120494	8 ATF22K18	8 ATCHRIV61	55 SYCCYSEPGT	2 090912	L AE001224	35 AT 365270	54 AL353604	7. AEOO3566	1 AEU02330	B AC023104	40 AC019951	
,	Query	Match Length DB ID	66.4 2142	26.4 4176	26.4 125803 8	26.4 198402 8	21.3 2792	21.3 128598	12.1 15727	11.9 156995	11.8 101370	11 7 11836 1	000000000000000000000000000000000000000	11./ 102149 9	-	
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1 (bases 1 to 2142)
Martin,W.F.
                                                                                                                                                                                                   Homo sapi
Drosophil
Drosophil
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Eubacterial origin of nuclear genes for chloroplast and cytosolic glucose-6-phosphate isomerase from spinach: sampling eubacterial gene diversity in eukaryotic chromosomes through symbiosis dene 214 (1-2), 205-213 (1998)
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AL049182 Plasmodiu
         Mus muscu
Mus muscu
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                                         Homo sapi
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Nowitzki,U., Flechner,A., Kellermann,J., Hasegawa,M.,
                                                                                                                                                                                                                                                                                                                                                   Human DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOJ00265 2142 bp mRNA PLN (25-AUG-1998.
Spinacia oleracea mRNA (nuclear-encoded) for chloroplast
                                                                                                                                              Ношо
                                                                                                                                                                   Homo
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AC008025 H
AC027702 H
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AC016012 B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="nuclear encoded chloroplast GPI"
84. ,1940

    . 2142
    /organism="Spinacia oleracea"
/db_xref="taxon:3562"

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TITLE

VERSION

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QLVMESIGKEFDLGNKVNGGITVYGNKGSTDOHATTQURNGVHFFATFIEVRDR
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AVGITXASLVNINAYHQPGYBRGKKAAALQKRVLAVLNRASCKDPUEDTITEEVA
DHCHCPDDIEMIXKIIAHMAANDRVILABGDCGSPRSIKAFLGECNVDELYA"
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1 (bases I M. 4.1.7)

Yu,T.S., Lue,W.L., Wang,S.M. and Chen,J.

Mutation of Arabidopsis chloroplastic phosphoglucose isomerase
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63; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /function="glycolysis, gluconeogenesis"
/product="glucose-6-phosphate isomerase"
467 c 490 q 592 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.4%; Score 199.2; DB 79.0%; Pred. No. 8.8e-51 Live 0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   490 g
                                                                                                                           /codon_start=1
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264. 1937
/gene="GPIP"
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Arabidopsis thaliana
/gene="GPIP"
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/ULDAGE LOID - "MGETRRHSVDVP LITRILVALRRVRSLRDPCTTSMSKFASLLDNV
KWETGSNNG ISLOFVERHODACKAADAPVG I JPFGSYS I MEELESGCDLHKLSSK VI
NVEGDAGSRSSRENGSEDLSVKGRDLACNAPST SHVEEAGSGGRYRTHY STKLASSVGE
YGSRLGSPMNSTNHSY YGDEDVDPFDSQSNRCGOT TV WORRTPR YKRGSNGSSVDEYPL
LPGNGNGESDVYPSHFYLSRLSOKFRPRSTOCT ITV WORRTPRY KRGSNGSSVDFEYPL
LFGRGRGTGKTSTSK IFAAALNCLSQAAHSRPCGLUSCFWGTLLNSLDSTILGRITSVY
LEHGRGTGKTSTSK IFAAALNCLSQAAHSRPCGLUSCFWGTLLNSLDSTINGSNGSSVL
NRPSYLRSLIKSASLPPVSSRRYFT I IDECQLLCQFTWGTLLNSLDNFSOHSVFILVT
SELEKLPRNYLGRSOKY HFSKVCDADITSK LAKA ICTEEG I DFDQGAVDFIASKSDGSL
RADAEIMLDQLSLLGKR ITTSLAY KLIGVYSDDELLDLLDLAASSDFSNIYTRARELAR
SKIDPWALSSOK YHFSKVCDADITSK LAKA ICTEEG I DFDQGAVDFIASKSDGS
RADAEIMLDQLSLLGKR ITTSLAY KLIGVYSDDELLDLLDLAASSDFSNIYTRARELAR
SKIDPWARSKOKYTHATISLAY KLIGVYSDDELLDLLDLAASSDFSNIYTRARELAR
SDAEKGGERRONETYBESVARTATDENGRONI NKDVELESSTSSGCGEDVIR
SDAEKGGERRONETYBESVARTYDLCCSDELKRELMKRGRLITSLTYTTSLEPERY
TPOHYARARGSWKLTAADSFQSVLGCNVEIQMNLY I SACSSPRASARAASLEFGLFSCS
RRMLHKSYLTTRIDSDCASERPAYTNSLRSCOGNVURARRSCARAAASLEFGLFSCS
RRMLHKSYLTTRIDSDCASERPAYTNSLRSCOGNVURARSSARAASSRRSCSSDQG
                                                Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Brassicales;
Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosome 4 can be viewed at: http://websyr.mips.blochem.mpg.de/proj/thal/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(171, .601,689, .883,983, .1159,1250, .1469,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(171. .601,689. .883,983. .1159,1250. .1469,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aquifex aeolicus, PIR2:A70460
Contains ATP/GTP-binding site motif A (P-loop) [GPRGTGKT]"
                                                                                                                                                                                                                                                                                 Submitted (03-FEB-1999) MIPS, at the Max-Planck-Institut fuer blochemic. Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: schuelle@mips.blochem.mpg.de,mayer@mips.blochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similarity to DNA polymerase III gamma subunit -
                                                                                                                                           Bevan,M., Wedler,H., Wedler,E., Wambutt,R., Hoheisel,J.,
Mewes,H.W., Mayer,K.F.X. and Schueller,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="DNA polymerase III like protein"
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                                                                                                                                                                                                                                                   sequencing, project.
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/number-1
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/numbor-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="GI:4220511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1556. .2980))
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EU Arabidopsis sequenc
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                         Arabidopsis thaliana
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. .2210,2365. .2433,2522. .2629,2891. .2943,3034. .3172,
. .3415,3507. .3585,3675. .3741,3827. .3961)
                                                                                                                                                                                                                                                                                                        join(<338. 856,1067. .1186,1384. .1482,1566. .1649,
1932. .2076,2146. .2210,2365. .2433,2522. .2629,2891. .2943,
3034. .3172,3259. .3415,3507. .3585,3675. .3741,3827. .>3961)
/gene="PGI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NTDPAGIDHQIAQLGPELASTLVVVISKSGGTPETRNGLLEVQKAFREAGLNFAKQGV
AITQENSLLDNTARIEGWLARFPWYDWVGGRTSIMSAVGLLPAHLQOINVRENLTGAA
LMDEATRTTSIKNNPAALLAMCWYWASNGVGSKDMVVLPYKDSLLLFSRYLQQLVMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGKEFDLDGNTVNOGITVYGNKGSTDQHPYIQQLRDGVHNFFATFIEVLRYRPPGHDW
ELEPGVTGGDYLFGMLQGTRSALYANGRESISYTIOEVTPTSYGAITALYERAVGLYA
SIVNINAYHOPGVEAGKKAAABVLALQKRVLSVLNEATCKDPVEPLTLEEIADRCHAP
EEIEMIYKIIAHMSANDRVLIAEGNCGSPRSIKVYLGECNVDDLYA"
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                                                                                                               Submitted (15-JAN-1999) Institute of Molecular Biology, Academia Sinica, Taipei, Taiwan 11529, Republic of China Location/Qualifiers
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Arabidopsis thallana DNA chromosome 4, BAC clone F22K18 (ESSAII
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                                                                                                                                                                                                                                                                                                                                                                                                 /product="phosphoglucose isomerase precursor"
<338, .>3961
/gene="PGI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="phosphoglucose isomerase precursor"
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affects starch synthesis and floral initiation
                                                                                                                                                                                                               /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
                                             2 (bases 1 to 4176)
Yu,T.S., Lue,W.L., Wang,S.M. and Chen,J.
Direct Submission
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/gene="PGI"
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17638. 19720
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1947. .19720)
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PRRASTIHPPILSGLRWMYPVRRTYWFDIYKNIDKITLNRCPVLV1HGTADDVDPF
HGRQLMELCQEKYEPLMLKGGNHCDLEILFPBYIGHLKRFVSAVEKSASKRNSSFSRR
MGGCEQPPRHSVDAPRKSKDGREKPRKSIDRLRFQGYKLSHIEKPEKLKVPFEEMERS
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                                                                                                                                                                                                                                                                                                                                                                                                                /note="similarity to putative protein F6118_70
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18965. .19052
                                                                                                                                                                                                                                                           17638. .17939
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1 Similarity 77.4%;
96; Conservative C
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join(13250. 13789,14106. 14207,14535. 14816,14914. 14979)
/gene="F22K18.30"
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ESQDVSEGDESEGDASEGDVSEGDESEGDVSEGAVSERAREPEPESEEAKLFVGNLAVD
VROALALMIFEGAGTVVELARYTYNETEDQSRGFGFTWSSVDEAETAVEKFNYKDLAV
RLITVNKAAPRGSRFBRAPKYEPAFRYVONDANDYDNGKLEQLESEHGKVVEARVY
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                                                                                                                                                                                                                                                       join(8981...9090,9370..10119,10217..10571)

gene="F22KK8.20"

Anote="strong similarity to pectate lyase, Musa acuminata,
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/note="27bp aag tandem repeat"
8981. .9090
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                                                                  complement(1556. .2980)
/gene="F22K18.10"
                             complement(1470. .1555)
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13790. .14105
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10217. 10571
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/number=3
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10120. .10
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11715. 11796,11890. 11957,12026. 12213,12305. 14416, 14692. 14793,14875. 15081,15183. 15236. 12213,12305. 14416, 15484. 15556,16085. 16198,16342. 16518)
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DSLDDIVEKKEYEYEQNYESQKDDADSSIKNIDWELSIYTKPEAEDGVSWKLIEDVQGT
EQSYEKQKQSPKKEEMEQYLSRDMSEQVTKSLPEEEQCVĢEYGAYDKLEAQDVLTINK
LEESQQTEQSYEKEDTKKNISSKKEDIKQNLSMDQSEQLYKSPPEDEKCVEVYEGSDK
DDNTYEALKKKVKEMQKTIEYPMSIQSAEEKQSPSFNIIDDTLSPGEYFKMRRSRSCR
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PYRDSKLTRILQNSLGGNARTAIICTMSPARSHLEGSRNTLLFATCAKEVTTNAQVNL
VVSEKALVKOLQRELARMENELKNLGPASASSTSDFYALMLKQKEELIARMEEQIHEL
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Contains ATP/GTP-binding site motif A (P-loop)
AA89-96;Kinesin motor domain signature and profile
AA225-336
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join(7612. -7808,8031. .8267,8480. .8526,8657. .8775,
8876. .9036,9206. .9315,9402. .9501,9574. .9697,9790. .9918)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Brassicales;
Brassicaceae; Arabidopsis.
1 (bases 4709 to 5139)
                                                                                                                                                                                                                                                                                 Zimmermann, W., Grueneisen, A., Wambutt, R., Kalicki, J., Wohldmann, P., Smith, A., Mewes, H.W., Lemcke, K. and Mayer, K.F.X.
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                                                                                                                                                       Robben, J., Grymonprez, B., Volckaert, G, Mewes, H.W., Lemcke, K. and
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Wedler,H., Wedler,E., Wambutt,R., Mewes,H.W., Lemcke,K. and
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/gene="AT4g24160"
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KEEVYKKWGVELSSKRRSLQYTHKLWNNNTKDIEHCKEASLIATUVGFVDSTLTPKE
ISDCTILPELAMAQLIRPIROLSPOCNHHFRNIKSPPRRITRPAPPEALKFYVIVAE
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ADDVGDSYDDDTETESEDEEEGSDEYTAMAARWFDGLISGNYVELTKEVYSLOSVDFDR
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               RERTMQHHSTHSDDTDTKTMKPENTDDGGEKTEFERQQSQIIELWQVCNVPLVHRTYF
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/gene-"AT4924170"
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PGVEAGKKAAASILELQKAIISTLQNESGPIALEALATKVQAPEQVETVYKIVRHLAA
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qgnikpptapkftdlaigiggsalgpofvaqalapnfpplaihfidnsdpdgidryl
nclkaqdklkstlvyttsksggtpeprnglabtkayfeaqglhfadyayavtmgskl
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GVTLGGTGKESGKRHPTLGENVVVGAGAKVLGNIAIGDNVRIGAGSVVLRDVPADFTV
VGVPGRMVHPSGERVNPLEHGKLPDSEGKVIRLLERIELLEOVATLGOOGSEQAME
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Sakamoto,T., Wada,H., Nishida,I., Ohta,H. and Murata,N.
Sakamoto,T., Wada,H., Nishida,I., Ohta,H. and Murata,N.
Sequence analysis of a DNA fragment from Synechocystis PCC6803
Sequence analysis of a DNA fragment from Synechocystis and containing genes homologous to cysE (serine acetyltransferase) and pgi (glucose-6-phosphate isomerase)
Plant Mol. Biol. 29, 187 (1995)
Plant Mol. Biol. 29, 187 (1995)
                                                                                                                                                                                                                                                       Submitted (27-NOV-1992) to the DDBJ/EMBL/GenBank databases. Toshio Sakamoto, Graduate University of Advanced Studies, Molecular Biomechanics; Myodaiji, Okazaki, Aichi 444, Japan (Tel:0564-55-7602, Fax:0564-53-7400)
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glucose-6-phosphate isomerase; serine acetyltransferase.
Synechocystis sp. (strain:PCC6803) DNA.
Synechocystis sp.
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54.2%; Pred. No. 4.8e-09;
tive 0; Mismatches 110; Indels C
                                                                                                          Bacteria; Cyanobacteria; Chroccoccales; Synechocystis.
1 (bases 1 to 2792)
Sakamoto, T.
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/product="serine acetyltransferase"
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/organism="Synechocystis sp."
/strain="PCC6803"
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gene
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of diaminopimelate-D-alanyi-D-glutamyi-2,

enthranilate synthase component I; aspartate carbamoyltransferase;

anthranilate synthase component I; aspartate carbamoyltransferase;

carbonic anhydrase; catabolite gene activator protein; cyclase;

cytochrome CytM; cytochrome c oxidase folding protein; cyclase;

factor IS; extragenic suppressor SuhB; fatty acid desaturase;

factor IS; extragenic suppressor SuhB; fatty acid desaturase;

hemolysin; hydrogenase expression/formation protein HypC; inner

membrane protein; melibiose carrier protein; membrane bound protein

LytR; ornithine acetyltransferase; oxygen independent

coprophorphyrinogen III oxidase; pantothenate synthetase;

photosystem II DI protein; polyA polymerase; regulatory components

transduction histoline kinase; serine acetyltransferase; tRNA-II;

Synechocysiis sy, (strain:PCC6803) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3-chlorobenzoate-3.4-dloxygenase; 30s ribosomal protein S1; 30s ribosomal protein S2; 50s ribosomal protein L9; 50s ribosomal protein L9; ABC transporter; Cobb protein; DNA primase; GDP-mannose pyrophorylase; GTP cyclohydrolase II; H+/Ca2+ exchanger; PetG subunit of the cytochrome b6f complex;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaneko,T., Sato,S., Kotani,H., Tanaka,A., Asamizu,E., Nakamura,Y., Myajima,N., Hirosava,M., Sugiura,M., Sasamoto,S., Kimura,T., Hosouchi,T., Matsuno,A., Muraki,A., Nakazaki,N., Naruo,K., Okumura,S., Shimpo,S., Takeuchi,C., Wada,T., Watanabe,A., Saquence analysis of the genome of the unicellular cyanobacterium synechocystis sp. strain PCC6803. II. Sequence determination of the DNA Res. 3 (3), 109-136 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (28-JUN-1996) to the DDBJ/EMBL/GenBank databases. Satoshi Tabata, Kazusa DNA Research Institite, Laboratory of Gene Structure 2; 1523-3, Yanauchino, Kisarazu, Chiba 292, Japan (E-mail:tabata@kazusa.or.jp, Tel:+81-438-52-3933,
                                                                                                                                                                                                                                                                                                                                                                                     D90912 128598 bp DNA BCT 07-FEB-1999
Synechocystis sp. PCC6803 complete genome, 14/27, 1719644-1848241.
D90912 AB001339
1711 ATGCTCTGGCGGAAACGAAGGCAGTATTTGAAGCCCAGGGCCTTCATTTTGCCGATTATG 1770
                                                                                                                      1771 CGGTGGCGGTGACCATGCCCGGCAGTAAACTTTCCCAGCAGGCCCAGACGGAACAATGGT 1830
                                                                                                                                                                                                                            1831 TACAAGCTTTTCCCATGCAGGATTGGGTGGGTGGGAGAACCTCTGAGTTATCGGCGGTGG 1890
                                                               181 gtgttgcaattactccaagaaaattctctgttggataacactgctagaatagaggggggg 240
                                                                                                                                                                                  241 tagctcggtttcctatgtttgattgggttggtggtaggacttcagaaatgtctgctgtgg 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GIASADKKSGRTAARGLVHSTIHFGGRIGYLVEVNCETDFVARGDRFKDLVNDVAMQI
AACPNVEY VSVADIPQEMVAKEKEIEMGRDDLGKRPANIKEKIVGGRIDKRLKELSLL
DQPYIKDQNLTIEELVKQAIAELGENIQVRRFIRFNLGEGIEKAETNFAEEVAAAAKG
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NLSVAVAVVLIGVYLLSLVFSNGTHAYLYDVGVAENMEMPELGEDVSBPEPPFEEKD
NLSVAVAVVLIGVYLGYAVESELLVGSLEVAPESLGITALFTGVIVLPIIGNAAFHATA
VTVAMKDKMDLSMSVVNGSSLQIAFFVAPVLVIVGWAIGQPMDLNFNPFELVAVLVAV
LIVNSISSDGTSNWLESILLIATYALVALAFFFHPTLV"
COMPLEMENT (4954. 5535)
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LAIPANVTVLCIGKSTYARAGIIANLTPGEAGWCGHLTLEFSNSSSADCRIYANBGIV
                                                                                                                                                                   SRVTTHLEPLEDPKSWQHPDEFPPSAPLNRDKPN"
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/gene="rps2"
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3809. .4927
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/transl_table=11
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qalddqlmevakfbivdtvfpebmedliltfrevllnaied"
7640. 8098
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IAKNENAIGIQIYTCIIAYLILKLLVIPKEAGTTMLDKLRYLQAFWCEKISYVHWLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MIDIVKADLNSAVHAEAMIQLMNEYACDPWGGGEELPNYVKANL
PEBLAKREPSAHIILAEVDSKPAGLLVCLEGESTFACKPLLNIHDVIYSLPYRGKGLSK
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DISTLDSHVSSIMIKQDS"
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QRQAIIAQKAQQWLEQLDPLSGEGIWFADLAKHYPSTLAAAIALLNNEST"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDSTIVSITSKLAWNLGFHQVKVFSGINLSTGIPGGIVIHFGQGHDNKYGNETIEETP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGVAVMDRGFCDLQRIKRLQKENNKYHVLRIKNNIKLEKLANDNYMVGTGKNKIESR
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PIHRKTAIKELAKEAGHEVLFLPKYSPDLNDIEHDFSALKRARMYAPIDTSLDEIIRS
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QLLFFEGEDCDISYETRRGKYQNQPQSVTLPRV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 64; DB 2;
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54.2%;
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Best Local Similarity 54.2'
Matches 130; Conservative
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Submitted (06-MAR-1998) The Institute for Genomic Research, 9712
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                                                                                                                                        121 atggtctactagaagtacagaaagccttcagagatgcggggctgcaattctcgaaacagg 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treponema pallidum section 40 of 87 of the complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25477 CGGTGGCGGTGACCATGCCCGGCAGTAAACTTTCCCAGCAGGCCCAGACGGAACAATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spirochaetales; Spirochaetaceae; Treponema.
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AE001224.1 GI:3322761
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Treponema pallidum
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ANPRIRTAILKARAANMPKDNIERAIKKGTGELSGSSYEELVYEGYAPGGVATUVEVL
PYDKRARAANNRNLEGRNGGRLGSAGSVSYMENRKGVIEXDSEQVDEEALMELALEAG
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Complement (1655. 3262)
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TLETLSNELEVAHVLRQAGLEPHTQEVAVTSETSPLANNPQYLASFYMDDFIGGRYSS
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complement(3326. .4672)
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complement(5525. 7072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(5525. .7072)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FAVCEFIRLNRGLLLLSLVLEGFVVPSFDPWLDSLGNWALCLPRLQPVYRALIEIPFV
GLARFYNTMIAGGLVAGALCYLPCYALARCAVTAYRTYLYPKIHHATIFFLVRNAPLC
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QRGRVNFWSLSMACASVLALLGLVYLIRNVIARRVVIGGSEAVFGARCEAAVVDLDLF
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TSGALPPRRAKRQRVRSSNPLIAKIQEKAAELAAPVSFGAGFSALKAQWDPRILLERE
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KTAQSLTTRKRLGGVIFCLSATSLPCC"
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9851, 10600
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101394 101393; gap of 100 bp 101394 109454; contig of 8061 bp in length 109454 109554; gap of 100 bp 109555 1010702; contig of 1148 bp in length 110703 110802; gap of 100 bp 110803 112576; contig of 1174 bp in length 112577 112676; gap of 100 bp 112577 1139381; contig of 26705 bp in length 1139382 139481; gap of 100 bp 1139482 134860; contig of 900 bp in length 1139482 148660; contig of 900 bp in length 148661 14860; gap of 100 bp in length 126995; contig of 8235 bp in length.
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45192 a 31015 c 30671 g 48611 t 1506 others
                                                              75492 75591: gap of 100 bp 75592 909121: contig of 15320 bp in length 90912 90702: contig of 8059 bp in length 99071 99170: gap of 100 bp 99071 99170: gap of 100 bp 99171 101293: contig of 2123 bp in length 101293: contig of 2123 bp in length
                           77: gap of 100 bp
75491: contig of 13914 bp in length
61477: contig of 24719 bp in length
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                           61577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
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                                                         ö;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 156995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (06-UUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CBIO 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator ET-amersham; 18% of reads Chemistry: Dye-terminator ET-amersham; 18% of reads Consensus quality: 148967 bases at least Q40 Consensus quality: 152162 bases at least Q30 Consensus quality: 154190 bases at least Q20 Insert size: 155495; sum-of-contigs un-of-contigs Quality Quality coverage: 4.30x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                    2650 CITGAGACCACGCTITITATITIGGTATCAAAGAGTGGTACGACGCTIGAAACACTCAGT 2591
                                                                                                                                                                                                                                               123 ggtetactagaagtacagaaagcettcagagatgeggggetgeaattetegaaacagggt 182
                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL365270 156995 bp DNA HTG 07-JUL-200C
Homo sapiens chromosome 1 clone RP11-99A8, *** SEQUENCING IN
PROGRESS ***, 16 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
       Score 36.2; DB 1; Length 15727;
Pred. No. 2.2;
0; Mismatches 78; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10301 10400: gap of 100 bp in length 10401 13921: contig of 3521 bp in length 13922 14021: gap of 100 bp 104022 27982: contig of 13961 bp in length
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                                                                                                                                                                                                                                                                                                                                  183 gttgcaattactcaagaaaattctctgttggataacactgc 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coverage: 4.65x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Sanger Centre
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HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:8980271
            Query Match 12.1%;
Best Local Similarity 51.6%;
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct
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AL365270/c
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COMMENT

KEYWORDS

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                               46917 AAAGGTTTACAAGGAGAATGGAAAGCAATAATAGAAGGAAACTTGAAGGTCACTAACAAG 46858
                                                                                                                                                                                                                                                         46857 GAAAGACAATAGAAATTGTAAATATCCAGGTAAATAAAATTAGAGTATTATTATTGCCTCT 46798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assembly program: XARP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator ABI; 3% of reads
Chemistry: Dye-terminator Big Dye; 45% of reads
Chemistry: Dye-terminator ET-amersham; 50% of reads
Quality: 99056 bases at least Q40
Consensus quality: 100022 bases at least Q30
Consensus quality: 100489 bases at least Q30
Insert size: 101270; sum-of-contigs
Insert size: 114210; 4.1% error; agaróse-fp
Quality coverage: 0.00x in Q20 bases; sum-of-contigs Quality
Coverage: 0.00x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL353604 101370 bp DNA HTG 09-AUG-2000
Homo sapiens chromosome 1 clone RP5-1180c18 map p32.3-34.2, ***
                                                                                                                                                                                                                 180 ggtgttgcaattactcaagaaaattctctgttggataacactgctagaatagaggatgg 239
                                                                                                          120 aatggtctactagaagtacagaaagccttcagagatgcgggggctgcaattctcgaaacag 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (08-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 11, 2000 this sequence version replaced gi:9717057.
                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
  11.9%; Score 35.6; DB 85; Length 156995; 52.7%; Pred. No. 4.5; tive 0; Mismatches 69; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence. It currently * consists of 2 contigs. The true order of the pieces * is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76801 76900: gap of 100 bp in length. 76901 101370: contig of 24470 bp in length. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code: SC
Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----- Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                        240 ttagctcggtttcctatgtttgattg 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; HTGS_PHASE1; HTGS_DRAFT
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                      Local Similarity 52.7
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Query Match
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/organism="Homo sapiens"

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Read.T.D., Brunham,R., Shen,C., Gill,S.R., Heidelberg,J.F.,
Nhite,O., Hickey,E.K., Peterson,J., Umayam,L.A., Utterback,T.,
Berry,K., Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B.,
Bowman,C., Dodson,R., Gwinn,M., Nelson,W., DeBoy,R., Kolonay,J.,
Direct Submission Salzberg,S.L., Elsen,J. and Fraser,C.M.
Direct Submission The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
On Jun 1, 2000 this sequence version replaced gi:7190921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60694 TCACTIGGAATITITITAAATATIGAGTAATICAGAGACTAACCAACAGGCCAGAGGTA 60635
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[ Chases 1 to 11836]
Read, T.D., Brunham, R., Shen, C., Gill, S.R., Heidelberg, J.F., White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T., Berry, C., Downan, C., Dodson, R., Welson, W., DeBoy, R., Caven, B., McClarty, G., Salzberg, S.L., Elsen, J. and Fraser, C.M. Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                    120 aatggtctactagaagtacagaaagccttcagagatgcggggctgcaattctcgaaacag 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 ttagctcggtttcctatgtttgattgggttggtggtaggacttcagaaatgtctgctgtg 299
                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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Chlamydia muridarum, section 83 of 85 of the complete genome.
                                                                                                                                                                                                                                                                                                11.8%; Score 35.4; DB 64; Length 101370;
49.7%; Pred. No. 4.9;
tive 0; Mismatches 91; Indels 0;
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                                                                                                                                                                                                             100 others
                               / Clone="RP5-138.02" |
// Clone="RP5-138.02" |
// Clone="RP5-1180018" |
// Clone="lb="RP5-1180018" |
1. 76800 |
// Once="assembly_fragment:00905.0" |
// Once="assembly_fragment:01232.0" |
24879 a 24116 c 25164 g 27111 t 100 c
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Nucleic Acids Res. 28 (6), 1397-1406 (2000)
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/db_xref="taxon:9606"
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/gene="TC0894"
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                          /chromosome="1
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AE002356.2 GI:8163342
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/translation-"MITSELNAAQVTAVTAPLQPVLVLAGAGAGKTRVVSHRILYLIE
EAQLDPSQILAITFTNKAAKELNERVLTQCNFPDYRGIPMVSTFHSLGVYILRRSIQL
LDRQSNFAIYDQSDSEKLIKQCLRKLNLDNKLCNAMQFTISQAKNRLQDPEDLDSREY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="WIDGIOTCSFGATHRLTAKSTVSLEMPLATHNLQEGASASAKLE ADFIRAEQILAEMQEIRSSLEQSLETLIPRE" complement(2323. .3012)
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PAKEHYEALRSTPFDQVKVJLGQDPYHGEGGAHGLSESVPKGGALDESPENTFOEL
PREHYEALRSTPFDQVKVJLGVPPKHGGGAHGLSESVFKGADLADY
THITPVLWGSAARKKODLFQTKHQHAILACPHPSPLAAHRGFFGCHFSKINYLLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MKILIASSHGYKVRETKAFLKKIGEFDIFSLVDYPSYTPPKETG
ETPERNAIOKGVFAAQTFRCWTIADDSMLIIPALGGLPGKLSASFSGEHASDKDHRKK
LLEEMLLLENPIDRSAYFECCVVLVSPFGKIFKAHASCEGTIVFKERGSSGFGYDPLF
SKHDYKQTYAELPEETKNOYSHRAKALAKLQPYVEMAFANHLLARNESL"
                                                                                                                                                                                                                                                                                                                     MTRADTGRIWVPTSPOVPDAOSAYFYAATGVIGALSITNIGIGYTLPFKVLGAPWIDG
HKVAQELNKAKLPGVKFLPFWYEPFFGKFKMEICSGVLLVLQDPKTFLPMETQSVILG
VLKMLYPKEVEQAFLLLDRLAPRRKAIQTLLGRSEFLNVCLQKQYVTWPLRTMCVEGR
                                                                                                                                                                                                                                       ALISHSAAINQQEHSLCVFDQHKGICKLSALCTLEHGYFGASIAETPGYDPVLAGIH
VVSLFSSKEIPSEVIEACDVFVYDVQDIGVRSYSFISALLQVVKASASSNKELIVLDR
PNPMGGDMVDGPLPDKEALPAIPYCYGMTPGELALLYRAWYAPNATVTVVPMQGWTRS
                                                                                                                                                                                                            /translation="MKVVCKLVMVALLFPSMGHALVQVGLERIFQEEKYLEKIRGKRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="conserved hypothetical protein; identified by
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/note="conserved hypothetical protein; identified by Glimmer2; putative"
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/note="similar to GB:M63176 PID:153062 SP:Q53727;
identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to GB:M20681 SP:P11169 PID:306821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      identified by sequence similarity; putative /codon_start=1
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/transl_table=11
/product="conserved hypothetical protein"
/protein_id="AAR39690.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="conserved hypothetical protein"
/protein_id="AAF39689.1"
                                                                                                                        /product="conserved hypothetical protein"
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/protein_id="AAF39691.1"
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/db_xref="G1:7190926"
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/gene="TC0896"
complement(2099. .2326)
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complement(2323. .3012)
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/gene="TC0898"
3093. .4997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALMITROHENRIARCOPAGISKKIOLPIAKLIVFLROALASIPWCPAAGFPNSLKTPB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to GB:D10483 SP:P00379 GB:J01609 GB:V00276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GB:X05108; identified by sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /producT-"conserved hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence similarity; putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAF39695.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(7094. .7825)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(6405. .7115)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
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5001, .6281
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                            Insert size: 170000; agarose-fp
Insert size: 160349; sum-of-contigs
Quality coverage: 3.9 in Q20 bases; agarose-fp
Quality coverage: 4.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                    Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
                                                                     Sequencing vector: M13; M77815; 100% of reads
                                                                                                                                                                                                                                                                                               Consensus quality: 150591 bases at least Q40 Consensus quality: 15557 bases at least Q40 Consensus quality: 1556001 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ap of 100 bp contig of 25335 bp in length ap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig of 11625 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167: gap of 100 bp 86875: contig of 19008 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86975: gap of 100 bp 106760: contig of 19785 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contig of 29854 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1573: contig of 1573 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1574 1673: gap of 100 bp
1674 3543: contig of 1870 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p of 100 bp contig of 1958 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5602 5701; gap of 100 bp 100 bp 10 length 5702 7732; contig of 2031 bp in length 7833 10667; contig of 2835 bp in length
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contig of 2835 bp in length
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10768 13917: contig of 3150 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p of 100 bp contig of 3364 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              up of 100 bp contig of 3852 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59: gap of 100 bp 39422: contig of 5863 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22: gap of 100 bp
46446: contig of 6924 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46: gap of 100 bp 56042: contig of 9496 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="RP11-733018"
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Center clone name: 733_0_18
..... Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27089: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106761 106860: gap of 132195: cont.
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17482 20415: conf
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17381: con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56142: gap of
67767: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3544 3643; gap of 3644 5601; cor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Chatcon, L., Bucknin, J., Barna, N., Beckerly, R., Beda, F., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cocke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Fitzhugh, W., Fortset, C., Gage, D., Galagan, J., Farreira, P., Fitzhugh, W., Fortset, C., Gage, D., Galagan, J., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Macdonald, P., Marquis, N., Macbwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Connor, T., O'Divar, T.M., Peterson, K., Peterson, K., Santos, R., Severy, P., Spencer, B., Stange-Thoman, D., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirtell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., D., Tone, C., Man, C., M., N., Waman, D., Ye, W.J., Chander, A., and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (08-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, NA 02141, USA On Mar I, 2000 this sequence version replaced gi:6939348.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens chromosome X clone RP11-733018 map X, WORKING DRAFT SEQUENCE, 19 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7121 GGTTTTGTGGAATCAAGAAAAGGAATAAAAGGGGGGGGCCATGAATTTTTAGATCAGCTA 7062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 ggtctactagaagtacagaaagccttcagagatgcggggctgcaattctcgaaacagggt 182
                                                                                                                       /note="similar to PID:169414; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.7%; Score 35; DB 1; Length 11836; 56.5%; Pred. No. 5.1; tive 0; Mismatches 50; Indels (
                                                                                                                                                                                                                                                    pyrophosphokinase/dihydropteroate synthase"
/protein_id="AAF39696.1"
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                             complement(8273, .9625)
                                                                             complement(8273. .9625)
                                                                                                                                                       similarity; putative"
/codon_start=1
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Best Local Similarity
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Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
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/db_xref="taxon:7227"
7305 c 7379 q 9395 t
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.7%; Score 35; DB 48; Length 162149; 61.5%; Pred. No. 6.8; tive 0; Mismatches 35; Indels 0;
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13226. .162149
/note="assembly_fragment"
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/note="assembly_fragment"
56143. 67767
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67868. 86875
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27190. :33459
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20516. 23137
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23238. 27089
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                       1674. .3543
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Matches 56; Conservative
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Auzny, D.M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K., Bodota, B., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Bunac, C., Bodota, B., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Bunac, C., Bodota, B., Bouck, J., Carter, M., Chacko, J., Cork, C., David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N., Duyan-Rocha, S., Durbin, K.J., Fernandez, C., Ferraguto, D., Dugan-Rocha, J., Frantz, P., Ganeel, R., Gorrell, J. H., Guevara, W., Harris, K., Hernandez, J., Hodgson, A., Hodues, M., Harlis, K., Hernandez, J., Hodgson, A., Hodues, M., Kelly, S., Kondejwski, N., Kong, Y., Kovar, C., Leal, B., Li, Z., Lichtarge, O., Liu, J., Liu, W., Logan, O., Lozado, R.J., Lu, J., Liu, W., Logan, O., Lozado, R.J., Lu, J., Liu, W., Logan, O., Lozado, R.J., Lu, J., Lu, S., Nash, S., Paxton, S., Parton, B., Perez, L., Pu, L., Oswal, G., Parish, B., Paxton, S., Parks, A., Sucagang, R., Tabor, P., Taylor, T., Vasquez, L., Vinson, R., Vo, O., Wahbah, M., Watlington, S., Weinstock, G., Yu, W., Zhou, X., Nelson, D., and
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Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pteryota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophildae, Drosophila.
This sequence was identified as CDM:10211508 by the submitter. For more information on this record e-mail to fly@celera.com.
For more information on this record e-mail to fly@celera.com.
For more information on this record e-mail to fly@celera.com.
For more information of the replaced

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Oualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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Best Local Similarity 49.2%; Pred. No. 7.6;
Matches 91; Conservative 0; Mismatches 94; Indels 0;
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TITLE JOURNAL REFERENCE AUTHORS

COMMENT

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11.5%; Score 34.6; DB 36; Length 148447;
                                            g of 1845 bp in length
f unknown length
g of 1670 bp in length
f unknown length
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J of 1666 bp in length
k unknown length
of 1455 bp in length
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of 1039 bp in length
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contig of 9406 bp in length
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/db_xref="taxon:7227"
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                                                                                                                                                                                                                                            Chemistry: Dye-terminator Big Dye: 17% of reads
Assembly program: Phrap; version 0.980611
Consensus quality: 105301 bases at least Q40
Consensus quality: 119508 bases at least Q20
Consensus quality: 126701 bases at least Q20
Estimated insert size: 132501; sum-of-contigs estimation
Q20 bases; sum-of-contigs estimation
                                      Submitted (16-SEP-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Feb 18, 2000 this sequence version replaced gi:5902992.
                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 52 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sap of unknown length contig of 847 bp in length gap of unknown length contig of 847 bp in length contig of 877 bp in length contig of 820 bp in length gap of unknown length gap of unknown length contig of 919 bp in length gap of unknown length contig of 876 bp in length gap of unknown length gap of unknown length contig of 832 bp in length gap of unknown length contig of 832 bp in length gap of unknown length gap of unknown length contig of 823 bp in length gap of unknown length gap of unknown length gap of unknown length gap of unknown length contig of 1227 bp in length gap of unknown length
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gap of unknown length
contig of 1054 bp in length
gap of unknown length
contig of 852 bp in length
gap of unknown length
contig of 1052 bp in length
gap of unknown length
contig of 1103 bp in length
contig of 1132 bp in length
gap of unknown length
contig of 1139 bp in length
gap of unknown length
gap of unknown length
gap of unknown length
grountig of 804 bp in length
grountig of 804 bp in length
grountig of 804 bp in length
grountig of 976 bp in length
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of 866 bp in length
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of 965 bp in length
unknown length
                                                                                               Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                 Sequencing vector: M13; L08821
                                                                                                                                                                                      Center project name: DRGW Center clone name: RPC198-5M7
                                                                                                                                                                                                                       .--- Summary Statistics
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2 (bases 1 to 148447)
Worley, K.C.
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                              Direct Submission
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KEYWORDS
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DOE Joint Genome Institute.

Direct Submission

Submitted (Jours 2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 18, 2000 this sequence version replaced 91:8810396.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC073779 207585 bp DNA HTG 18-JUL-2000
Mus musculus clone RP23-389E9, WORKING DRAFT SEQUENCE, 18 ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Consensus quality: 196805 bases at least Q40 consensus quality: 203855 bases at least Q30 consensus quality: 205855 bases at least Q30 consensus quality: 205194 bases at least Q30 consensus quality: 205194 bases at least Q20 bestimated insert size: 206785; sum-of-contigs estimation Quality coverage: 5.94 in Q20 bases; agarose-fp estimation Quality coverage: 6.55 in Q20 bases; aum-of-contigs estimation.

* NOTE: This is a 'Working draft' sequence. It currently * consists of 18 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces
                                                                                                                          63453 ATAGCATTGGAATCATTCAACCTGCTATTTTTAGCCGGAATAACAAAGTCTTTCTGTG 63512
                                                                                                                                                                                                                               63513 ATACGGATATAATGCTATACATTGAGGCTTTTTATATTACTAAGATAAATTTTTTAATAA 63572
                                                                                                                                                                                                                                                                                                              214 ataacactgctagaatagagggatggttagctcggtttcctatgtttgattgggttggtg 273
                                                                         94 agagoggaggacacctgaaacccgcaatggtctactagaagtacagaaagccttcagag 153
                                                                                                                                                                              154 atgoggggctgcaattctcgaaacagggtgttgcaattactcaagaaaattctctgttgg 213
                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 24555: contig of 24555 bp in length 24655; gap of unknown length 24656 26633: contig of 1977 bp in length 2653 26732: qap of unknown length 26733 40387: contig of 13655 bp in length
                           94; Indels
49.2%; Pred. No. 9;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------Genome Center
Center: Joint Genome Institute
Center Code: JGI
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HTG; HTGS_PHASE2; HTGS_DRAFT.
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DOE Joint Genome Institute.
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                           91; Conservative
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     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 63633 CGAGG 63637
                                                                                                                                                                                                                                                                                                                                                                                             274 gtagg 278
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                                Matches
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SOURCE

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. ( pases 1 to 235066) McCombie, W.R., Baker, J.P., Bahret, A., Bal, H., Dedhia, N.N., de la Bastide, M., Huang, E.N., King, L., Kirchoff, K.A., Miller, B., Nascimento, L.U., O'Shaughnessy, A.L., Preston, R.R., Rodriguez, M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACO74208 235066 bp DNA HTG 19-JUL-2000
Mus musculus clone RP23-62A16, *** SEQUENCING IN PROGRESS ***, 22
unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 91664 TGAGGGCCCAGAAAGTTCCCTCAGAAGGCCTCTTCACTTGGTTTGGTTTGATTTGG 91723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 51.6%; Pred. No. 9.4;
Matches 79; Conservative 0; Mismatches 74; Indels 0;
46487: gap of unknown length
46664: contig of 6177 bp in length
46664: contig of 6177 bp in length
96506: contig of 43926 bp in length
96528: contig of 43926 bp in length
96528: gap of unknown length
161230: contig of 16372 bp in length
112830: gap of unknown length
114129: gap of unknown length
115766: contig of 1627 bp in length
115766: contig of 1627 bp in length
115765: contig of 1627 bp in length
115865: gap of unknown length
138129: contig of 1627 bp in length
138129: contig of 1371 bp in length
138129: contig of 13812 bp in length
138129: gap of unknown length
138120: contig of 11812 bp in length
138229: gap of unknown length
18552: gap of unknown length
197426: contig of 11812 bp in length
19756: contig of 12174 bp in length
200791: contig of 2536 bp in length
203527: gap of unknown length
203527: gap of unknown length
204273: contig of 2536 bp in length
204273: contig of 3212 bp in length
204273: contig of 3212 bp in length
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57071 a 49938 c 48076 g 50778 t 1722 others
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/organism="Mus musculus"
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/clone="RP23-389E9"
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AC074208.1 GI:9280702
HTG; HTGS_PHASE1.
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46665
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Direct Submission
Submitted (19-701-2000) Lita Annenberg Hazen Genome Sequencing
Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring
Harbor, NY 11724, USA
                                                                                                                                                                       Center: Lita Annenberg Hazen Genome Center, Cold Spring Harbor
                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'vorking draft' sequence. It currently consists of 22 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
Shah, R.S., Shekher, M., Spiegel, L.A., Toth, K. and Vil, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44540: contig of 44540 bp in length
44627: gap of unknown length
66112: contig of 21485 bp in length
66199: gap of unknown length
85282: gap of unknown length
10212s: contig of 16843 bp in length
102211: gap of unknown length
116936: contig of 14725 bp in length
116936: contig of 14725 bp in length
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g of 11971 bp in length
f unknown length
g of 11588 bp in length
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unknown length
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Context: mccomble@cshl.org
Context: mccomble@cshl.org
Center project name: RP23-62A16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig of 6506 bg of unknown locating of 4893 bg of unknown locating of 4547 bg of unknown locating of 4842 bg of unknown locating of 4403 bg octating of 4403 bg octating of 4803 bg
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McCombie, W.R.
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/organism="Mus musculus"

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                                                                                                                                                                     0; Gaps
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                                                1863 others
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65290 a 55075 c 52677 g 60161 t
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Search completed: November 4, 2000, 13:43:05 Job time: 17634 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		DB	7	45	26	7	œ	7	7	7	_	7	7	10
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Direct Submission
Submitted (07-ocr-1997) to the DDBJ/EMBL/GenBank databases. Akihiko
Katsurada, Tezukayama Gakuin College, Deprt. of Nutrition; 4-2-2
Harumidal, Sakai, Osaka 590-01, Japan
(E-mail:LDD00647@niftyserve.or.jp, Tel:+81-722-96-1331,
Fax:+81-722-92-2135)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AE003845 Drosophil
AC010915 Drosophil
AC011677 Homo sapi
AC027571 Homo sapi
AL139163 Homo sapi
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Location/Qualifiers
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Eukaryota; Viridiplanta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; editocyledons; core eudicots; Rosidae; eurosids I; Fabalee; Fabaceae; Papilionoideae; Medicago.

1 (bases I to 1618). Shorrosh, B.S. and Dixon, R.A. Stress responses in alfalfa (Medicago sativa L.) XIX. Transcriptional activation of oxidative pentose phosphate pathway genes at the onset of the isoflavonoid phytoalexin response Plant Mol. Biol. 28 (5), 885-900 (1995)
                                                                                                                                                                 ELGSVESEWIKGELLISFLIETTADIFGIKDIKGDGYLVDKVLDKTGWKGTGKWTVQQA
AELSIAAPTIEASLDARFLSGLKEERVEAARVEKSGGIGDIVTDDHVDKOKLIDDVRK
ATAAKICSYRAGMILIRAKSIEKGHODKLGELARIUKGGCIIRAIFLDRIKQAYERN
PULAMILVDPEFAREIIDYOSAWRRVVCLAINSGISPPGMSASLAYFDTYRRELPAN
LVQAQRDYFGAHTYERVDIEGSYHTEWFKLAKQSKKLDYCISANQDFPNKCNIFCSDC
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                                                                                          /translation="Maopstgiglagiavmgonlalniaekgfpisvynrtyskydety
Verrkoegenldvygyhdperyhsiokprynithikacapvdotiktisaymekgdci
IDGGNEWYENTERREKDVAELLYLGLGVSGGEEGARNGPSIMPGGSFBAFKYIEDI
LLKVAAQVPDSGPCYTYIGKGGSGNFVKMIHNGIEYGDMQLIAEAYDVLKSVGKLSNE
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Submitted (06-DEC-1994) Theo Fahrendorf, Samuel Roberts Noble
Foundation, Plant Biology Division, 2510 Sam Noble Parkway,
Ardmore, OK 73402, USA
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Pred. No. 4.1e-30;
0; Mismatches 43; Indels 2;
                             /product="6-phosphogluconate dehydrogenase",
/protein_id="BAA22812.1"
/db_xref="GI:2529229"
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/cultivar="Apollo"
/sub_species="sativa"
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/EC_number="1.1.1.44"
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PERAKQEGULPLYGFHDPEAFVNSIERERVIIMLUKAGAPVEGTTKTLSAYLEKGDCI
IDCDNEWYENTERREKEVALGIITYLGWGVSGGEEGARRGESWMFGGESEARKYFIEDI
ELKVAAQVPDSGPCYTYIGNGSGSNEYKMIHKGIEYGDMGJIAEAYDYLKSYGKLTNE
ELGSAFTEWNKGELLSTIETTADIFGIKDNGDGYLVDKYLDKTGWKGTGKWTVQQA
ALTAARCSYAGGWINITRAKSAEKGWDLALGELTTDOQVPKKGLIDDVRK
PNLANILVYDPERAKEIIEROTAWRRYVSLSVNSGISLPGMSASIAYFDDRIKQAYDNR
LVQAQRDXFGAHTYERVDIEGSYHTEWFKLAKQSKII
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 96240)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lin, X., Kaul, S., Town, C.D., Benito, M., Creasy, T.H., Ronning, C.M., Koo, H., Fujii, C.Y., Utterback, T., Barnstead, M.E., Bowman, C.L., White, O., Nierman, W.C. and Fraser, C.M.
Arabidopsis thaliana 'IGF' BAC 'Filal2' genomic sequence near
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Lin,X. and Kaul,S.
Lin,X. and Kaul,S.
Direct Submission.

Submitted (1-MAY-2000) The Institute for Genomic Research, 9712
Submitted (1-MAY-2000) The Institute for Genomic Research, 9712
Submitted (1-MAY-2000) The Institute for Genomic Research, 9712
On Jun 2, 2000 this sequence version replaced 917769972.

* NOTE: This is a 'working draft' sequence. It currently
consists of 17 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 ctcaatattgcttgaaaagggcttcccaattccggttaacaacggaaccatttccaaggt 172
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Arabidopsis thaliana chromosome III clone IGF-F11A12, ***
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                                                                                                            /product="6-phosphogluconate dehydrogenase"
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/db_xref="G1:603221"
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                                        /tissue_type="cell suspension culture"
7. .1467
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                                                                                                                                                                                                                                                                                                                                                                                                       /note="24 A nucleotides"
'db_xref="taxon:56147"
'clone="019"
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will

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Zea mays 6-phosphogluconate dehydrogenase isoenzyme B mRNA, partial
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             of 22087 bp in length
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gap of unknown length
contig of 13139 bp in length.
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of 2962 bp in length
                                                           of 2072 bp in length
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             22087:
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JOURNAL

TITLE

FEATURES

CDS

JOURNAL

REFERENCE AUTHORS

SOURCE

TITLE

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URL:http://www.dna.affrc.go.jp:82/, Tel:81-298-38-7441, Fax:81-298-38-7468)

The orientation of the sequence is from SP6 to T7 of the PAC clone. Genes were predicted from the integrated results of the Genes were predicted from the integrated results of the following:GENSCANI.0, BLASTX.0 as well as SplicePredictor (October 1998 version). The genomic sequence was sparched against the non- redundant database NRP (PIR. SWISSPROT, GENBERT, DBB) from MAFF DNA bank and the cDNA sequence database at RGP. Protein similarities of the coding regions were searched against NRP with BLASTP2.0. ESTS represent the identified cDNA sequences using BLASTP2.0. ESTS represent the identified cDNA and RGP clone ID. This sequence of this clone has an overlap with POS41H01 clone, DDDJ:ADDJ:ADDJSALTANI.0 and CASTPANI.0 with the corresponding DDBJ accession no.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGEEGVRERASSGAGDGASHIRCPCSSPPTLLGKSGTPPSGVRGRERESGGIGEMKSM
APTSVBLLRSAGSAGEEVELAGSGGPSLLTGKSEEVAVAHEEGARGHRIRQAAVSSAA
TPGPDGHRVRPPPADVTTRRGIRREEAPASGPTDVVCAAMRRGLMVAAAVPPPPRRP
TPHRRHLPTSTFNHRHYYPCWLRRSREGKRAAAEREVEGRAAETPLPASEVRENK
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join(2761. 3848,5363. 5544,5878. 5959,6846. 7125)
/note="hypothetical protein"
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PWECRYADEFTALAAASSLGEFINCPKNLRNDDAGPWSLHLPAATACLSMESCWYSVR
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                                                                                                                                                                                                                                                                                                                                                                                                 This clone ends at the position 26,826 of P0541H01. Detailed information on overlap and assembly quality together with annotation of this entry at annotation of this entry at http://www.dna.affrc.go.jp:82/genomicdata/GenomeFinished.html. Location/Qualifiers
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/note="hypothetical protein"
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/codon_start=1
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15374. .15492)
/note="hypothetical protein"
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/db_xref="GI:7363270"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Oryza sativa"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/chromosome="6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MALTRIGLAGLAVMGONLALNIAEKGFPISVYNRTTSKVDETVQ
RAKARGNLPYYGFHDPASFVNSIQKPRVVIMLVKAGAPVDQTIATLAAHLEQGDCIID
GGNERYENTERREKAMEERGLLYLGMGVSGGGEGARNGPSLMPGGSFDAYKYVEDIVL
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                                                                                Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.

1 (bases 1 to 634)
Padegimas, L. S. and Reichert, N.A.
Isolation of genes and regulatory sequences implicated in hypersensitive response from Zea mays nematode-resistant line MP307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="6-phosphogluconate dehydrogenase isoenzyme B"/protein_id="AAC79950.1"
/db_xref="G1:3925225"
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                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (06-DEC-1997) Department of Plant and Soil Sciences,
Mississippi State University, Box 9555, Mississippi State, MS
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
clone:P0029D06
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AP001552
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26.3%; Score 60.2; DB 7; Length 634;
Best Local Similarity 67.1%; Pred. No. 1.6e-07;
Matches 100; Conservative 0; Mismatches 48; Indels
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Sasaki,T., Matsumoto,T. and Yamamoto,K. Direct Submission
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Padegimas, L.S. and Reichert, N.A.
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/db_xref="taxon:4577"
100. .>634
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                                               Zea mays.
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                                                                          Zea mays
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VERSION
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
TITLE
                                                                          ORGANISM
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                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
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KEYWORDS

RESULT

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LOCUS

SOURCE

CDS

LTR

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/translation="MOIEPTWHQCIVQWQGDKIEIVPANREQSCSRRRLGTAAPTRRP
DIPPLSPPESRRPTLPAASAAAPSRQPPRPASGQRHSISGSGSALRLSGLRI"
J1897. 21769
/note="5", LTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RYLLROGIA-ROGINET BESINDRONFALLAND VOOL SOLUTION AGEN THE VAROLL OKQUIRCCSMETRY SCILKELGDEN'A LIADESSDISHKEQLVVCLARTYDRADGNILITSPRI OKQVIRCCSMETRSCILKTELGDEN'A LIADESSDISHKEQLVVCLARTVDKLGGYCGRE LAVVHVAGTSSLQLKTALGOSLLTSHILTTOTHGGOTDGASNMKGEVKGKOWLPNIEG OYSRLLNIVGTSSLQKRDADGLATSHILTTOTHGGOTDGASNMKGEVKGKOWLPNIEG OYSRLLNIVGTSTERDMLENDYRAQKIKKA LANLGETASGGSLNOEMALARDEDTRNGS GYTNEFONSLORDODLYNMASJVGTSKRWOONDRINGERGGIGKTSTSCIKYSIDIP AMDAKYVPHGREGHEYPYQTIDDHYRREVYTGVIENINGESTLGKYTSFCIKYSIDIP AMDAKYVPHGREGHEYPYQTIDDHYRREVYTGVIENINGELENNFDESVSMELLLCWARNOENSTRADGNINGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNNIGGIGNGNAGNIGGIGNNIGGI
DGGDRREDGDSRRRGRRHIAATRMRGAAARARGREGEGVLTGVRPATREETTTNGDAA
                                                             ELQDTLREEMREVRGREGVHGEREPWPTAAAMEGLTGTRRTTAFDGGIRWRRGRRAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(29217. .30334,31321. .31609,31701. .31862))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation-"MEKSSIALLFQKHEAKKNACDLFIPHVDEGSSIPAVNDAPIDED
IVVDEGVCEETEEDTVVDDAPPPDVVVDEVSIETKEESLPIYDVDDLEHDPGLRVPIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFDANDQDAARRGY ILKGPCHLMAFNFPSRK IYGKDRRFSVIWFHKYPWIEYSVDKDA
TFCEVCYLFGKESGKFVTGGWHNWNVGAKALDKHVGGTSSDHNFAQEKYNLFVKKGCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LYKCKWQLGDPSKRTLSLRCSAPQNIPDRMRYLGCSYGYLIFSYYENCLLVDWYTGAK
VKPPKLQSAGNKETYYG ILTAPLNLPISHLLLCSRSSIFYWQYGTNSKSEHPEGERI
LQIYLFKGEFFAMDFHHRLHTWRFAPQLSWQEYGYVWGEEMFYGVHFKPWLVISGDMI
LMLDLSYGIHHSYGFPGTFQVFRLDFSAQTAKWMKWEKLENSALFYSLDRRNPTFSCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="WYOIKIKKKKRDEVLVATRLGEKVESLQALRHUGRVSGDDDAGE
RRPLRRCRRAQCGPKSKVGLDWLGLPWIITSLTHPPPRLASTPIGRAAAAAAVATAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSSPAHPGKLRVSKRSWTGAAGSGSGEDHGRRRRRPSPRQRSSPLSAKGLMDSMLHQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IALLSSFQDLLAFSGTCRSWRAALSSFPSIYTFTFPPLHLKPDIPNSHPHCSSFRYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NPERWGGKSNCIYVAKPSEDSDEPWTAVELGQPIPGATHCVPYSHPLLRTEGHCSQLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="c1:7363276"
/translation="MQSPSKVSEASGSAPPATSVIEGWAELPEGLLHSIVALLGSFLD
LLAFTGTCHGWRAARSSYPSKSNFRTILPPLLVRPNVRVKAPYSSNGHRKLRSCEVID
LANNNTPLRCQIPQETLQRMHFAGSSHGQLICCRRGYCLVVDVFTGAEVSPPRLPFSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCDEFYYCGILTAPITSPNSHLIISTQSSLEDWPVGSDSWSELKLPVNRVDQIVEFNG
QLIAVIEYSLYTLQLAPILKLEKIKTLWWDNMNECPYMRPWFVVCGDMLLIVDHYISF
SFGAPVLYRPYRLDMSTKPAKWVEVKKLENWALFIGGDARSPPFSFKNPERWGGRSNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYYAHYSQPLSLHGLGDDADAVWDPNTDDNLVFKRNWYRQLQALWVYPSMFYSAGDGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(34717. .34935,35401. .35912,36242. .36363,36470. .36542,36626. .36754,36936. .37247,37336. .38617,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(21843. 22489,22572. 23072,23168. 24293)
/note="Similar to Arabidopsis thaliana DNA chromosome 4,
BAC clone F1788; putative protein. (AL049482)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38724. 39212))
/note="Similar to Arabidopsis thaliana DNA chrmosome V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAC clone TM021B04; N. tabacum membrane-associated salt-inducible protein. (AF007271)"
                                                                                                                                                                            join(19096. .19172,20123. .20329,20389. .20395)
                                                                                                                          SGGRRSGKGGGGRNDRGHGRERWKEEKGGEECGEAL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32671. .33849
/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                             /protein_id="BAA93017.1"
/db_xref="G1:7363273"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/protein_id="BAA93018.1"
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/db_xref="G1:7363275"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="BAA93021.1"
/db_xref="GI:7363277"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="GI:7363274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNCLVTFIERDMYMRKT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEWYLPSFINGVDO"
                                                                                                                                                                                                                                                                                /codon_start=1
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/note="3' LTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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LTR

CDS

CDS

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GKLNDMLMFYANYRRDIVPSTSVFNFNYSSLOKOKLHGKVTHLWEOMLEANVAPNOF
TYTVYIGSYAREGMLEEAMDAFGEMKRRRFVPEEATYSLLISLCAKHGKGEEALGLYD
EMKYKSIVPSNYTCASVLTLYKNEDDYSKALGLSESMEONKYTVPDEVITYGLIVRIYGK
LGLYEDAQRMFREIDRAGLLSDEOTYVAMAQVHMYONYDRALOYLDAMRARNYFSQ
FSYSALLRCHVAKEDVDAAEDTFRALSNYGPPDVFCCNDLLALYMRLGHLDARRALII.
WARREALQFDEDLCVTYLEVCCKTSINKDTDNLTEVIONEGSSSKYLNPTDSSTLSM
                                                                                                                                                                                                                                     LKSLLDKPGGLSSVSQLIMKFREGSTDEAKFLYEHLTELGAKPDDTAIJTLIVQYGQ
AQQLEGAQKLEETASTSFPVGGSVINAMVDALCRCGKTEEAYRLFMELLDQGHNGDAV
ISILVTHITKQEKFQPERNIIYRCLHDEAELDYVVNTFIKSMLESGLDNYFLLAVS
IYDRMISSGIPREMOTFNIMISVYGQGKLEKADYFWYNTSTRGHLESGLDNYFLLAVS
YGKAGLHNEAEIIFQEMQKNNHVPDSHTYLALIRAYTEGKCYSKAEERIQMALKSNNT
PSCTHFNHLISAFLKEGQIDEAQRMYNQMEERGIFALLRAYTEGKCYSKAEERIQMALKSNNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(40023 .40413.40774 .40971,41292 .41464,
41783 .42027,42111 .42288,42719 .42901,43197 .43301,
44137 .44274,44361 .45353)
/note="ESTS C74776(E51022),C26123(C116681) correspond to a
                                                                                                                                                                                                                                                                                                                                                                                                                          LFFETACRLIKPDSFILSAAFHLYEHSGRESEAGDVLDAINNSGASFLRNLKYGSKLE
QIQPKWWSIVKSGPLFPQKAHGVPLKYKQRSPWCCSVEQVVAREGEVDAAQRFGSRDA
VVAAVRAARATASCSSPSSADMREAMASFVAKLTFREMCFVLHELRGWRQARDFFAWM
                                      KLQLCYEPSVVAYTILLRIYGQVGKVKLAEVTFLEMLQAGCEPDAVACGTLLCAYARW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPPVAAQGRRRRSSESVDSAPQNEGFSDDDDSCSVSQESAHNFHGGRGGTTÄAQEGRR
AQVVTFGVTEDSRYESKEFDDVSEQYVAVTKKEKRGRTCSRCGKRKWESKESCTVCDA
RFCSYCVLRAMGSMPEGRKCITCIGQPIDESKRSKLGKGSRILSRLLSPLEVRQILKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation-"magagavggsnwBEMvRRmLPPGTTIPEAPANLDYSIALEYDGP
PVSYELPRIDPVDLPAIPTAQPVSGPLVPGRSNGVVAPVVRPVFMPPVHRKQDAHRAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKECQANQLRPEQLIINGFPLNPDEMASLLSCQRPPQKLKPGRYWYDKESGLWGKEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
1 (bases 1 to 1686)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF061838 1686 bp mRNA PLN 08-JUN-2000
Zea mays strain W64A x A182E putative cytosolic 6-phosphogluconate
dehydrogenase (pdh2) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A (uses 1 to 1000)

Nitrate regulation of the oxidative pentose phosphate pathway in maize (Zea mays L.) root plastids: induction of 6-phosphogluconate dehydrogenase activity, protein and transcript levels Plant Sci. 134 (2), 129-140 (1998)

(bases 1 to 1686)

Redinbaugh, M.G. and Bailey-Serres, J.
Characterization of cDNAs encoding cytosolic and a putative plastidic 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50458 ACTAGAATTGGTCTTGCTGGCCTTGGGGTCATGGGGCAGAACCTTGCCCTCAACATTGCA S0517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 acaagaataggccttgctggattggctgttaatgggcaaaatctggcactcaatattgct 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 tgaaaagggcttcccaattccggttaacaacggaaccatttccaaggttattgggccata 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            region of the predicted gene.
Similar to Arabidopsis thaliana cultivar Landsberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.3%; Score 60.2; DB 8; Length 150120; 64.2%; Pred. No. 1.8e-07; iive 0; Mismatches 58; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50577 TCAGCGCGCAAGGTAGAAAGCTTCCTGTGTACGGGTTCCA 50621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 agacgaagcaaaccaggaaggaaaccttcaatttatggggaacaa 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             extra-large G-protein (AF060942)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="BAA93022.1"
/db_xref="G1:7363278"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVHDHVQRYDSSTCD"
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plastidic 6-phosphogluconate dehydrogenase
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25.1%; Score 57.4; Di
Best Local Similarity 64.2%; Pred. No. 1.1e
Matches 102; Conservative 0; Mismatches
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Padegimas, L.S. and Reichert, N.A.
                                                                                                                                                                                                                                                                                                      /strain="W64A x A182E"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                      /organism="Zea mays"
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1 (bases I to 1818)
Redinbaugh, M.G. and Campbell, W.H.
Nitrate regulation of the oxidative pentose phosphate pathway in maize (Zea mays L.) root plastids: induction of 6-phosphogluconate dehydrogenase activity, protein and transcript levels plant Sci. 134 (2), 129-140 (1998)

2 (bases I to 1818)
Redinbaugh, M.G. and Balley-Serres, J.
Characterization of CDNAs encoding cytosolic and a putative
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RAKABGNLPVYGFHDPASFVKSIQKPRVVIMLVKAGAPVDQTIATLAAHLEQGDCIID
GGNEWYENTERREKAMEERGLLYLGMVVSGGEEGARNGPSLMPGGSFEAYKVVKDIVL
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Zea mays strain W64A x A182E putative cytosolic 6-phosphogluconate
dehydrogenase (pdh1) mRNA, complete cds.
                                               Tobses 1 to 1686)
Redinbaugh, M.G., Campbell, W.H. and Bailey-Serres, J.
Direct Submission
Submitted (28-APR-1998) USDA, ARS/Dept. Plant Path., OARDC/OSU, 1680 Madison Ave., Wooster, OH 44691, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 acaagaataggccttgctggattggctgttaatgggcaaaaatctggcactcaatattgct 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="NADPH producing dehydrogenase of the oxidative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49; Indels 1; Gaps
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25.6%; Score 58.6; DB 7; Length 1686;
Best Local Similarity 66.4%; Pred. No. 4.9e-07;
Matches 99; Conservative 0; Mismatches 49; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pentose phosphate pathway; PGD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAC27703.1"
/db_xref="G1:3342802"
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                                                                                                                                                                                                                                                                                /strain="W64A x A182E"
/db_xref="taxon:4577"
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99. .1547
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.

1 (bases 1 to 2392)
Padegimas, L. S. and Reichert, N.A.
Isolation of genes and regulatory sequences implicated in hypersensitive response from Zea mays nematode-resistant line MP307
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/db_xref="G1:3342800"

/translation="MALTRIGLAGLAVMGONLALNIAEKGFPISVYNRTTSKVDETVO

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GGNEWFWTBERREAMERGLIZLGMGYSGGEBGARNGPSLAMGGSFBAYKIEDILL

KVAAQVPDSGPCVTYIGKGGSGNFVKNVHNGIEYGDMQLIABAYDVLKSVGKLTNSEL

KVAAQVPDSGPCVTTIETTADIFGIRDDNGEBYLDWKUJAKTGMKGTGKWTVQDABE

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LVDPEFAQERIDRAGAANRTVVCLAINNGVSTFGMSAGIAYFDSYRRDRLPANLVQAQR
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Pred. No. 1.1e-06;
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/translation="MALTRIGLAGLAVMGONLALNIAEKGFPISVYNRTTSKVDETVO
RAKVEGNLFVFGFHDPASFVSSIQKPRVVIMLVKAGAPVDQTIATLAAHLDQGDCIVD
GGNEWYENTERREKAMEERGLLYLGMGVSGGEEGARNGPSLMPGGSFEAYKYIEDILL
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Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
1 (bases 1 to 645)
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Zea mays 6-phosphogluconate dehydrogenase isoenzyme A mRNA, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MALTRIGLAGLAVMGQNLALNIAEKGFPISVYDRTTSKVDETVQ
RAKVEGNLFVFGFHDPASFVSSIQKPRVVIMLVKAGAPVDQTIATLAAHLDQGDCIVD
                                                                                                                                                                                                         /product="6-phosphogluconate dehydrogenase isoenzyme A"
/protein_id="AAC79957.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1867 ACGAGAATTGGCCTCGCCGGCTCGCGGGTCATGGGACAGAACCTTGCCCTCAACATCGC- 1925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="6-phosphogluconate dehydrogenase isoenzyme A"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 tgaaaagggottcccaattccggttaacaacggaaccatttccaaggttattgggccata 184
Submitted (06-DEC-1997) Department of Plant and Soil Sciences. Mississippi State University, Box 9555, Mississippi State, MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
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Isolation of genes and regulatory sequences implicated
hypersensitive response from Zea mays line MP307
                                                                                                                                                                                                                                                                                                                                                                                                                                    25.1%; Score 57.4; DB 7; Length 2392; 64.2%; Pred. No. 1.1e-06; Live 0; Mismatches 56; Indels 1
                                                                                                                                                                                                                                                                                                                                                               7 others
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/db_xref="G1:3925223"
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                                                                                                     /organism="Zea mays"
/db_xref="taxon:457"
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                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                  KVAAQVPDSGPCVTYIGK"
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                                                                                                                                            1858. .>2392
/note="6pgdh(A)"
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/note="6pgdh(A)"
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Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Brassicales; Brassicaceae; Arabidopsis.
1 (bases I to 11122)
Shinn, P., Khan, S., Brooks, S., Buehler, E., Chao, Q., Dunn, P., Kim, C., Walker, M., Altafi, H., Araujo, R., Conn, L., Conway, A.B., Gonzalez, A., Hanssen, N.F., Huizar, L., Kremenetskaia, I., Lenz, C., Li, J., Liu, S., Davis, R. W., Federspiel, N.A., Theologis, A. and Ecker, J. B.
Genomic sequence for Arabidopsis thaliana BAC F22C12 from
GGNEWYENTERREKAMEERGLLYLGMGVSGGEEGARDGPSLMPGGSFEAYKYIEDILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (16-JuL-1999) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA (bases 1 to 11122)
Chao, Q., Brooks, S., Buehler, E., Johnson-Hopson, C., Khan, S., Kim, C., Shinn, P., Altafi, H., Bel, B., Chin, C., Chiou, J., Choi, E., Conn, L. Lee, J., Lenz, C., Li, J., Liu, A., Howing, B., Koo, T., Lam, B., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Palestspiel, N., Theologis, A. and Ecker, J., Davis, R.,
Direct Submission
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Submitted (09-JUN-1999) Arabidopsis thaliana Genome Center,
Department of Biology, University of Pennsylvania, 38th Street and
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
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                                                                                                                                                                                                                                                                                                               120 ACGAGAATTGGCCTCGCCGGCCTCGCGGTCATGGGACAGAACCTTGCCCTCAACATCGC- 178
                                                                                                                                                                                                                                                                 65 acaagaataggccttgctggattggctgttaatgggcaaaaatctggcactcaatattgct 124
                                                                                                                                                                                                                                                                                                                                                                           125 tgaaaagggcttcccaattccggttaacaacggaaccatttccaaggttattgggccata 184
                                                                                                                                                                                                                                                                                                                                                                                                                      179 GGAGAAAGGGTTCCCCATCTCGGTCTACGACAGGAACCTCCAAGGTTGATGAGACCGT 238
                                                                                                                                                                                                                            1; Gaps
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Genomic sequence for Arabidopsis thaliana BAC F22C12 from
                                                                                                                                                             24.4%; Score 55.8; DB 7; Length 645; 63.5%; Pred. No. 3.3e-06;
                                                                                                                                                                                                                         57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 agacgaagcaaaccaggaaggaaaccttcaatttatggg 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 GCAGCGCCAAGGTCGAAGGAACCTCCCAGTGTTTGG 277
                                                      117 t
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                      KVAAQVPDSGPCVTY IGK'
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FEATURES

COMMENT

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LCFKDBDELKKTVDWGSIRGRQKCVVRETEKDKYTFECIRWKCKWSLDAARLEEHGLV
BITKCNTPHTCCPIGPDNYDVEFAADEIECLIRVQPTLTIEELRNWWFENFGDMLATS
BROAARQENYTKKYFGWDDQSFRYLPNIMAAFHSSNGLVVDWOYKLFPPNEFASFRSVF
WAFPQSIEGFOHCRPLIVVDTKDLKGKYPMKLMIASGVEADDCYFPLAFAFTTEVSSD
TWWWFLSGIREKYTQRKDICLISRPHPDILDVINEPGSQWQEPWAYHMFCLDDICTQF
HYVFQDDYLKNILVYEAGSTSKKEEFDSYMNEIEKKNGEARKKULDQFPQYQWAQHDSG
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YTKPVMDQLEKLMTDSIPHVVMPLEKGLFQVTEPLQEDEWIYQLSEWSCTCGEFQLKK
PCHYLAVOFCKEKKINPLQYUDDCYSLDRLYKTAATFSPVPEVAAMPEASGVPTLFP
PVILPPPNVSGKSQWKTTPRTINDKAKVPPSDEELRNAIVDILKYVDLKTTALADVIK
RLVNVPVFCCWNGCIKDGTNGIYYEGSNYRMTTVKGKTKFNELLDHLYQVTGLDRKRS
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VIDPATCSSPSDILGGSSKRQKTDIHVKLERETDRNSESDGVVHLVDSSTLNKDSISG
HVSKPCMSSLMLDDHDLRVGLCFKDGDELKKAVDWCSLKAQQKCVVRETAKDEYIFEC
IRWKCKWSLGAARMKKHGLVEIIKYTGPHTCHPIVPEDFKSEFETDEIERAVRYMPTQ
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DAANKYFPLAFAYTKEVSTDIWRWFLIGIREKVTQRKGLCLISSPHPDIIAVVNESGS
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QRITQQEIVDNNSGSAGILVKVVNSGALKPCLLPRLMIDDDHDMHLGLCFKDRDELKK
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CDQSFEDLPKLMAAIHSSNGLLVDWKYDLFPNPKFASFRGVFWAFSQSIEGFHHCRPL
IIVDTKNLNCKYQWKLMIASAYDAADNFFLLAFATTELSTDSWRWFLSGIRERYTQR
KGLCLISSPDPDLLAVINGSGSQWQDPWAYNRFCLRHLLSQFSGIFRDYYLEDLVKRA
GSTSQKEEFDSYMKDTEKNUSEAKKWLDQFPQNQWALAHDNGRYGIMEIETTTLFED
FNVSHLDNHVLTGYVLRLFDELRHSFDEFFCFSRGSRKCGNYYTEPYTEKLAESRKDS
VTYDVWPLDNNAFQYTAPQENDEWTVQLSDCSCTCGFEQSCKFPCHALAVCKLIKIN
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IKLVELYLEVKSTSEGVIDPAACSSPLENLGSSLKRQRTQEATGYVTHSSVKLERVNG
LKVQGVDNSNGWIEDEADAALGNGSTHGYVDREMTNKNSGSDGVEQVYTLIANNAESR
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LISTPSWTVVLMAMETLREHVMLLCYTNACIKYGSDGVYYEGSSPKKIRVKRNTEFNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(979. .3122,3735. .5930,6862. .6892,6983. .7068,7655. .9286,9346. .10019,10228. .10279,10673. .10816,11047. .13429,13585. .13835,14366. .14645))/note="similar to maize transposon MuDR mudrA protein isolog gill946355"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QTCLDVVNSGLKISTECCKFLKEQQPCLCDVTKTSKIKTNVLSSRLKSCVVFLSRDD1
Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J.,
                       Liu,S., Mukharsky,N., Nguyen,M., Palm,C., Pham,P., Sakano,H., Schwartz,J., Southwick,A., Thaveri,A., Toriumi,M., Vaysberg,M., Yu,G., Davis,R., Federspiel,N., Theologis,A. and Ecker,J. Direct Submission
                                                                                                                                                                                                                 Submitted (28-JUN-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA on Jul 16, 1999 this sequence version replaced 91:5030434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAF24584.1"
/db_xref="G1:6692119"
                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .111222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product-"F22C12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="F22C12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /chromosome="1
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join(20892. 20993,21210, 21310,21520, 21694,21780. 21976,
22063. 22162,22282. 22387,23017. 23183)
/note="similar to vacuolar ATPase 91,3600058"
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AELSVAAPTIAASLDCRYLSGLKDERENAAKVLREAGLKEEIGSASSGIDKKRLVDDV
RQALYASKICSYAQGMNLLRAKSLEKSWNLNFGELARIWKGGCIIRAVFLDRIKKAYQ
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IIDGGNEWYQNTERRISEAEGKGLLYLGMGVSGGEEGARNGPSLMPGGSFQAYDNIKD
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GGVFLVTIHPPPDYPFKPRYAFRTRVFHPNVNSGSICLDIIKEGWSPALTISKVLL
SIGSLICTPROPDDPLVPETHAMYKTDRAKYESTARSWTQKYAMG"
complement(join(18031, .18617,18685, .19861)) '
/note="putative receptor kinase emb[GAA23040.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="G1:662117"
/translation="MOIFLFFFSLICFVLISSQTLEDDKRALLHFLSSFNSSRLHWN
/translation="MOIFLFFFSLICFVLISSQTLEDDKRALLHFLSSFNSSRLHWN
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DFPSDFTNIKSLTHTYLQHNILSGPLLAIFSELKNLKYLDLSNNGFNGSIPFSLSGTN
SLOVLNLANNSFSGEIPNLHLPKLSQINLSNNKLIGTIPKSLQRFQSSAFSGNNLTER
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KRLKEVVVGRREFEQQMEIIGMIRHENVAELKAYYSKDDKLAVYSYYNHGSLFEILH
GNRGRYHRVPLDWDARLRIATGAARGLAKIHEGKFIHGNIKSSNIFLDSQCYGCIGDV
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VPTGGENMDLASWIRSVVAKEWTGEVFDMEILSQSGGFEEEWVEMLQIGLACVALKQQ
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KKAKVHAPEIIVDKDIFLPFAPSDDDPHALSCAGGVVLASRDGKIVCENTLDARLEVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRNKLPEFCSKGSFLEMCVDPKVALRQGWCSLMSDSNFITKEKLRDAKSMNPTGRRCP
DPNGVEKKSMCYSSCKTQGFMGGSCQGHKGNYMCECYEG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EAEKKKIRQEYEKKEKQVDVRKKIDYSMQLNASRIKVLQAQDDIVNAMKEEAAKQLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KK<u>Ö</u>RKTPFGLSQLAFLLILSAACVLCVSGLSFIMITCFGKTRISGKLRKRDSSSPPGN
                                                                       RVFGDEDQSFRVMPKLISAFHSSNGLLVDWQYDLFPNPDFASFRGVFWSFSQSIEGFQ
HCRPLIVVDTKSLNGKYQLKLMIASGVDAANKFFPLAFAVTKEVSTDSWRWFFTKIRE
                                                                                                                                                      KVTQRKDLCLISSPLRDIVAVVNEPGSLWQEPWAHHKFCLNHLRSQFLGVFRDYNLES
                                                                                                                                                                                          LVEQAGSTNQKEEFDSYMNDIKEKNPEAWKWLDQIPRHKWALAHDSGLRYGI1EIDRE
                                                                                                                                                                                                                             ALFAVCRGFPYCTVAMTGGVMLMFDELRSSFDKSLSSIYSSLNRGVVYTEPFMDKLEE
                                                                                                                                                                                                                                                                     FMTDSIPYVITQLERDSFKVSESSEKEEWIVQLNVSTCTCRKFQSYKFPCLHALAVFE
                                                                                                                                                                                                                                                                                                    KLKINPLOYVECYTYDEOYCKTYAATFSPVPDVAAWPEDCRVPTLFPPSQOLSPNT" complement(join(15674. .15817,15904. .16008,16075. .15196, 11703. .17102)
//note="similar to ubiquitin-conjugating enzyme E2-17 Kd splp35135; similar TO ESTS gb!R84048, gb!T45251, gb!AA041165, gb!T21697, emb|Z29145,
AVDWWCIRRRRNCIVRETEKEMYTFECVRWKCKWSLRAARMEEHGLVEITKYTGPHTC
                                       SHEYPNDFESEFAADEIERVVRIQPTLSIAELKKWWKEKTGYELQTSKMRDGKLEVIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23882. .25345
/note="putentive 6-phosphogluconate dehydrogenase
dpl BAA22812: similar to ESTs emb[F15308, emb[15307, qb]T21894, qb]A1997770.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental/product="F22C12.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAF24559.1"
/db_xref="G1:6692094"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAF24560.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAF24583.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAF24582.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ERPHIAQVLKLIEDIRSVDAE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="F22C12.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="F22C12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb|T20867"
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ANLVQAQRDLFGAHTYERTDRPGAYHTEWTKLARKNH"

CDS

62048 AICTCGCATAGGICTCGCCGGICTCGCAGICAIGGGACAAAACCICGCCTTAAACAICGC 61989

Op δλ

184 aagacgaagcaaaccaggaaggaaaccttcaatt 217

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complement(join(25806. .26028,26204. .26373,26722. .28161,
28379. .28489,28868. .29284))
/note="Mypothetical protein"
/codon_start=1
/evidence=not_experimental
                                                                                                                                                                                                                      ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sato,S., Kotani,H., Nakamura,Y., Kaneko,T., Asamizu,E., Fukami,M., Miyajima,N. and Tabata,S.
Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence features of the 1.6 Mb regions covered by twenty physically assigned Pi clones
                                                                                                                                                                                                                                                                             Db 23899 ATCCCGAATCGGTCTCGCCGGACTCGCCGTGATGGGCCAAAACCTCGCCTTAAAACATCGC 23958
                                                                                                                                                                                                                                                                                                                                                                       23959 -CGAGAAAGGTTTCCCAATCTACAATCGAACCACTTCCAAAGTCGACAAAGCC 24017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AB005233 79837 bp DNA PLN 20-NOV-1999
Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone: MBK23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (02-JUL-1997) to the DDBJ/EMBL/GenBank databases. Yasukazu Nakamura, Kazusa DNA Research Institute, Laboratory of Gene Structure 2; 1532-3, Yana, Kisarazu, Chiba 292, Japan (E-mail:Yunakamu@kazusa.or.jp, Tel:+81-438-52-3935,
                                                                                                                                                                                                                                                   64 aacaagaataggccttgctggattggctgttaatgggcaaaatctggcactcaatattgc 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui plclone:MBK23.
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                             124 ttgaaaagggcttcccaattccggttaacaacggaaccatttccaaggttattgggccat 183
                                                                                                                                                                                                                 1; Gaps
                                                                                                                                                              22.9%; Score 52.4; DB 7; Length 111222; 63.0%; Pred. No. 3.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 50.8; DB 7; Length 79837; Pred. No. 0.00011; 0; Mismatches 57; Indels 1;
                                                                                                                                                                          Pred. No. 3.8e-05;
N. Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 24018 TAGATCGAGCGCCGTCGAAGGAAACCTCCCAGT 24051
                                                                                                                                                                                                                                                                                                                                                                                                                                       184 aagacgaagcaaaccaggaaggaaaccttcaatt 217
                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Mitsui Pl"
25977 a 14362 c 13908 g 25590 t
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                                                                                                               /product="F22C12.6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="MBK23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AB005233.1 GI:2264305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 79837)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.2%;
                                                                                                                                                                               Local Similarity 63.09
nes 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .79837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AB005233
                                                                                                                                                           Query Match
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AB005233/c
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Administration of traineres, catallilli, nowillillate; nowil.

By Stren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo saptens chromosome 17, clone hRPK.502_F_1

Upublished

2 (bases 1 to 170453)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,

Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Berow, A.,

Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A.,

Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K.,

Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C.,

Funke, R., Gage, D., Galagan, J., Howland, J.C., Jones, C., Kann, L.,

Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J.,

Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J.,

Marduis, J., Niloff, M., O'Connor, T., O'Donnell, P., Paviln, B.,

Peterson, K., Pollara, W., Riley, R., Roberts, D., Roy, A., Severy, P.,

Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A.,

Tesfaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A.,

Nirele, T., Wu, X., Wyman, D., Ye, W.J. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Micretet Submission

Micretet Submission

Micretet Submission

Submitted (20-FEB-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 170453)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Carny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dazrellano, K., Depayre, E., Devon, K., Dewar, K., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Jones, C., Karatas, A., Lehoczky, J., Lieut, C., Locke, K., Macdonald, P., Marduis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Maloff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stolanovic, N., Stone, C., Subramanian, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J. and Zody, M., Wagner, A., Derberts, A., Dermer, J., Naman, D., Ye, W. J., and Zody, M., Dermer, A., Dermer, J., Naman, D., Ye, W. J., and Zody, M., Dermer, J., Nermer, J.
                                                                                                                                                  Homo sapiens chromosome 17, clone hRPK.502_F_1, complete sequence.
AC006600
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (28-FEB-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 1, 1999 this sequence version replaced 9:4309870.
All repeats were identified using RepeatMasker: Smit, A.F.A. 6 Green, P. (1996-1997)
                                                                                                                28-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://ftp.genome.washington.edu/RM/RepeatMasker.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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/clone="hRPK.502_F_1"
                                                                                                                                                                                                                                     AC006600.4 GI:4309964
                                                                                            170453 bp
                                                                                                 AC006600
                                                                                                                                                                                                                                                                                                                                            human.
RESULT 12
AC006600/c
                                                                                                                                             DEFINITION
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                                                                                                 LOCUS
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ij

Gaps

1;

64 aacaagaataggccttgctggattggctgttaatgggcaaaatctggcactcaatattgc 123

1 Similarity 62.3%; 96; Conservative

Local

Matches

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/clone_lib="RPCI-11 human BAC library"
/map="17"
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/rpt_family."MIR"
complement(16804. 16875)
/rpt_family="L2"
18053. 18195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(11335, .11458)
/rpt_family="MER69A"
complement(11619, .11674)
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complement(593..1090)

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1477. 1635

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2171..2861

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Gaps

16.7%; Score 38.2; DB 10; Length 170453; 53.7%; Pred. No. 0.64; tive 0; Mismatches 68; Indels 0;

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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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144986 184799: contig of 39814 bp in length.
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32881 32980: gap of 100 bp

32881 41040: contig of 8060 bp in length

41041 41140: gap of 100 bp

41141 48535: contig of 7395 bp in length
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122840 144885: contig of 22046 bp in length
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86256: contig of 14218 bp in length
                                                                                                                                                                                                                                                          2144 2243: gap of 100 bp
2244 6178: contig of 3935 bp in length
6179 6278: gap of 100 bp
6279 10043: contig of 3765 bp in length
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32880: contig of 5499 bp in length
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    . 2143
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    244. .6178

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG 26-WAR-2000 HOMO sapiens chromosome 17 clone RP11-45J24 map 17, WORKING DRAFT SACHES, 17 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON Mar 26, 2000 this sequence version replaced g1:6751809. All repeats Were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
       Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                  1819 GAAGGAAAAGAGAGTTATTGTGGACAAGAGTCCCTATGAGCAAAGTAATTGGCAATGAGA 1760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center clone name: 45_J_24

Center clone name: 45_J_24

Sequencing vector: M13, M7815; 96% of reads
Sequencing vector: Plasmid; n/a; %-0.f%% of reads
3.81991814461119Chemistry: Dye-terminator Big Dye; 100% of
                                                                                                                128 aaagggetteceaatteeggttaacaaeggaaeeattteeaaggttattgggeeataaga 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently * consists of 17 contigs. The true order of the pleces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality coverage: 3.8 in Q20 bases; agarose-fp Quality cov.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assembly program: Phrap; version 0.960731
Consensus quality: 164567 bases at least Q40
Consensus quality: 174814 bases at least Q30
Consensus quality: 179219 bases at least Q20
Insert size: 182000; agarose-fp
Insert size: 183199; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 184799)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 17, clone RPI1-45J24
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                                                                                                                                                                                                                                                                                                                        1759 GTATTTCCAACAGAAAGGCCCCTCTCA 1733
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                                                                                                                                                                                                                                               188 cgaagcaaaccaggaaggaaaccttca 214
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2 (bases 1 to 184799)
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reads

human.

ORGANISM

REFERENCE AUTHORS

JOURNAL REFERENCE

TITLE

AUTHORS

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RESULT 13 AC015724/c

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woulin, P., Crepineau, F., Kloareg, B. and Boyen, C.
Isolation and characterization of six cDNAs involved in carbohyrate
biosynthesis in Laminaria digitata (Phaeophyta) - Utilization of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - CNRS UPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                          37009 AAAAGAGCCTCTCTCTTTATCTGTGAAAGAGCAAAAATCCTCCTCACCTTGCCTGG 36950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 aaagggetteecaatteeggttaacaaeggaaceattteeaaggttattgggeeataaga 187
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Submitted (16-NOV-1998) Boyen C., Laboratoire de Biologie
Moleculaire et Cellulaire des Algues, Station Biologique -
9042, BP 74, 29682 Roscoff cedex, FRANCE
                                                                                                                                                                                                                                                                                                                               Length 184799;
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Laminaria digitata mRNA 6-phosphogluconate dehydrogenase.
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/gene="6PGDH"
/EC_number="1.1.1.44"
/codon_start=1
/product="6-phosphogluconate dehydrogenase"
                                                                                                                                                                                                                                               1608 others
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6-phosphogluconate dehydrogenase; 6PGDH gene.
                                                                                                                                                                                                                                                                                                                          Score 38.2; DB 38;
Pred. No. 0.64;
0; Mismatches 68;
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/db_xref="taxon:80365"
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          /note="assembly_fragment"
72039. 86256
72039. 86256
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86357. .100509
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100610. .122739
7note="assembly_fragment"
122840. .144885
7note="assembly_fragment"
144966. .184799
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1. .3158
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68. .1660
56231. .71938
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53.7%;
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Laminaria digitata
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Best Local Similarity 53.7'
Matches 79; Conservative
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LDI130772
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Submitted (06-JUN-2000) to the EMBL/GenBank/DDBJ databases on May 5, 2000 this sequence version replaced gi:7242501.

IMPORTANT: This sequence is unfinished and does not necessarly represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage, etc. . even if efforts are made to eliminate these contaminating sequences. The following BAC sequence is oriented
                                                                                                                                                         AERSTAAPTWAAALDARYMSGRKGERVEAAKTLKGFST IPQVPKAQLIEDMKAALYCS
KCSYAQMULIKAASEHFEWGVDLGECRIWKGGCIIRAAFLDDIKNAYIKNADLDN
LLVDPFITSQILEROAMRRVVTLCVASGAAPAARAVVTLOVASG
RDFFGAHTYERVDKEGVFHCLWDDTHKEIATSPAHGGRTLIGSLENLFRPLCMGCLM
                                           /translation="MSASALSDVGLYCLAVMGONFALNMASHGFSVSVSNRSPEKVDA
TVARAKEEGNLPLRGFKDPKSFVDSLSKPRKIVLLVQAGAAVDATIATLSELLEEGDI
LVDGGNEWFPNSQRRAKELEPKKIMFVGMGVSGGEEGARNGPSLMPGGPREAYDALSP
                                                                                                                IISKCAAQVDGPCTTYLGSIGSGNYVKMVHNGIEYGDMQLIAEVYDVLKHVAGLTNDE
LSATFTDMNQGELQSFLIEITAVIFSRKDDLTSSGHVVDKILDKTGMKGTGRWTVQEA
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of library RPCI-11 from chromosome 14 of Homo sapiens (Human),
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 206247)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 taggoottgottgattggotgttaatgggoaaaatottggoaotcaatattgottgaaaag 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 TIGGECTCTATGCCTTGGCGGTCATGGGACAGAACTTCGCGCTCAACATGGCGAG-CCAC 151
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Upstream BAC (overlapping the T7 end) : R-718G2
Downstream BAC (overlapping the SP6 end) : R-1023122
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                                                                                                                                                                                                                                                                            630 t
                                                                                                                                                                                                                                                                                                                                                                   16.2%; Score 37.2; DE ilarity 56.3%; Pred. No. 1.2; Conservative 0; Mismatches
/protein_id="CAB61332.1"
                                                                                                                                                                                                                                                         SSTVVSVAYCGMKYYIGSLSFT"
                   /db_xref="GI:6453557"
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Range : bases
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63683
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Search completed: November 4, 2000, 13:33:25 Job time: 17054 sec

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November 4, 2000, 11:52:01; Search time 4352.3 Seconds (without alignments) 582.439 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                 7189864 seqs, 3091403243 residues
                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                     OM nucleic - nucleic search, using sw model
                                                                                                                                                  IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                         US-09-300-482-14
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Maximum DB seq length: 200000000
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117: qb_qss18:*
118: qb_qss10:*
119: qb_qss10:*
120: qb_qss20:*
121: qb_qss21:*
123: qb_qss22:*
124: qb_qss22:*
125: em_qss14:*
126: em_qss14:*
127: em_qss16:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ipt	E363077 DG	E216/05 HV_C	130bl MCGU	E493869 WHE1	W563648 LG1_	53025 DG1_9	4610 SCU0	970 RICR28	97862 WHE0	97880 WHEO	DAST WHEU	14643 SCHO	76879 1.61	6839 LG1	36858 LG1	77090 DG1_	33238 WHEO	50009 AV551	26953 AV52	94267 WHE1	08515 AUU6	4720 ML10	19/8/ LJNE	2211/ SM0/112. 5081/ FCT/0170	AW586409 EST318032	65745 MtBA02B1	65743 MtBA02B0	95821 NF099E09	88619 NF009F08	0243 sm42	99197 EST30600	96464 NXCI_018	5410 EST317	41175 EST34527	8880 MTD011.H	58600 MtBA25E0	5788 AV425788	58071 MtBA22A0	8	50451 EST31549	406682 AV4066	er O
ID	BE36307	BE21670	BE41306	BE49386	AW56364	BE36302	BE41461	D24970	BE49786	BE49788	BE42523	BE4	AU29667	AW28683	AW28685	AW67709	BE40323	AV55000	AV52695	BE49426	AU06851	AW25472	AW/L9/B	BE02211	AW58640	AL36574	AL36574	AW69582	AW68861	BE02024	AW29919	BE49646	AW58541	BE34117	BE42886	AL36860	AV42578	AL36807	AL38284	AW5604	AV40668	C7442
DB	35	34	35	9 6	23	35	35	36	36	36	3	36	3 5	7.5	21	23	35	19	19	36	15	21	4.5	3.2	0 6	14	14	24	23	32	21	36	23	32	32	14	18	14	14	23	18	36
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ALIGNMENTS

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Eukāryota; Virīdiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; Liliopsida; Poales; Poaceae; Sorghum.
1 (bases 1 to 530)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Dark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
                                                                                                                                                                                                                                                                                                                                                                                                Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                 Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt
 BE363077 530 bp mRNA EST 20-JUL-2000
DG1_9_F06.b1_A002 Dark Grown 1 (DG1) Sorghum bicolor CDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 GITGICALCATGCITGICAAGGCIGGIGCACCAGTIGACCAGACCAITGCGACGCICGCA 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
20-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 84.6%; Score 346.8; DB 35; Length 530; Best Local Similarity 91.7%; Pred. No. 9.4e-81; Matches 366; Conservative 0; Mismatches 33; Indels 0;
                                                                                                                                                                                                                                  An EST database from Sorghum: dark-grown seedlings Unpublished (2000)
Contact: Cordonnier-Pratt MM
Department of Botany
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High quality sequence stop: 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                  Email: mmpratt@uga.edu
                                                                        BE363077.1 GI:9304634
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BE216705 729 bp mRNA EST 25-JUL-2000
HV_CEb0011E16f Hordeum vulgare seedling green leaf EST library
HVCDNA0005 (Erysiphe infected & control) Hordeum vulgare cDNA clone
HY_CEb0011E16f, mRNA sequence.
                                                                                                                                                                                   Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.

1 (bases 1 to 729)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo Wood, T., Saski, C., Schwartzbeck, J., Slmmons, J., Choi, D.W., Main, D. and
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                                                                                                                                                                                                                                                                                                             Development of a genetically and physically anchored EST resource
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100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
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88.0%; Pred. No. 1e-74;
tive 0; Mismatches
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/db_xref="taxon:4513"
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High quality sequence stop: 678.
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Unpublished (2000)
Contact: Wing RA
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Matches 352; Conserva
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BE413061 886 bp mRNA EST 24-JUL-2000
MCG015.E05R990625 ITEC MCG Barley Leaf/Culm Library Hordeum vulgare
CDNA clone MCG015.E05, mRNA sequence.
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Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.
1 (bases 1 to 886)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anderson, O. A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Larmann, R.G., Holton, T., Jacquenin, J.M., Jia, J., Joudrier, P., Langridge, P., Lazo, G. R., Lin, J.J., McGuire, P., Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warburton, M. and Wenzel, G.
International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 gtacaacaggacaacctccaaggtggacgagaccgtgcagcgtgccaaggcagaaggaaa 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 egeggtcatggggcagaaccttgccctcaacattgcagagaaagggttccccatctgt 70\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
358 AGAAAGGAGGAGAAGGCGATGGAGGAGCGTGGACTCCTCTACCTCGGTATGGGTGTTTC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.0%; Score 323.8; DB 35; Length 886; 88.0%; Pred. No. 1.1e-74; ive 0; Mismatches 48; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="MCG015.E05"
/clone_lib="TTEC MCG Barley Leaf/Culm Library"
/tissue_type="leaf/culm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Institute for Plant Genetics & Crop Plant Research Corrensstr. 3, D-06466 Gatersleben GERWANY Tel: 49 39482 5521 Fax: 49 39482 5137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: a_graner@ipk-gatersleben.de
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
                                            186 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="etiolated"
224 c 258 q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 88.0°
Matches 352; Conservative
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                                                                                                                                                                                                                                                                                                                                                              barley.
Hordeum vulgare
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Gundblished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.
1 (bases 1 to 466)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="WHE0284_C07_E14"
/clone_lib="Wheat drought-stressed seedling cDNA library"
/tissue_type="Seedling Without endosperm"
/dew_stage="Five old seedling"
/lab_host="E. coll SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The structure and function of the expressed portion of the wheat genomes – Drought stressed seedling cDNA library
Close, T.J., Fenton, R.D., Han
                                                                                                                                                                                                              BE471136 466 bp mRNA EST 28-JUL-2000 WHE0284_C07_E142S Wheat drought-stressed seedling cDNA library Tritticum aestivum cDNA clone WHE0284_C07_E14, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                         Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., He'S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Stratagene SK primer.
                                                                          371 tggaggaaaggaggtgcccgcaacggcccgtccttgatg 410
                                                                                               /organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cultivar="Chinese Spring"
/db_xref="taxon:4565"
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BE471136.1 GI:9561627
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BE493869 547 bp mRNA EST 02-AUG-2000
WHE1276_F08_K16ZS Secale cereale anther cDNA library Secale cereale
CDNA clone WHE1276_F08_K16, mRNA sequence.
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/dev_stage="Anther"
/dev_stage="Anther"
/lab_host="E. col; Sour"
/note="Vector: Lambda Uni 2AP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown in the
greenhouse. Anthers were harvested and pooled from early
meiosis to late meiosis. The tissue, total RNA, and
poly(A) RNA were prepared (Butler, Ross and Gustafson) at
University of Missouri, Columbia. A CDNA library was
made, and the cDNA clones were in vivo excised to give
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US Department of Agriculture, Agriculture Research Service, Pacific
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( bases 1 to 547)
Anderson, O.D., Butler, E., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Gustafson, J.P., Han, P. S., Hsia, C. C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Ross, K., Seaton, C.L. and Tong, J.C. The structure and function of the expressed portion of the wheat
                                                49 GGCGTCATGGGCCAGAACCTTGCCCTCAACATTGCAGAGAAAAGGGTTCCCCATCTCTGT 108
                                                                                                                                               131 ccttcccgtctacggcttccatgaccccgcgtcctttgtgaagtccattcagaagccacg 190
                                                                                                                                                                              251 ageteaettggageaggggggaetgeategatggggggaacgagtggtaegagaaeee 310
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Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
Location/Qualiflers
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/clone="WHE1276_F08_K16"
/clone_lib="Secale cereale anther cDNA library"
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800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
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Contact: Olin Anderson
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11 cgcggtcatggggcagaaccttgcctcaacattgcagagaaagggttcccatctcgt 70

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Query Match

78.2%; Score 320.6; DB 35; Length 466;
Best Local Similarity 87.5%; Pred. No. 6.6e-74;
Matches 350; Conservative 0; Mismatches 50; Indels 0;

/db_xref="taxon:4558"

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pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
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Sorghum bicolor

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; Liliopsida; Poales; Poaceae; Sorghum.

1 (bases 1 to 519)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW563648 519 bp mRNA EST 19-JUL-2000
LG1_245_A11.bl_A002 Light Grown 1 (LG1) Sorghum bicolor cDNA, mRNA
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                                                                                                                                                                                                                                                                                                                                      71 gtacaacaggacaacetecaaggtggacgagaccgtgcagcgtgccaaggcagaaggaaa 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 agctcacttggagcagggggactgcatcatcgatgggggaacgagtggtacgagaacac 310
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Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C. and Pratt,L.H.
An EST database from Sorghum: light-grown seedlings
Unpublished (2000)
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                                                                                                                                Ouery Match 77.8%; Score 319; DB 36; Length 547; Best Local Similarity 87.2%; Pred. No. 1.8e-73; Matches 349; Conservative 0; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           371 tggaggaaaggaggtgcccgcaacggcccgtccttgatg 410
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Fax: 706 542 1805
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/organism="Sorghum bicolor"

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/clone_lib="Light Grown 1 (LG1)"
/roto="Organ: 10- to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site_1: XhoI; Site_2: EcoRI
The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
I dayanoliophyta; Liliopsida; Poales; Poaceae; Sorghum.
1 (bases 1 to 516)
Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt
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                                                                                                                                                                                                                                                                                                                                                        cttcccgtctacggcttccatgaccccgcgtcctttgtgaagtccattcagaagccacgg 191
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The University of Georgia
The University of Georgia
The University of Georgia
The Toto 542 1860
Fax: 706 542 1805
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                                                                                                                                                                                    76.7%; Score 314.6; DB 23; Length 519; 91.7%; Pred. No. 2.5e-72; Live 0; Mismatches 30; Indels 0;
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High quality sequence stop: 516
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Contact: Cordonnier-Pratt MM
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below Phred quality 16. The
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BE363025.1 GI:9304582
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                                                                                                                                                                                                                         Matches 332; Conservative
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0
                               /do xref="taxon:4558"
/db xref="taxon:4558"
/clone_lib="Dark Grown 1 (DG1)"
/note="Organ:5-day-old dark grown seedlings; Vector:
Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Centre for Plant Conservation Genetics, Southern Cross University PO Box 157, Lismore NSW 2480 AUSTRALIA
Tel: 61 2 6620 3409
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCGGTCATGGGGCAGAACCTTGCCCTCAACATTGCAGAAAAGGCTTCCCCATCTCTGTC 215
                                                                                                                                                                                                                                                             72 tacaacaggacaacetecaaggtggacgagaccgtgcagcgtgccaaggcagaaggcaaae 131
                                                                                                                                                                                                                                                                         132 cttcccgtctacggcttccatgaccccgcgtcctttgtgaagtccattcagaagccacgg 191
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                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                              gcggtcatggggcagaaccttgccctcaacattgcagagaaagggttccccatctctgtg 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE414610 743 bp mRNA EST 24-JUL-2000
SCU011.F01.R990714 ITEC SCU Wheat Endosperm Library Triticum
aestivum cDNA clone SCU011.F01, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                              Query Match 76.5%; Score 313.6; DB 35; Length 516; Best Local Similarity 91.7%; Pred. No. 4.5e-72; Matches 331; Conservative 0; Mismatches 30; Indels 0;
                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Triticum aestivum
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AUTHORS
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.
1 (bases 1 to 456)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    333 AACGCTCGCAGCACCACCTGGAGCAGGGGGGACTGCATCGTTGATGGAGGGAACGAAGTGGT 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 CCCCCGGGCTGCAGGAATTCGGCACGAGCTCGCCCTCAACATTGCGGAGAAAGGGTTCCC.152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 catetetgtgtacaacaggacaacetecaaggtggacgagaccgtgcagcgtgccaaggc 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa cDNA clone R2869_1A, mRNA
                                                                                 1...743
/organism="Triticum aestivum"
/oultivar="Wyuna"
/db_xref="taxon:455"
/clone="SCU011:F01"
/clone_lib="TPEC SCU Wheat Endosperm Library"
/tissue_type="endosperm"
/nsue_type="endosperm"
/note="Vector: Bluescript II SK(-)"
/note="Vector: Bluescript II SK(-)"
/note="Vector: Bluescript II SK(-)"
                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                  Score 295.2; DB 35; Length 743; Pred. No. 3.1e-67; 0; Mismatches 65; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 tgggtgtctctggaggaaaggaggtgcccgcaacggcccgtccttgatg 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minobe, Y. and Sasaki, T.
Rice CDNA from root
Unpublished (1995)
Contact: Vazo Minobe
National Institute of Agrobiological Resources
Email: tholton@scu.edu.au
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/qenome.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rice Genome Research Program
2-1-2 Kannondai, Tsukuba
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Best Local Similarity 83.9%;
Matches 344; Conservative
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Tel: 0298-38-7441
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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US Department of Agriculture, Agriculture Research Service, Pacific
US Department of Agriculture, Agriculture Research Service, Pacific
USES Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.

Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.

I (bases 1 to 472)

Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J.,
Seaton, C.L. and Tong, J.C.

The structure and function of the expressed portion of the wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE497862 472 bp mRNA EST 04-AUG-2000 WHE0957_D04_H07ZS Wheat pre-anthesis spike cDNA library Triticum aestivum cDNA clone WHE0957_D04_H07, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252 gctcacttggagcagggggactgcatcatcgatggggggaacgagtggtacgagaacacg 311
                                                                                                                                                                                                                                                                                                                                                                                                                            70 GCGGTCATGGGGCAGAACCTTGCCCTCAACATTGCAGAAAAGGGTTCCCTATCTCTGTC 129
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                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                            DB 36; Length 456;
                                                                                                                 /strain="Nipponbare, sub_species Japonica"
/db_xref="taxon:4530"
/clone="R26621A"
/clone="lib="Rice root"
/note="Prepared from seedling root."
104 c 130 g 112 t 3 others
                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 55; Indels
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                                                                                                                                                                                                                                                                                                      70.8%; Score 290.4; DB 3
85.6%; Pred. No. 5.2e-66;
                                                                                                /organism="Oryza sativa"
Fax: 0298-38-7468
Email: minobe@rtcs0.riken.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            372 ggaggaaaggaggtgcccgcaacggcc 399
                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                  Query Match 70.8%
Best Local Similarity 85.6%
Matches 332, Conservative
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                                                                                 1. .456
                                      PROJECT = 'RGP'
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                                                                                 source
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                                                          FEATURES
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Fax: 5105595818

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/UNIQUISHE TITLICUM aeSILVUM"
/UNIQUISHE "TITLICUM aeSILVUM"
/UD xref="taxon:4565"
/Clone="WHEED957_LOA_LH07"
/Clone="WHEED957_LOA_LH07"
/Clone="Lib="Whee pre-anthesis spike cDNA library"
/Lissue_type="Spike before anthesis"
/Lissue_type="Spike before anthesis"
/Act_stage="Adult plant"
/Lab_host="E. coll SOLR"
/Abb_host="E. coll SOLR"
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/Iab_host="E. coll SOLR"
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/Iab_host="Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performéd in the OD Anderson lab (all other authors)."
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Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.
1 (bases 1 to 474)
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WHE0957_B09_D17zS Wheat pre-anthesis spike cDNA library Triticum
aestivum cDNA clone WHE0957_B09_D17, mRNA sequence;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 CGCCGTCATGGGGCAGAACCTTGCCCTCAACATTGCAGAAAGGCTTCCCCATCTCTGT 171
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                     Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Stratagene SK primer.
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70.8%; Score 290.2; DB 3
Best Local Similarity 87.8%; Pred. No. 5.9e-66;
Matches 316; Conservative 0; Mismatches 44
                                                                                                                                                                   /organism="Triticum aestivum"
                                                                                                            Location/Qualifiers
Email: oandersn@pw.usda.gov
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                                     Unpublished (2000)
Contact: Olln Anderson
Contact: Oll Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: Tambda Uni-ZAP XR, excised phagemid; Site_1: EcoRI; Site_2: XhoI; Plants were grown in the greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors).
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The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library
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                                                                                                                                                                              Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                         /clone_1b-"WHE0957_B09_D17"
/clone_lib-"Wheat pre-anthesis spike cDNA library"
/tissuc_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
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                                                                                                                                                                                                                                                                                                    /organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
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                                                                                                                                        Tel: 5105595773
                                                                                                                                                             Fax: 5105595818
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1...31. /organism="Triticum aestivum" / organism="Triticum aestivum" / oultivar="Chinese Spring" / dultivar="Chinese Spring" / fultivar="Chinese Spring" / downson:4565" / clone_lib="Wheat unstressed seedling shoot cDNA library" / clone_lib="Wheat unstressed seedling shoot cDNA library" / tissue type="Fitolated shoot" / dev_stage="Five day old seedling" / lab_host="E. coli SOLR" / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole / sole
                                                                                  Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.

1 (bases I to 512)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han ...,P.S., Haia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.
The structure and function of the expressed portion of the wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
West Area, Western Regional Research Center
Tel: 5105595773
Tel: 5105595718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 agotcacttggagcagggcgactgcatcgatggggggaacgagtggtacgagaacac 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 AGCACACCTGGAGCAAGGTGACTGCATCGTTGACGGAGGAAACGAGTGGTATGAGAACAC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 ggagaggaggagaaggccatggaggagggcgcctnctgtatcttggcatgggtgtctc 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 CGCGGTCATGGGCCAGAACCTTGCCCTC-ACATTGCCGAGAAA-GCTTCCCCATCTCTGT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 cgcggtcatggggcagaaccttgccctcaacattgcagagaaagggttccccatctctgt 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: oandersn@pw.usda.gov
Sequence have been trifmmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.4%; Score 288.6; DB 35; Length 512; 85.8%; Pred. No. 1.6e-65;
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                                              Triticum aestivum
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bread wheat
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Matches 320;
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/tissue_type="Anther"
/dev_stage="Anther"
/dev_stage="Andit plant before anthesis"
/lab_host="E. coli SOLR"
/lab_host="E. coli SOLR"
/lab_host="E. coli SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI: Site_2: XhoI; Plants were grown in the
greenhouse. Anthers were harvested and pooled from early
melosis to late melosis. The tissue, total RNA, and
poly(A) RNA were prepared (Butler, Ross and Gustafson) at
University of Missouri, Columbia. A cDNA library was
made, and the cDNA clones were in vivo excised to give
pBluescript phagemids in the TJ Close lab (Choi, Close,
Fenton) at the University of California, Riverside.
Plasmid DNA preparations and DNA sequencing were performed
in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                  BE495944 454 bp mRNA EST 02-AUG-2000
WHE1259_B05_C092S Secale cereale anther cDNA library Secale cereale
cDNA_clone WHE1259_B05_C09, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
TH: 510559573
Fax: 5105595818
                                                                                                                                                                                                                                                                                                                                                                                            Secale cereale
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Secale.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anderson, O.D., Butler, E., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Gustafson, J.P., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Ross, K., Seaton, C.L. and Tong, J.C.
The structure and function of the expressed portion of the wheat genomes - Anther cDNA library from rye
99 CGCCGTCATGGGGCAGAACCTTGCCCTCAACATTGCGGAGAAAGGCTTCCCCCATCTCTGT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
Location/Qualifiers
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                                                                   /organism="Secale cereale"/cultivar="Blanco"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:4550"
/clone="WHE1259_B05_C09"
                                                                                                                                                                                                                                                                                                   BE495944
BE495944.1 GI:9662537
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BE495944
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Manollophyta; Liliopsida; Poales; Poaceae; Triticum.

I (bases 1 to 781)

Anderson, O. A. Appels, R., Bailey, P., Blake, T., Close, T., Cloutier S., Dubcovsky, J., Feuillet, C., Gale, M., Jia, J., Joudirer, P., Laro, G. R., Lih, J.J., McGuire, P., Ogihara, Y., Langiade, P., Lazo, G. R., Lih, J.J., McGuire, P., Ogihara, Y., Sorrells, M., Warburton, M. and Wenzel, G., Shariflou, M., Sorrells, M., Warburton, M. and Wenzel, G. International Triticeae EsT Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae Unpublished (2000)

Contact: Holton T Censervation Genetics, Southern Cross University Po Box 157, Lismore NSW 2480 AUSTRALIA

Fax: 61 2 6620 2409
251 agctcacttggagcagggggactgcatcgatggggggaacgagtggtacgagaacac 310
                                                                                                                                                                                                                                                        79 ggacaacctccaaggtggacgagacgtgcagcgtgccaaggcagaaggaaaccttcccg 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE414643 781 bp mRNA EST 24-JUL-2000 SCU011.H10.R990714 ITBC SCU Wheat Endosperm Library Triticum aestivum cDNA clone SCU011.H10, mRNA sequence.
BE414643.1 GI:9412489
                                                                                                            191 ggtggtgatcatgctcgtcaaggccggcgccagttgaccagaccatcgcgacgctcgc
                                                                                                                                                                                                                                                                                                                                          311 ggagaggaggaggagggccatggaggagcgccctnctgtatcttggcatgggtg 366
                                                                                                                                                                                                                                                                                                                                                                       399 CGAAAGGAGGAGAAAGCGATGGAGGAGCGTGGACTCCTCTACCTCGGGATGGGTG 454
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/clone_isCuO11.H10"
/clone_lib="TFEC SCU Wheat Endosperm Library"
/tissue_type="endosperm"
/note="Vector: Bluescript II SK(-)"
/note="Vector: Bluescript II SK(-)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: tholton@scu.edu.au
International Triticeae EST Cooperative (ITEC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://wheat.pw.usda.gov/genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cultivar="Wyuna"
/db_xref="taxon:4565"
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/clone_lib="Light Grown 1 (LG1)"
/clone_lib="Light Grown 1 (LG1)"
/note="Organ: 10- to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site_l: Xhol; Site_2: EcoRI
; The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
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                                                                                                                                                                                                                                                                                                                                                               AW286879 463 bp mRNA EST 19-JUL-2000
LG1_222_F04.bl_A002 Light Grown 1 (LG1) Sorghum bicolor cDNA, mRNA
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to exclude PolyA, vector and regions threshold for highest quality sequence
tcatgetegteaaggeeggegegecagttgaceagaceategegaegetegeageteaet 258
                                                                                                                                 gggagaaggccatggaggagcgcggcctnctgtatcttggcatgggtgtctctggaggaa 378
                                                                                                 404 GGGAGAAGGCGATGGAGGAGCGTGGACTCCTCTACCTCGGGATGGGTGTTTCCGGAGGAG 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .463
/organism="Sorghum bicolor"
/db_xref="taxon:4558"
                                                                                                                                                                                                                                                                                  464 AGGAGGGTGCCCGCCATGCCCATGATG 495
                                                                                                                                                                                                                                                                 379 aggagggtgcccgcaacggcccgtccttgatg 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: JEN REV
High quality sequence stop: 341
POLYA=No.
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below Phred quality 16. The
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The University of Georgia
Plant Sciences Building, Rm
Tel: 706 542 1860
Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                               AW286879.2 GI:6858816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mmpratt@uga.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                 AW286879
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AW286879
LOCUS
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COMMENT
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KEYWORDS
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AI783104

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AI622577 486058F10 AI711616 605058C06

A1947960 A1622577 A1711616 AQ844969

AW288562 AI745746

AL371121

AI896020 EST265463 AW288562 618067F10 AI745746 605076F04 AI947960 603031G04

AL371121 MtBA42A06

AU088734 575 bp mRNA EST 31-MAR-2000 AU088734 Rice shoot Oryza sativa cDNA clone S4976, mRNA sequence. AU031584 369 bp mRNA EST 30-OCT-1998 AU031584 Rice cDNA from immature leaf including apical meristem Oryza sativa cDNA clone E61890_2Z, mRNA sequence. AU031584 121 agctctatatttggcgctgcggacccaggagccatcatatctgtgctgaggagagcgtc 180 Gaps 0; Query Match
Best Local Similarity 83.2%; Pred. No. 1.3e-39;
Matches 183; Conservative 0; Mismatches 37; Indels 0; // State of the control of the contr 181 gagggctctcagaacaaaactgattttggtgtttctgct 220 Japan 305 Tel: 0298-38-7441 Fax: 0298-38-7468 Email: tsasaki@abr.affrc.90.jp Location/Qualifiers AU031584.1 GI:3767474 AU088734.1 GI:7378463 PROJECT ='RGP'. Oryza sativa. Oryza sativa S4976_8Z. Ibaraki, source DEFINITION ACCESSION VERSION KEYWORDS SOURCE DEFINITION ORGANISM BASE COUNT ORGANISM ACCESSION TITLE JOURNAL RESULT AU031584 VERSION KEYWORDS REFERENCE AUTHORS FEATURES COMMENT SOURCE ORIGIN g g δ g ŏ à

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D22889 RICC1720A R C98335 C98335 Rice C73011 C73011 Rice AL380932 MtBB55E04

AU088734 AU088734 AU031584 AU031584

AU088734 AU031584

C98335 C73011

SUMMARIES

AL380933 MtBB55E04 AW350186 GM210007B AW348508 GM210002B BE359923 DG1_58_DO BE034126 MG05C09 M

Oryza sativa.
Oryza sativa.
Oryza sativa.
Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Eukaryota, Viridiplantae; Poales; Poaceae; Oryza.
1 (bases 1 to 369)
Sasakl,T. and Yamamoto, K.
Rice cDNA from immature leaf including apical meristem
Unpublished (1997) Mayoristications and the second of the control of t ö REFERENCE AUTHORS TITLE JOURNAL

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C98335 499 bp mRNA EST 19-OCT-1998 C98335 Rice callus Oryza sativa cDNA clone C1720_62, mRNA sequence. C98335.1 GI:3761081
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Magnoliophyta, Liliopsida, Poales, Poaceae, Oryza.
1 (bases 1 to 499)
                                                                      /clone_lib="Rice callus"
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/note="Wector: pBluescript II SK+;,Site_1: SalI; Site_2:
/note="Wector: pBluescript II SK+ phagmid in the SalI-NotI site of pBluescript II SK+ phagmid."
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                                                /strain="cultivar Nipponbare, sub_species Japonica"
/db_xref="taxon:4530"
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/db_xref="taxon:4530"
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National Institute of Agrobiological Resources
Rice Genome Research Program
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Fax: 0298-38-7468
Email: tsasaki@abr.affrc.go.jp
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Rice cDNA from callus
Unpublished (1994)
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Sasaki, T. and Minobe, Y.
Rice cDNA from callus
Unpublished (1994)
Ontact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
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/note="Organ: leaf; immature leaf including apical
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Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
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Fax: 0298-38-7468
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1 (Dases 1 to 472)
Sasail, T. and Yamamoto, K.
Rice cDNA from panicle at flowering stage
Unpublished (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C73011 Rice panicle at flowering stage Oryza sativa cDNA clone E2703_2A, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 AGGTTGATGGTGTGTCTTGGTTCCACCATTGATGTGGCTGCATCTGCTGGGGCTAACT 65
                                                                                                                        Gaps
                                                                                           88 GAGAAAGAAGTACCCATCCCTTGACATCGAGGTGATGGTGGTCTGGGTCCTTCCACCAT 147
                                                                                                                                                                                    138 tgcggacccaggagccatcatatctgtgctgaggaagagcgtcgagggctctcagaacaa 197
                                                                                                                                                                                                    Gaps
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Pred. No. 2.8e-28;
0; Mismatches 31; Indels 0;
                                ö
    DB 36; Length 499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Rice panicle at flowering stage" /dev_stage="flowering stage"
                                 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program.
Score 150.2; DB 3
Pred. No. 2.6e-36;
0; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: tsasaki@abr.affrc.go.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="Nipponbare"
/db_xref="taxon:4530"
/clone="E2703_2A"
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                                                                                                                                                                                                                                                    198 aaactgattttggtgtttctgct 220
                                                                                                                                                                                                                                                                                268 AAGCTGATCTGTGGTTTTGTACT 290
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Best Local Similarity 82.2%;
Matches 143; Conservative
    47.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 c
                    Best_Local Similarity 83.74
Matches 170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 0298-38-7441
Fax: 0298-38-7468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa.
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         Query Match
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/note="Vector: pBluescript pSK: Site_1: ECORI; Site_2:
/note="Vector: pBluescript pSK: Site_1: ECORI; Site_2:
Xho1; Plants were grown in an aeroponic chamber on
nitrogen-rich medium for 21 days. Three days before
inoculation with Sinorhizobium meliloti, the medium was
inoculation with Sinorhizobium meliloti, the medium was
replaced by N-free medium. Root nodules (+ short adjacent
root segments) were harvested 4 days post inoculation.
CDNA was prepared from polyA+ enriched RNA. The CDNA was
directionally 1sqated into Uni-zap XR vector from
Stratagene and packaged using Giapack Gold packaging
extracts. Plasmids containing cDNA inserts were
mass-excised from phage stocks using Exassit helper phage
and propagated in SOLR cells. Clone ordering and
sequencing was performed by the Centre National de
Sequencage (Genoscope, Evry, France)."
Sequencage (Genoscope, Evry, France)."
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Medicago.
                                                                                                                                                                                                      AL380932 504 bp mRNA EST 03-AUG-2000
MLBB55E04F1 MtBB Medicago truncatula cDNA clone MtBB55E04 T3, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRX cedex - France
Email: seqref@genoscope.cns.fr
Contact: Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes Microspanismes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Journet, E. P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O., Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Glaninazzi-Pearson, V. and Gamas, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Medicago truncatula ESTs from Sinorhizobium meliloti-induced root
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email : Mt-estétoulouse.inra.fr Website
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="symbiotic root nodules"
/dev_stage="harvested 4 days post inoculation with
Sinorhizobium meliloti"
167 tgaggaagaggtcgagggctctcagaacaaaaactgattttggtgtttctgct 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.5%; Score 118.4; DB 14; Length 504; 74.5%; Pred. No. 2.1e-26; Live 0; Mismatches 51; Indels 0;
                              http://sequence.toulouse.inra.fr/Mtruncatula.html).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Medicago truncatula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:3880"
/clone="MtBB55E04"
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                                                                                                                                                                                                                                                                                                                                   AL380932.1 GI:9680684
                                                                                                                                                                                                                                                                                                                                                                                                                         Medicago truncatula
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61 ctaggtccttcaaccatagacgtggccgcatctgctggggccaattgcatcgtcggg 120

ò a ò qq δ g

121 agetetatatttggegetgeggaeceaggageeateatatetgtgetgaggaagagegte 180

181 gagggctctcagaacaaaa 200

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Anotes "Vector: Bilescript psk; Site_1: EcoRI; Site_2:
XhoI; Plants were grown in an aeroponic chamber on
nitrogen-rich medium for 21 days. Three days before
inoculation with Sinorbizobium meliloti, the medium was
replaced by N-free medium. Root nodules (+ short adjacent
root segments) were harvested 4 days post inoculation.
CDNA was prepared from poly4+ enriched RNA. The CDNA was
directionally ligated into Uni-zap XR vector from
Stratagene and packaged using Glapack Gold packaging
extratcs. Plasmids containing cDNA inserts were
mass-excised from phage stocks using ExAssit helper phage
and propagated in SOLR cells. Clone ordering and
sequencing was performed by the Centre National de
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Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Medicago.
                                                                                                                                                                                                                                                                                                                                                                         AL380933 542 bp mRNA EST 03-AUG-2000
MtBH55E04R1 MtBB Medicago truncatula cDNA clone MtBB55E04 T7, mRNA
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Genoscope - Centre National de Sequencage
BP 191 91006 ENFY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email:
MT-est@toulouse.inra.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Journet, E.P., Grespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O., Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Gianinazzi-Pearson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ,V. and Gamas,P. Medicago truncatula ESTs from Sinorhizobium meliloti-induced root
                                                        121 agctctatatttggcgctgcggacccaggagccatcatatctgtgctgaggaagagcgtc 180
239 TTAGGGCCTTCAACCATAGATGTGGCTGCATCAGCGGAGCGAATTGCATTGTTGCTGGA 298
                                                                                            /tissue_type="symbiotic root nodules"
/dev_stage="harvested 4 days post inoculation with
Sinorhizobium meliloti"
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Location/Qualifiers
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86 c 123 g 151 t
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/db_xref="taxon:3880"
/clone="MtBB55E04"
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                                                                                                                                                                          181 gagggctctcagaacaaaa 200
                                                                                                                                                                                                                               359 GAGAAATCACTGTAAACATA 378
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/clone="Gm-riol-104"
/clone="Gm-ri021-2639"
/clone_lib="Gm-ri021"
/tissue_type="root"
/lab host="Xil0-Gold"
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Xho1; Library Gm-ri021 is a sequence driven, reracked set of the original library Gm-cl04 which was prepared from root cDNA. The mRNA was isolated from entire roots of 8 day old 'Williams' seedlings which were propagated on paper towels with distilled water. Stratagene's cDNA Synthesis Kit (catalog #200401) was used to synthesize the cDNA. The Gm-cl004 library was constructed by Dr. Paul Keim & Virginia H. Coryell, Department of Biology, Box5640, Northern Arizona University, Riagateff, Az 86011
/ emmil: paul keim@nau. virginia.coryell@nau.edu. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Computational Biology
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 638)
Vodkin, L., Keim, P., Shoemaker, R., Retzel, E., Khanna, A., Coryell, V.,
Erpelding, J., Raph, C., Shoop, E., Pardinas, J., Liu, L. and Lewin, H.
Erpelding, J., Raph, C., Shoop, E., Pardinas, J., Liu, L. and Lewin, H.
Orpublished (1999)
Other_ESTS: A142690
Contact: Vodkin, L.O., PI, A Functional Genomics Program for Soybean (NSF 9872565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lewin, H. A., Director, Keck Center for Comparative and Functional Genomics
                                                                                                                AW350186 638 bp mRNA EST 01-FEB-2000 68010007910612R Gm-r1021 Glycine max cDNA clone Gm-r1021-2639 3', AW350186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA 1911: (217) 244-6147 Fax: (217) 333-4582 Email: 1-vodkin@uiuc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134. For further information call: (800) 430-0030 or (314) 427-3222 FAX:(888)919-3324 or (314) 427-3324 or contact:clones@genomesystems.com or info@genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ystems.com web site:www.genomesystems.com Seq primer: 5'-TTTTTTTTTTTTTTTTTTT(A/C/G)-3'.
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    .638
    /organism="Glycine max"

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228 GAGAAATCACTGTAAACATA 247
                                                                                                                                                                                                                                                                                             AW350186.1 GI:6847896
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Gaps

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51; Indels

Score 118.4; DB 14; Length 542;

.le-26;

Pred. No. 2.1e 0; Mismatches

Query Match 37.5%; Best Local Similarity 74.5%; Matches 149; Conservative

Query Match Best Local 3

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Magnoliophyta; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabalee; Fabaceae; Papilionoideae; Glycine.

[ (base 1 to 736) Vodkin, L., Keim, P., Shoemaker, R., Retzel, E., Khanna, A., Coryell, V., Erpelding, J., Raph, C., Shoop, E., Pardinas, J., Liu, L. and Lewin, H. A Functional Genomics Program for Soybean (NSF 9872565)

Contact: Vodkin, L.O., PI, A Functional Genomics Program for Soybean (NSF 9872565)
                                                                                                                                                                                                                                                                                                                             ö
http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html.
Reracking was performed by Genome Systems, St. Louis, http://www.genomesystems.com, and sequencing by the Keck Center for Comparative and Functional Genomics, University of Illinois, http://www.life.uiuc.edu/biotech/keck.html."

144 c 106 g 190 t 24 others
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Badyan R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
Tel: (217) 244-6147
Fax: (217) 333-4582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available through: Genome Systems, Inc. 4633 World barkway Circle St. Louis, Missouri 63134. For further information call: (800) 430-0030 or (314) 427-3322 FAX: (888) 919-3324 or (314) 427-3324 or contact:clones@genomesystems.com or info@genome
                                                                                                                                                                                                                                                                                                                                                                                                                61 ctaggtccttcaaccatagacgtggccgcatctgctggggccaattgcatcgtcgctgga 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 TTAGGGCCTTCAACCATAGATGTGGCCGCATCAGCAGGGGCAAACTGCATTGTTGCTGGA 212
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GM210002B12C3R Gm-r1021 Glycine max cDNA 3', mRNA sequence.

    gataaaggtgcgcacactgagaaagaagtacccttcccttgacatagaggttgatggtggt

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Pred. No. 1.2e-25;
0; Mismatches 50; Indels
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/db_xref="taxon:3847"
/clone_lib=@n=rl021"
/issue_type="root"
/lab_host="XL10-Gold"
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/note-"Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; Library Gm-r1021 is a sequence-driven, reracked set

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of the original library Gm-c1004 which was prepared from root cDNA. The mRNA was isolated from entire roots of 8 day old 'Williams' seedlings which were propagated on paper towels with distilled water. Stratagene's cDNA Synthesis Kit (catalog #200401) was used to synthesize the cDNA. The Gm-c1004 library was constructed by Dr. Paul Keim & Virginia H. Coryell, Department of Biology, Box5640, Northern Arizona University, Flagstaff, AZ 86011, email: paul.keim@nau.edu, virginia.coryell@nau.edu. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Computational Biology
                                                                                                                                                                                                                                                                     Centers, University of Minnesota,

The property of Minnesota,

Reracking was performed by Genome Systems, St. Louis,

http://www.genomesystems.com, and sequencing by the Keck
Center for Comparative and Functional Genomics,

Iniversity of Illinois,

http://www.lin.i. 29 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE359923 165 bp mRNA EST 20-JUL-2000
DG1_58_D09.g2_A002 Dark Grown 1 (DG1) Sorghum bicolor CDNA, mRNA
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Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
TTE: 706 542 1860
Fax: 706 542 1805
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1 (bases 1 to 165)
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High quality sequence stop: 163
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181 gagggeteteagaacaaaaactgatt 206
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Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta: dudioctyledons; core eudicots; Caryophyllidae;
Caryophyllales; Alzoaceae; Mesembryanthemum.
1 (bases 1 to 749)
Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M., Ferrea, H.K. Kawasaki, S., McColluogh, A., Michalowski, C.B., Palacio, C.,
Furctional Genomics of Plant Stress Tolerance
Unpublished (2000)
Contact: Michalowski, C.B.
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                                                 1..165'.

/Organism="Sorghum bicolor"

/db_xref="taxon:4558"

/clone_lib="Dark Grown 1 (DG1)"

/rote="Organ: 5-day-old dark-grown seedlings; Vector:

/note="Organ: 5-day-old dark-grown seedlings; Vector:

/note="Organ: 5-day-old dark-grown seedlings; Vector:

//note="Organ: 5-day-old dark-grown seedlings; Vector:

//note="Organ: 5-day-old dark-grown seedlings; Vector:

//note="Organ: 7-day-old dark-grown seedlings; Vector:

//note="Organ: 7-day-old dark-grown seedlings; Vector: 7-day-grown                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="5-6 weeks"
/note="grown in hydroponics, stress 400 mM NaCl (in 0.5
Hoagland's), 30 h stress"
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                                                                                                                                                                                                                                                                                                                                                                                                                DB 35; Length 165;
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/db_xref="taxon:3544"
/clone_lib="MG"
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 33.7%; Score 106.6; DB 35; Length Best Local Similarity 96.5%; Pred. No. 7.9e-23; Matches 109; Conservative 0; Mismatches 4; Indels
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An open reading frame exists.
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; endicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.

E (bases 1 to 483)

Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D.,
Rang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brasseka, P.,
Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R.,
Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T.,
Policky J., Suzuki, G., Argentine, C., Shah, S., Nobriga, A., Murry, L.,
Turner, C., Krikorian, S., Elder, L. and Hanson, D.
Arabidopsis thaliana Gene Expression MicroArray
Contact: David Smoller, Ph. D.
Genome Systems, Inc., a wholly owned subsidiary of Incyte
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/note="cDN library was made from selected clones from the mabidopsis thaliana Ohio State clone set."
109 c 111 g 133 t
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                                      121 agetetatatittggegetgeggaeeecaggageeateatatetgtgetgetgaggaagagegte 180
61 ctaggtccttcaaccatagacgtggccgcatctgctggggccaattgcatcgtcgctgga 120
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Fax: 314-427-3324
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/db_xref="taxon:3702"
/clone="701495920"
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Alarge Scale analysis of CDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected CDNA libraries
Contact: 7, 175-180 (2000)
                                                                                                                                                                                                               Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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                                                                                    mRNA EST 23-JUL-2000
thaliana roots Columbia Arabidopsis thaliana
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Kazusa DNA Research Institute
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/clone="RZ74e06F"
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/clobe_libran_a. thaliana, Columbia Col-0, rosette-3"
/tissue_type="rosette"
/dev_stage="d - 7 weeks"
/dev_stage="d - 7 weeks"
/note="Vector: pSPORT; Site_1: NotI; Site_2: SalI; CDNA
library was derived from untreated rosette tissue from
Arabidopsis thaliana, Columbia Col-0, at 4 - 7 weeks.
Plants were grown in 1:1:1 peat moss/vermiculite/perlite
soil at 22 deg. C +/- 3 deg. C under constant light, and
watered with fertilizer. CDNA synthesis was initiated
using a NotI-Oligo(dT) primer. Double-stranded cDNA was
blunted, ligated to SalI adaptors, digested with NotI,
size=selected, and cloned into the NotI and SalI sites of
the pSPORT vector."

64 a 160 c 123 g 168 t 4 others
                                                                                               Chen, J., Moniyama, M., Chan, E., Mooney, M., Carroon, B., Gillilland, D., Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P., Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T., Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobriga, A., Murry, L., Turner, C., Krikorian, S., Elder, L. and Hanson, D.
Arabidopsis thaliana Gene Expression MicroArray
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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10593 Lambda-PRL2 Arabidopsis thaliana cDNA clone 146H5T7, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4633 World Parkway Circle, St. Louis, MO 63134, USA Tel: 877-577-2733
Fax: 314-427-3324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"
/cultivar="Columbia Col-0"
                                       Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 619)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: service@genomesystems.com.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: David Smoller, Ph.D.
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1. .619
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Anote—"Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day gerninated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA.
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 317)
Newman, T., deBruiln, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, C.
                                                                                                                                                 Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones plant Physiol. 106, 1241-1255 (1994)
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Best Local Similarity 64.6%; Pred. No. 1.2e-17;
Matches 148; Conservative 0; Mismatches 80; Indels 1; Gaps
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                                                                                                                                                                                                                                                                                                                                Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg.,E.
                                                                                                                                                                                                                                                 On Apr 14, 1993 this sequence version replaced gi:692577.
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                                                                                                                                                                                                                                                                                Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7 dye primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Dogoriation	1 :	557311 486093	564778 LG1_301_	56 D43256 Ri	15297 EST39797	5534 EST28127	34861 NZ11008e	128 E	99786 EST310	43964 WHE112	56975 MtBA11	54881 ML13	55839 ML923	82995 EST242	, AWB010.	AV52249	EST304491	953823 nbeb00	SNAESTF09	AV551048	AZ046382 nbeb0085N	;182d02	IIT-HSP-	AU074940 AU074940	AU061833	9215	Tetra	175E	F1538U ATTS5628 G1 AT260448 T.D04319 5	2	528 70368	677 RPCI-23	4575 RPCI-2	748 B	5517	24 qh22h09.x	8320 Dros	905 E	1194 ox12h07	153 mp80h08.	21197 EST29/66	BE109286 UI-R-BJI-	31/40 UI-R-C4:	20509 cm44f04	0111000000
d.	1	AI65731	3 AW564	256	4 BE20529	9 AW03553	3 AW58486	5 AW93375	2 AW39978	5 BE44396	AL36697	AW25488	AW25583	11 AI482995	BE40008	8 AV52249	1 AW256424	113 AQ953823	7 L33519	9 AV551048	14 AZ0463	3 AW56984	0 AQ24032	5 AU07494	15 AU061833	2 AW484099	4 CNS05	6 BE52961	4	##007TU	21 CNS00	, '	AZ0645	9 B	_	AI217424	21	AA32790	AI034194	12	0 AW22119	33 BE109286	PITECMW 7	0.440	DE0703
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ALIGNMENTS

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                                                                                                 Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
1 (bases 1 to 573)
Walbot,V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW564778 423 bp mRNA EST 19-JUL-2000 LG1_301_C06.bl_A002 Light Grown 1 (LG1) Sorghum bicolor cDNA, mRNA
                                                                                                                                                                                                                                                                                      AI657311 573 bp mRNA EST 05-MAY-1999
486093C03.y1 486 - leaf primordia cDNA library from Hake lab Zea
mays cDNA, mRNA sequence.
AI657311. GI:4753401
                                                                                                                                               Maize ESTS from various cDNA libraries sequenced at Stanford University
University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbotestanford.edu
Email: walbotestanford.edu
C column: 03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
95.2%; Score 285.6; DB 12; Length 573;
Best Local Similarity 97.0%; Pred. No. 4.1e-79;
Matches 291; Conservative 0; Mismatches 9; Indels 0;
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AW564778
AW564778.1 GI:7218656
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Sorghum bicolor
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bukaryota; Vilidipsida; Poales; Poaceae; Sorghum.
1 (bases 1 to 423)
Cordonier-Pratt, M.-M., Gingle, A., Marsala, C. and Pratt, L.H.
An EST database from Sorghum: light-grown seedlings
Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:4558"
/clone_lib="Light Grown 1 (LG1)"
/folce="Organ: 10- to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site_l: XhoI; Site_2: EcoRI
; The library was made from poly-A RNA in the cloning
vector lambda Zap II. Clones to be sequenced were
prepared by mass excision."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                              Email: mmpratteuga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
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1 (bases 1 to 330)
Uchimiya, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D43256 330 bp mRNA EST 04-NAY-1998 D43256 Rice callus cDNA (H.Uchimiya) Oryza sativa cDNA clone SS131,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 aactggcaactactcttgtaattgtcatttctaagagcggaggcacacctgaaacccgca 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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Contact: Hirofumi Uchimiya
Institute of Mol. & Cell. Bioscience, Department of Cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 23; Length 423;
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                                                                                                                                                                                                                                                                                                                                                                    /organism="Sorghum bicolor"
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High quality sequence stop: 420
                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                 Department of Botany
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                                                                                                                                                                                  Tel: 706 542 1860
Fax: 706 542 1805
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1 (bases 1 to 550)
Fedorova, M., Pierson, B.L., Samac, D.A., Vance, C.P., Gantt, J.S., Peng, H., Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, T.E. and Fraser, C.M.
ESTs from one month old nitrogen-fixing root nodules of Medicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids I,
Fabales, Fabaceae, Papilionoideae, Medicago,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
Tel: 612-625-7219
Fax: 651-649-5058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 cttcagagatgcggggctgcaattctcgaaacagggtgttgcaattactcaagaaaattc 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 tctgttggataacactgctagaatagagggatggttagctcggttcctatgtttgattg 265
                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE205297 550 bp mRNA EST 27-JUN-2000
EST397973 KVO Medicago truncatula cDNA clone pkVO-21015, mRNA
                                                                                                                                                                                                                                                                                                                                                                   DB 36; Length 330;
                                                                                                                                                                                                                  /clone="SS131"
/Clone_lib="Rice callus cDNA (H.Uchimiya)"
/tissue_type="callus"
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                       32;
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University of Minnesota
                                      Tokyo 113, Japan
                                                                                                                                                                                                                                                                                                                                                            74.6%; Score 223.8; DB 3
88.4%; Pred. No. 8.8e-60;
tive 0; Mismatches 32
                 The University of Tokyo
1-1-1 Yayol, Bunkyo-ku, Tokyo 113, Japan
1-1-1 3-3812-2111(ex.7844)
Fax: 03-3812-2910
Email: huchimiya'gtansei.cc.u-tokyo.ac.jp
PROJECT= Uchimiya.
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More information is available at. .
                                                                                                                                                                            /organism="Oryza sativa"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: vance004@maroon.tc.umn.edu
                                                                                                                                                                                                                                                                                  84 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Carroll P. Vance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE205297.1 GI:8748593
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Email: mjharrison@noble.org
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                                                                                                                                                                                                                                                                                           /tissue_type="Seedling roots"
/dev_stage="Seedling roots"
/dev_stage="Imaediately prior to inoculation with
Sinorhizobium melilor! (0 hour)"
/lab_host="E. coli strain Solx"; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2:
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
1; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 419)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW035534 419 bp mRNA EST 15-SEP-1999
EST281272 tomato callus, TAMU Lycopersicon esculentum cDNA clone
cLEC39G17 similar to glucose-6-phosphate isomerase, putative, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 aactggcaactactcttgtaattgtcattctaagagcggaggagcacctgaaacccgca 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 atggtctactagaagtacagaaagccttcagagatgcggggctgcaattctcgaaacagg 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 AIGGCIIGITAGAAGIACAAAAGGCCITITCGIGAAGCAGGAIIGGAITICCCAAAACAGG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 gtgttgcaattactcaagaaaattctctgttggataacactgctagaatagaggatggt 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 tagctcggtttcctatgtttgattgggttggtggtaggacttcagaaatgtctgctgtgg 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 AGCTAGCTTCGACATTGTAATTGTGATTTCAAAGAGTGGAGGCACCCCTGAGACTAGAA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 GIGTIGCTATAACACAGAAAACTCTTIGTIGGATAACACTGCCAGAATTGAGGGATGGT 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 gatttattgacaacaccgatcctgctgggattgatcatcaaattgctcaactaggacctg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.1%; Score 210.4; DB 34; Length 550; 81.3%; Pred. No. 1.6e-55; Live 0; Mismatches 56; Indels 0;
           Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
                                                                                                                                      /organism="Medicago truncatula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: David Frisch
Clemson University Genomics Institute
                                                                                                                                                                       /cultivar="genotype A17"
/db_xref="taxon:3880"
http://chrysie.tamu.edu/medicago
                                                                                                                                                                                                                                              /clone="pKV0-21015"
                                                                                                                                                                                                                                                                               /clone_lib="KV0"
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AW035534.1 GI:5894290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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ORIGIN
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                                                                      FEATURES
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100 Jordan Hall, Clemson, SC 29634, USA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Medicago truncatula/Glomus versiforme mixed EST library.
Medicago truncatula/Glomus versiforme mixed EST library
Eukaryota; mixed EST libraries.

[ bases 1 to 670]
Harrison, M.J., Liu, J., Peng, H., Gonzales, M., Ellis, L., Town, C.D.,
Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and Fraser, C.M.
ESTS from roots of Medicago truncatula after colonization with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 gigtigcaattactcaagaaaattctcigtiggataacacigciagaatagagggaiggi 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 aactggcaactactcttgtaattgtcatttctaagagcggaggcacacctgaaacccgca 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           352 TGGCCAGATTCCCTATGTTTGATTGGGTGGCGGGAAGAACCTCAGAATGTCTGCAGTTG 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-APR-2000
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library cDNA clone MHAM-7H23, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292 GTGTTGCCATTACACAAGAAAACTCATTGACAACACTGCTAGAATTGAGGGTTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 208.8; DB 19; Length 419; Pred. No. 4.8e-55;
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                                                                                                                            /organism="Lycopersicon esculentum"
/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2510 Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-223-5810
Fax: 580-221-7380
                                                                                                                                                                                                                              /clone_lib="tomato callus, TAMU"
/tissue_type="callus"
/dev_stage="25-40 days old"
/lab_host="XL1-Blue MRF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Samuel Roberts Noble Foundation
                                                                                                                                                                               /db_xref="taxon:4081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA
                                                                          Location/Qualifiers
                                                                                                                                                                                                      /clone="cLEC39G17"
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW584861.1 GI:7261915
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Contact: Harrison M.J.
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81.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 243; Conservative
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                                                     5 prime sequence.
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Best Local Similarity
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TITLE
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                                                                                                                                                                                                                                                                                    /tissue_trype_man.
/tissue_trype_man.
/tissue_trype_man.
/dev_stage="roots colonized with Glomus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post_incoulation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host="E. coli strain SOLR"
/lab_host="E. coli strain SOLR"
/note="Vector: pBluescript SK-; Site_1: EccRI; Site_2:
XhoI: CDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-incoulation with Glomus versiforme. The cDNA was
directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing CDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in SOLR cells."
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
1; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 538)
1 (bases 1 to 538)
1 (bases 1, v. Webalov, J., White, R., Matern, A.L., Holt, I.E., Liang, F., Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M., Kraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J., Generation of ESTs from tomato fruit tissue
                                                                                                                                                /organism="Medicago truncatula/Glomus versiforme mixed EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
Other name: MHAM-7c-D12; Date: 3/14/00; Updated to the Database of Expressed Sequence Tags (dbEST) on 04/27/00; More information is available at 'http://chrysie.tamu.edu/medicago'. Seq primer: T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST359601 tomato fruit mature green, TAMU Lycopersicon esculentum CDNA clone cLEF56016 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9tgttgcaattactcaagaaaattctctgttggataacactgctagaatagagggatggt 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aactggcaactactcttgtaattgtcatttctaagagcggaggcacacctgaaacccgca 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atggtctactagaagtacagaaagccttcagagatgcgggggctgcaattctcgaaacagg 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     578 GIGIIGCIATAACACAAGAAAACICITIGIIGGAIAACACIGCCAGAAIIGAGGGAIGGI 637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.8%; Score 191.4; DB 23; Length 670;
81.3%; Pred. No. 1.6e-49;
Live 0; Mismatches 51; Indels 0;
                                                                                                                                                                                            /cultivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
/clone="MHAM-7H23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                        /clone_lib="MHAM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW933758.1 GI:8109159
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                                                                                                                                                                       library
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AW933758
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1; Solanales; Solanaceae; Solanum; Lycopersicon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alcala, J., Vrebalov, J., White, R., Matern, A.L., Lakey, J., Holt, I.E., Liang, F., Hansen, T.S., Upton, J., Ronning, C.M., Craven, M.B., Fujii (C.Y., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Martin, G.B., Tanksley, S.D. and Giovannoni, J. Generation of ESTs from wild tomato (Lycopersicon pennellii)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xhol: cLEF - Fruit were tagged at the lons stage and harvested 3-5 days prior to ripening. Fruit were cut in half to verify the seeds were indeed 'immature' and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST310286 L. pennellii trichome, Cornell University Lycopersicon pennellii cDNA clone cLPT10F14 5', mRNA sequence.
AW399786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seeds and locules were discarded prior to freezing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97 gcggaggcacacctgaaacccgcaatggtctactagaagtacagaaagccttcagagatg 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 cggggctgcaattctcgaaacagggtgttgcaattactcaagaaaattctctgttggata 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 CTGGCCTGATATTCGCAAAACAGGGTGTTGCCATTACACAAGAAAACTCATTGCTTGACA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATCAAATTGCACAACTTGGCCCTGAGCTGGCTTCAACACTTGTTATTGTTATTTCAAAGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 atcaaattgctcaactaggacctgaactggcaactactcttgtaattgtcatttctaaga 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07 - FEB - 2000
                                                                                                                                                                                                                                                                             /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cirEF56016"
/clone_lib="tomato fruit mature green, TAMU"
/tissue_type="fruit pericarp"
/dev_stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.8%; Score 182.4; DB 25; Length 538; 80.7%; Pred. No. 1e-46; Live 0; Mismatches 51; Indels 0;
                                                Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 g
                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 ggacttcagaaatgtctgctgtgg 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 GAACCTCAGAATGTCTGCAGTTG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lycopersicon pennellii.
Lycopersicon pennellii
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                        Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     537 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 60.8%
Best Local Similarity 80.7%
Matches 213; Conservative
Unpublished (1999)
                                                                                                                                                                                                           5 prime sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW399786
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  JOURNAL
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                   FEATURES
                             COMMENT
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/tissue_type="Root"
/dev_stage="Five day old etiolated seedling"
/dev_stage="Five day old etiolated seedling"
/lab_host="E. coll DH10B"
/note="vector: Landad Uni-ZAP XR, excised phagemid
/note="vector: Landad Uni-ZAP XR, excised phagemid
/note="vector: Landad Uni-ZAP XR, excised phagemid
pBluescript SK; Site_1: ECORI; Site_2: XhOI; Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made in the
TJ Close lab (Choi, Close, Fenton) at the University of
California, Riverside. The CDNA clones were in vivo
excised to give pBluescript phagemids before
normalization was carried out. The mass excision of
phagemid library and normalization were done in HT Nguyen
lab by D. Zhang at Texas Tech University. Normalization
protocol used was that of Soares. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Far: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Medicago.

1 (bases 1 to 217)
Journet, E. P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="WHE1123_E08_J15"
/clone_lib="Wheat etiolated seedling root normalized CDNA
library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL366975 217 bp mRNA EST 03-AUG-2000
MtBAl1D05F1 MtBA Medicago truncatula cDNA clone MtBAl1D05 T3, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 aactggcaactactcttgtaattgtcatttctaagagcggaggcacacctgaaacccgca 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 487 AACTTAAATCTACTCTTGTAATTGTAATCTCTAAGAGTGGTGGTACACCTGAAACCCGGA 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 gatttattgacaacaccgatcctgctgggattgatcatcaaattgctcaactaggacctg 60
                                                                                                                                                                                                                      Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          547 ATGGTCTACTAGAAGTACAAAAAGCCTTCAGAGATGCTGGACTGGATTTTT 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22; Indels
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87.1%; Pred. No. 4.4e-32;
tive 0; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL366975.1 GI:9666728
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Best Local Similarity
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/db_xref="taxon:28526"
/clone="clpTp10F14"
/clone_lib="L. pennellii trichome, Cornell University"
/tissue_type="trichome"
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/dev_staqe="mixed stages"
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Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta;
Magnoliophyta: Liliopsida: Poales: Poaceae: Triticum.

1 (bases 1 to 597)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
The structure and function of the expressed portion of the wheat
genomes - Normalized root cDNA library
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81.6%; Pred. No. 1.8e-43;
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                                                                           Contact: David Frisch
Clemson University Genomics Institute
Clemson University
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Fax: 864 656 4293
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//dev_stage="harvested after 3 days of N-starvation"
//dev_stage="harvested after 3 days of N-starvation"
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//note="vector: pBluescript pSK; Site_1: EcoRi; Site_2:
XhOI; Plants were grown in an aeropoinc chamber for 14
days on nitrogen-rich medium followed by 3 days on N-free
medium. RNA was extracted from root tips (1-3 cm). cDNA
was prepared from polyA+ enriched RNA. The cDNA was
directionally ligated into Uni-zapxR vector from
Stratagene and packaged using Gigapack Gold packaging
extracts. Plasmids containing cDNA inserts were
mass-excised from phage stocks using Exassit helper phage
and propagated in SOLR cells. Clone ordering and
sequencing was performed by the Centre National de
Sequencage (Gence Order) "
Sequencage (Envir France)."
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Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
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                                                                                                      Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BE 191 91006 EVRY cedex - France
BE 191 91006 EVRY cedex - France
Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :
Mt-estétoulouse.inra.fr Website :
http://sequence.toulouse.inra.fr/Mtruncatula.html).
             Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Gianinazzi-Pearson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 gcaatggtctactagaagtacagaaagccttcagagatgcgggggtgcaattctcgaaac 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 agggtgttgcaattactcaagaaaattctctgttggataacactgctagaatagagggat 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 ctgaactggcaactactcttgtaattgtcatttctaagagcggaggcacacctgaaaccc 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CTGAGCTAGCTTCGACACTTGTGATTGTGATTTCAAAGAGTGGAGGCACCCCTNAGACTA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 133; DB 14; Length 217;
Pred. No. 2.5e-31;
0; Mismatches 46; Indels
                                       ,V. and Gamas,P. Medicago truncatula ESTs from nitrogen-starved roots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Medicago truncatula"
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1 (bases 1 to 501)
                                                                                                                                                                                                                                                                                                                                                /cultivar="Jemalong"
/db_xref="taxon:3880"
/clone="MtBAllD05"
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                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="MtBA"
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Best Local Similarity 78.4%;
Matches 171; Conservative
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                                                                            Unpublished (2000)
Contact: Genoscope
                                  and Gamas, P
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evaluation of expressed sequence tags from mint glandular trichomes Proc. Natl. Acad. Sci. U.S.A. 97 (6), 2934-2939 (2000) Contact: Lange, B.M.
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Probing essential oil biosynthesis and secretion by functional evaluation of expressed sequence tags from mint glandular trichomes Proc. Natl. Acad. Sci. U.S.A. 97 (6), 2934-2939 (2000) Contact: Lange, B.M. Institute of Biological Chemistry/Washington State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW255839 621 bp mRNA EST 15-MAR-2000 ML923 peppermint glandular trichome Mentha x piperita CDNA, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              393 AGCTAGAATCTACACTCGTGATAGTGGTTTCAAAGAGTGGAGGTACGCCCGAAACAAGAA 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Institute of Biological Chemistry/Washington State University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 76.9%; Pred. No. 6.1e-23;
Matches 130; Conservative 0; Mismatches 39; Indels '0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mentha x piperita"
/cultivar="Black Mitcham"
/db xxef="taxon:34256"
/clone_lib="peppermint glandular trichome"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="peltate glandular trichomes"
/cell_type="secretory"
/note="Vector: lamba ZAPII"
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                                                                                                                                                                                                                                                                                                  /organism="Mentha x piperita"
/cultivar="Black Mitcham"
/cultivar="1016 Mitcham"
/cultivar="1016"
/clone_lib="peppermint glandular trichome"
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/cell_type="secretory"
/note="Vector: lamba ZAPII"
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
I; Solanales; Solanaceae; Solanum; Lycopersicon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST242318 tomato shoot, Cornell Lycopersicon esculentum cDNA clone cLEB3B18 similar to glucose-6-phosphate isomerase, mRNA sequence. AI482995.1 GI:4386919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 564)
van der Hoeven, R.S., Matern, A.L., Vision, T., Holt, I.E., Liang, F.,
Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L.,
and Tanksley, S.D.
Generation of ESTs from tomato shoot meristem
Unpublished (1999)
Other_ESTs: EST242322
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-Tomato Shoot Meristem EST Library. Oligo-dT primed cDNA
library made from tomato vegetative shoots including
meristems and expanding leaves."
                                                                                                    61 aactggcaactactcttgtaattgtcatttctaagagcggaggcacacctgaaacccgca 120
                                                                                                                                                                                       121 atggtctactagaagtacagaaagcctt-cagagatgcgggggtgcaattctcgaaacag 179
                                                                                                                                                                                                                                                                                     487 AACGICIACIIGAAGIICAAAAAGCCIICCCGAGAGCCIGGICNIGGAIIICCCAAACAG 546
                                                    Gaps
                                                                              1 gatttattgacaacaccgatcctgctgggattgatcatcaaattgctcaactaggacctg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JUN-1999
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  34.7%; Score 104; DB 21; Length 621; 72.2%; Pred. No. 4.3e-22; Live 0; Mismatches 56; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Invopersion esculentum"
/oultivar="7A496"
/db_xref="taxon:4081"
/clone="cleBa818"
/clone=lib="tomato shoot, Cornell"
/tissue_type="shoot meristem"
/dev_stage="8 week old plants"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST
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Tel: 864 656 4366
Fax: 864 656 4293
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Clemson University
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1. .564
                                                                                                                                                                                                                                                                                                                               180 ggtgttgcaattactcaagaaaatt 204
                                                                                                                                                                                                                                                                                                                                                                      547 GGTCTTGCCAATTCCCAAAAAAT 571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 564 bp
                                     Matches 148; Conservative
                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI482995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tomato.
Query Match
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; Lillopsida; Poales; Poaceae; Triticum.
1 (bases 1 to 439)
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//dev_stage="meiotic stage no later than metaphase I"
//note="Vector: psport 1 (Life Technologies cat, no
18248-013); Site=1: SalI; Library constructed in psport 1
Directionally cloned using the Superscript plasmid System
for cDNA synthesis and plasmid clonding. M13.Reverse
sequencing primer used to obtain 5' sequence data. 1.4
Kbp average insert size."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Langridge P
Special Research Centre, Basic and Applied Plant Molecular Biology
Waite Campus, University of Adelaide, Glen Osmond SA 5064 AUSTRALIA
Tel: 61 8 8303 7368
Fax: 61 8 8303 7102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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Expressed Sequence Tags for Species of the Triticeae

Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                        BE400087 439 bp mRNA EST 21-JUL-2000
AWB010.F10F000328 ITEC AWB Wheat Meiotic Stage Library Triticum
61 aactggcaactactcttgtaattgtcatttctaagagcggaggcacacctgaaacccgca 120
                                                                                                                                           188 aattactcaagaaaattctctgttggataacactgctagaatagaggatggttagctcg 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="ITEC AWB Wheat Meiotic Stage Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: plangridge@waite.adelaide.edu.au
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                           aestivum cDNA clone AWB010.F10, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cultivar="Chinese Spring"/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="AWB010.F10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE400087.1 GI:9359555
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                                                                                                                                                                                                               121 atggtctactaga 133
                                                                                                                                                                                                                                                          552 ATGGCTTGCTAGA 564
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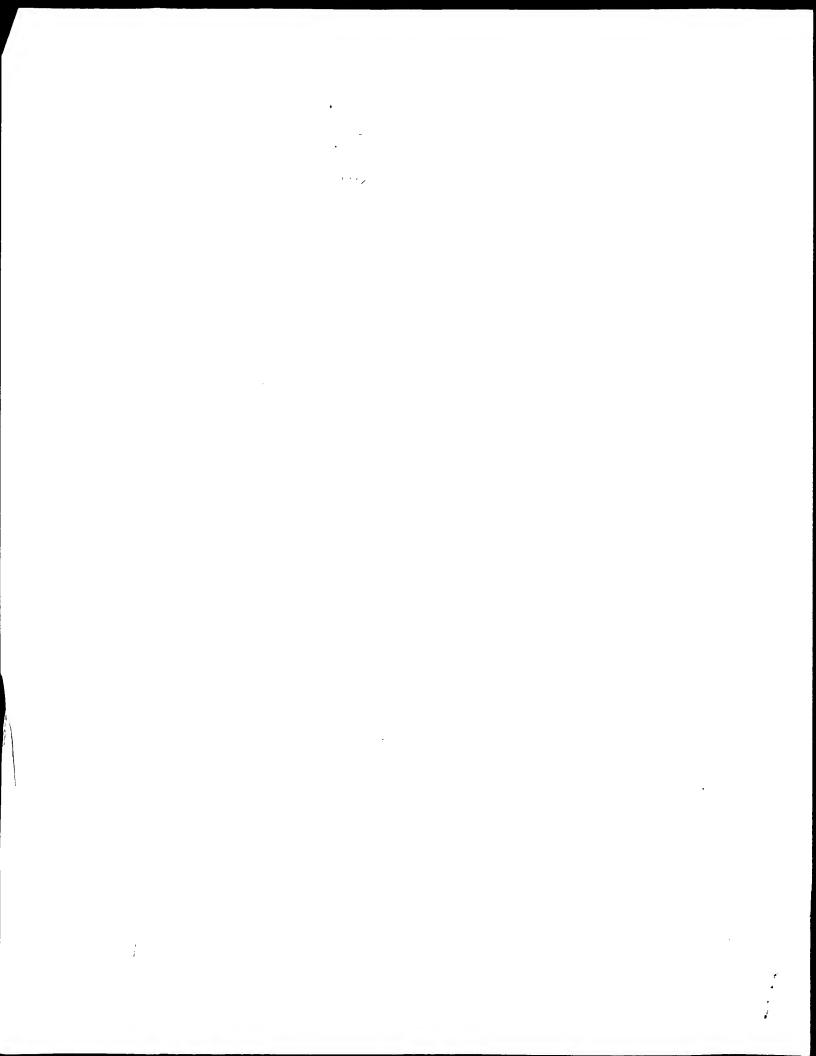
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Trachaptopsis thallana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; Brassicaceae; Arabidopsis; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis; Rosidae; eurosids II;
Brassicales; Darassicaceae; Arabidopsis; Consecution of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries

AL DNA Res. 7, 175-180 (2000)
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.

Location/Qualifiers

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//clone="Arabidopsis thaliana"
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                                                                                                               Sequence 1, Apsender 2, Apsender 3, Apsender 3, Apsender 13, Apsender 13, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 29, Apsender 
                                                                       Sequence 3,
Sequence 1,
             Sequence 1,
Sequence 3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09012030
Patent No. 5912169
GENERAL INFORMATION:
APPLICANT: SCHMIDT, Ralf-Michael, STITT, Marc, SONNEWALD,
APPLICANT: Use
TITLE OF INVENTION: Transketolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 44.3%; Score 170.4; DB 4; Length Best Local Similarity 67.4%; Pred. No. 3.6e.37; Matches 240; Conservative 0; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage. COMPUTER: IBM AT-compatible, 80486 processor OPERATING SYSTEM: MS-DOS version 6.0
  US-08-093-577-1
US-08-095-577-3
US-08-096-623A-1
US-08-096-623A-1
US-08-096-623A-1
US-08-075-904-1
US-08-14-309A-2
US-08-722-001-29
US-08-722-001-29
US-08-722-001-29
US-08-722-001-29
US-08-228-932-1
US-08-248-939-1
US-08-244-354-1
US-08-206-899-1
US-08-206-899-1
US-08-206-899-1
US-08-206-899-1
US-08-206-899-1
US-08-206-899-1
US-08-206-899-1
US-08-206-899-1
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APPLICATION NUMBER: US/09/012,030
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STREET: 1101 Connecticut Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,454
FILING DATE: 22-JAN-1996
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 2629 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
  1157
1157
1157
1157
50341
50341
1513
1513
1513
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Keil & Wei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
ORGANISM: Nicotiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDA
60..2289
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  CLASSIFICATION:
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LOCATION:
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US-09-012-030-1
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4 ccggcaccaagcctgacatcattgggttgggcaccggctccgagctggagatcgcgggca 63

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Sequence

us-09-300-482-356.rni

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2056 GGGAGCTTTTTGAAGAACAATCAGCCGACTACAAGGAAAGTGTCCTTCCATCATCTGTTA 2115
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                                                     244 aaggcaaggccattggcatcgacaagttcggcgcgagtgctcctgccgggacgatctaca 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 116; Indels
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APPLICANT: SCHMIDT, Ralf-Michael, STITT, Marc, SONNEWALD,
APPLICANT: WE THING APPLICANT: Transketolase
TITLE OF INVENTION: Transketolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage COMPUTER: IBM AT-competible, 80486 processor OPERATING SYSTEM: MS-DOS version 6.0 SOFTWARE: WordPerfect version 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/590,454
FILING DATE: 22-JAN-1996
CLASSIFICATION: 435
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1101 Connecticut Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 1, Application US/08590454
; Patent No. 5925535
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TYPE: nucleic acid
STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
ADDRESSE: Keil & We
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APPLICANT: Hamilton O. Smith
APPLICANT: J. Craig Venter
TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome
NUMBER OF SEQUENCES: 48
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2236 AGGAGTACGGAATTACAGCAGGCTGTTGTAGCTGCAGCTAAACAAGTTTCTTAG 2291
                                                                                                                                                                                                                                                                        304 aggagtacggcatcaccgtggagagcatcattgcaactgccaagagcttttaagag 359
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Sterne, Kessler, Goldstein & Fox 1100 New York Avenue, Suite 600
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                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 1025, Application PC/TUS9605320A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                9410 Key West Avenue
Rockville, MD 20850
United States of America
Johns Hopkins University
720 Rutland Avenue
Baltimore, MD 21205
United States of America
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APPLICATION NUMBER: 08/476,102
FILING DATE: June 7, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: June 7, 1995
ATTONNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Genome Sciences
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APPLICATION NUMBER: PCT/US96
FILING DATE: APT1122, 1996
CLASSIFICATION:
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TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1025:
SEQUENCE CHARACTERISTICS:
LENGTH: 1995 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Fric K. Steffe
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION:
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Owen White
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APPLICANT:
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APPLICANT: PICARD, Francois J.
APPLICANT: PICARD, Francois J.
APPLICANT: PICARD, Paul H.
TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
NUMBER OF SEQUENCES: 273
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                                                                                                                                                                                                      1650 CACACCTGAGTTAATCTTCATTGCGACAGGTTCTGAAGTGGAATTAGCAGTGCAAGCAGC 1709
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                                                                                                                                                                                                                                                                                                                                                              131 ctttgatgagcagtcggatgagtacaaggagagcgtcctccctgccgacgtcacagcgag 190
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                                                                                                                                 Gaps
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                                                                                                                               .;
0
                                                                                       Length 1995;
                                                                           19.9%; Score 76.8; DB 6; Length 151.8%; Pred. No. 4.9e-12; tive 0; Mismatches 162; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1950 TGGTTTCACTGTTGAAAACGTGGTAGCAAAAGCGAA 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             311 eggcatcaccgtggagagcatcattgcaactgccaa 346
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,840
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REJESTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 85,686,90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/743,637B
FILING DATE: 04-NOV-1996
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411 EAST WISCONSIN AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17, Application US/08743637B Patent No. 5994066 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                               Best_Local Similarity 51.8
Matches 174; Conservative
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TELEFAX: (414)277-5591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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ZIP: 53202-4497
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; TOPOLOGY: 111
PCT-US96-05320A-1025
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                                                                                Query Match
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SPECIFIC AND UNIVERSAL PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
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                                                                                                                                                                                                                                                                                                                             Query Match 13.4%; Score 51.6; DB 4; Length 1872; Best Local Similarity 47.3%; Pred. No. 2.9e-05; Matches 156; Conservative 0; Mismatches 174; Indels '0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304 aggagtacggcatcaccgtggagagcatca 333
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FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: QUARLES & BRADY
STREET: 411 East Wisconsin Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/304,732
FILING DATE: 12-SEP-1994
                                                                                                                                                                                                                       ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/08526840B Patent No. 6001564 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BERGERON, Michel G.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY. Paul H.
TITLE OF INVENTION: SPECIFIC AND
TITLE OF INVENTION: COMMON BACTE
TITLE OF INVENTION: COMMON BACTE
TITLE OF INVENTION: FROM CLINICA
NUMBER OF SEQUENCES: 177
CORRESPONDENCE ADDRESS:
ADDRESSEE: QUARLES & BRADY
                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                    1872 base pairs
                             SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO:
                                                 LENGTH: 1872 base pai
TYPE: nucleic acid
STRANDEDNESS: double
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STATE: Wisconsin
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LOCATION:
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 13.4%; Score 51.6; DB 5; Length 1872; Best Local Similarity 47.3%; Pred. No. 2.9e-05; Matches 156; Conservative 0; Mismatches 174; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Alitalo, et al.
TITLE OF INVENTION: FLT4, A NOVEL RECEPTOR TYROSIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                          REFERENCE/DOCKET NUMBER: 850586,90012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1016 CCTCCCACGAGCACCCCGAGTTCATCGTCA 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 aggagtacggcatcaccgtggagagcatca 333
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COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,011
                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Pseudomonas aeruginosa US-08-526-840B-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08340011
Patent No. 5776755
                    NAME: BAKER, Jean C. REGISTRATION NUMBER: 35,433
                                                                                                      TELEPHONE: (414) 277-5000
TELEPAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
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NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                       linear
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CITY: Chicago
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                                                                                                                                                                                                                                                                  TOPOLOGY:
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US-08-340-011-1
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2255 TATCTGTGCAGCGTGTGCAACGCCAGCGTGCGTCCTCCCCCCAGCGTGGCGTG 2314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2195 TTGGCGGACTCCAACCAGAAGCTGAGCATCCAGCGCGTGCGCGAGGAGGATGCGGGACGC 2254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 cctgccgacgtcacagcgaggatcagcatcgaggccgggtccactctcggctggcagaag 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 tacgicggagcccaaggcaaggccattggcatcgacaagticggcgcgagtgctcctgcc 290
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APPLICANT: Pajusola, Katri
APPLICANT: Armstrong, Elina
APPLICANT: Kaipainen, Jaana
APPLICANT: Kaipainen, Arja
APPLICANT: Kaipainen, Arja
TITLE OF INVENTION: FLT4, A RECEPTOR TYROSINE KINASE, AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291 gggacgatctacaaggagtacggcatcaccgtggagagagcatcattgcaactgcc 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 4195;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41.2; DB 2; Length 4
Pred. No. 0.023;
0; Mismatches 158; Indels
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COUNTRY: United States of America
ZIP: 66066-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPatible
APPLICATION NUMBER: 07/959,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08901710 Patent No. 6107046
                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEEX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4195 base pairs
                                                                               NAME: Meyers, Thomas C. REGISTRATION NUMBER: 36,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.7%;
                         FILING DATE: 09-OCT-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Alitalo, Kari
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                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                      nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20..3916
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                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 136; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
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Pred. No. 0.023;
0; Mismatches 158; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST
                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          28113/33824
                                                         APPLICATION NUMBER: US/08/901,710
  PC-DOS/MS-DOS
                                                                                                                                 APPLICATION NUMBER: 08/340,011
FILING DATE: 14-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,754
FILING DATE: 09-JUL.1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                    APPLICATION NUMBER: 07/959,951
FILING DATE: 09-0CT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 31, Application US/08222616
Patent No. 563517
GENERAL INFORMATION:
APPLICANY: Bennett, Brian D.
APPLICANY: Goeddel, David
                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 2811
TELECOMMUNICATION INFORMATION:
TELEBHONE: 312/474-6300
TELERAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Taai, Siao Ping
APPLICANT: Wood, William I.
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46.3%;
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Best Local Similarity 46.38
Matches 136; Conservative
                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20..3916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: cDNA
OPERATING SYSTEM:
                                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION:
US-08-901-710-1
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2206 TIGGCGGACTCCAACCAGAAGCIGAGCATCCAGCGCGIGCGCGAGGAGGAIGCGGGACGC 2265
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Pred. No. 0.024;
0; Mismatches 158; Indels 0
                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/222,616
FILING DATE: 4-APR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00586
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/826935
                                                         ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: Callfornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 821P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/25-981
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 31:
SEGUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 31, Application PC/TUS9504228
GENERAL INFORMATION:
APPLICANT: Genericch, Inc.
APPLICANT: Bennett, Brian D.
APPLICANT: Goeddel, David
                                                                                                                                                                                                                                                                  PC-DOS/MS-DOS
TITLE OF INVENTION: ANTIBODIES
                                                                                                                                                                                                                                                                                    SOFTWARE: patin (Genentech)
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illarity 46.3%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 136; Conserval
                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                            94080
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US-08-222-616-31
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APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
APPLICANT: Wood, William I.
TITLE OF INVENTION: PROFEIN TYROSINE KINASE AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291 gggacgatctacaaggagtacggcatcaccgtggagagcatcattgcaactgcc 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.7%; Score 41.2; DB 6; Length 4425; 46.3%; Pred. No. 0.024; tive 0; Mismatches 158; Indels 0
                                                                                                                                                                                                                                                                                                     3: 5.25 inch, 360 Kb floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 821P3PCT TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-1994
                                                                                                                                              ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNBER: 08/22516
FILING DATE: 04-APR-1994
ATTONNEY/AGENT INFORMATION:
NAME: WendY M. Lee
REGISTRATION NUMBER: 00,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 3, Application US/08340011; Patent No. 5776755; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Alitalo, et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 4425 bases
                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
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Best Local Similarity
Matches 136; Conserva
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                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                            94080
                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE
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PCT-US95-04228-31
                                                                                                                                                                                                                                                                                                                             COMPUTER:
                                                                                                                                                                                                                                        COUNTRY:
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2255 TATCTGTGCAGCGTGTGCAACGCCAAGGGCTGCGTCAACTCCTCCGCCAGGGGTGGCCGTG 2314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2195 TTGGCGGACTCCAACCAGAAGCTGAGCATCCAGCGCGTGCGCGAGGAGGATGCGGGACGC 2254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2315 GAAGGCTCCGAGGATAAGGGCAGCATGAATCGTGATCCTTCTCGGTACCGGC 2368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 gggacgatctacaaggagtacggcatcaccgtggagagcatcattgcaactgcc 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 10.7%; Score 41.2; DB 2; Length 4795; Best Local Similarity 46.3%; Pred. No. 0.024; Matches 136; Conservative 0; Mismatches 158; Indels 0
TITLE OF INVENTION: FLT4, A NOVEL RECEPTOR TYROSIN KINASE
                                                                         E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,011
FILING DATE:
CLASSIFICATION: 435
                                                                                                                          CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
IIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07/959,951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Meyers, Thomas C. RECISTRATION NUMBER: 36.987 REFERENCE/DOCKET NUMBER: 32.TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 09-OCT-1992 ATTORNEY/AGENT INFORMATION:
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TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 4795 base pairs
                           NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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20..4111
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                                                                         ADDRESSEE:
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; LOCATION:
US-08-340-011-3
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2255 TATCTGTGCAGCGTGTGCAACGCCAAGGGCTGCGTCAACTCCTCCGCCAGCGTGGCCGTG 2314

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 tegitegietectgggaactetitgatgageagteggatgagtaeaaggagagegtecte 170
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                                             APPLICANT: Armstrong, Elina
APPLICANT: Korhonen, Jaana
APPLICANT: Kaipainen, Arja
APPLICANT: Matikainen, Marja-Terttu
APPLICANT: Matikainen, Marja-Terttu
TITLE OF INVENTION: FLT4, A RECEPTOR TYROSINE KINASE, AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.7%; Score 41.2; DB 5; Length 4795; Best Local Similarity 46.3%; Pred. No. 0.024; Matches 136; Conservative 0; Mismatches 158; Indels 0
                                                                                                                                                                                                                                         E: Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28113/33824
TELECOMBUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                     STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/340,011
FILING DATE: 14-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,754
FILING DATE: 09-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/959,951
FILING DATE: 09-OCT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Aprelikova, Olga
Pajusola, Katri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 4795 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS: ADDRESSEE: Marshall,
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20..4111
                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                         Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
US-08-901-710-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231
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3138 TTGGCGGACTCCAACCAGAAGCTGAGCATCCAGCGCGTGCGCGAGGAGGATGCGGGACGC 3197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3018 GACCTCCTGGTGAACGTGAGCGACTCGCTGGAGATGCAGTGCTTGGTGGCCGGAGCGCAC 3077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 gagatcgcgggcaatgcggccgacgagttgaggaaggaggggaagacggtccgcgtcgtc 110
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                                        2315 GAAGGCTCCGAGGATAAGGGCAGCATGGAGATCGTGATCCTTGTCGGTACCGGC 2368
                                                                                                                                                                                                                                                                      APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsal, Slao Ping
APPLICANT: Wood, William I.
TITLE OF INVENTION PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 45
291 gggacgatctacaaggagtacggcatcaccgtggagagcatcattgcaactgcc 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41.2; DB 6; Length 9108;
Pred. No. 0.03;
0; Mismatches 158; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                             STREET: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Prancisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            821P3PCT
                                                                                                           RESULT 12
PCT-US95-04228-45
; Sequence 45, Application PC/TUS9504228
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/22616
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 00,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
                                                                                                                                                                                                      Genentech, Inc.
Bennett, Brian D.
Goeddel, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.7
Best Local Similarity 46.3
Matches 136; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9108 bases
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PCT-US95-04228-45
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APPLICANT:
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231 tacgtccgaagcccaaggccaatggcattggcatcgacaagttcggcgcgagtgctcctgcc 290

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3198 TATCTGTGCAGCGTGTGCAAGGCCTGCGTCAACTCCTCCGCCAGCGTGGCCGTG 3257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1003 GAAGAACGTCGTCGCCCCGGTCTCGCCTCGCGTGCGAGGTCCAGGTCGCGTACGCGAT 944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             883 CGAGAAGATCGAGAACGCCATCGGCGAGGTCTTCGACCTCCGCCCGGCCGCGATCAT 827
                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Melanie C.
APPLICANT: TANG, Li
TILE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 300622002120
CURRENT PELICATION NUMBER: US/09/320,878A
CURRENT PELICATION NUMBER: CIP OF 09/141,908
EARLIER FILING DATE: 1999-05-27
EARLIER FILING DATE: 1998-05-26
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1997-04-30
EARLIER FILING DATE: 1997-04-30
EARLIER FILING DATE: 1997-04-30
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1998-09-2-08
                                                                                                                                                                          3258 GAAGGCTCCGAGGATAAGGGCAGCATGGAGATCGTGATCCTTGTCGGTACCGGC 3311
                                                                                                       291 gggacgatctacaaggagtacggcatcaccgtggagagcatcattgcaactgcc 344
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APPLICANT: Horlick, Robert A.
APPLICANT: Damaj, Bassam B.
APPLICANT: Comaj, Bassam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes TITLE OF INVENTION: From Multiple Transfected Episomes File Reference: 0867/1D903021
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5; Length 1693;
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Pred. No. 0.02;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                           Sequence 23, Application US/09320878A Patent No. 6117659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Streptomyces venezuelae US-09-320-878-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 2, Application US/09130114; Patent No. 5976807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 10.6%;
Best Local Similarity 52.0%;
Matches 92; Conservative
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                                                                                                                                                                                                                                                                                 RESULT 13
US-09-320-878-23/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 23
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                                                                                                                                                                                                                                                                                                    gatgagtacaaggagagcgtcctcctgccgacgtcacagcgaggatcagcatcgaggcc 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 gggtccactctcggctggcagaagtacgtcggagcccaaggcaaggccattggcatcgac 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 gggttgggcaccggctccgagctggagatcgcgggcaatgcggccgacgagctgaggaag 86
                                                                                                                                                                                        Length 1931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: SARHAN, Fathey
APPLICANT: HOUDE, MATIO
APPLICANT: LALIBERT, Jean-Fran ois
TITLE OF INVENTION: DNA MOLECULES ENCODING FREEZING
TITLE OF INVENTION: TOLERANCE PROTEINS IN GRAMINEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 265 AAGGTGGCACCCAGGGAAACGTCGGTTACGTTGAACCTGCA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267 aagtteggegegagtgeteetgeegggaegatetaeaagga 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/106,981
                                                                                                                                                                                    9.4%; Score 36.2; DB 4;
45.6%; Pred. No. 0.4;
Live 0; Mismatches 153;
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UMBER: US/08/106,981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 163-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: VINCE COUNTY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08106981
Patent No. 5731419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                    Best Local Similarity 45.6 Matches 128; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                          ORGANISM: EBNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                    LENGTH: 1931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-08-106-981-5
                                                                                                                              US-09-130-114-2
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                                                                                        TYPE: DNA
                                                                                                                                                                                        Query Match
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; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: CDNA to mRNA
ORIGINAL SOURCE: Triticum Aestivum L.
US-08-106-981-5
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0; Query Match 9.2%; Score 35.6; DB 2; Length 1136; Best Local Similarity 51.2%; Pred. No. 0.49; Matches 83; Conservative 0; Mismatches 79; Indels 0; Gaps

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SUMMARIES

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Query Match Length DB ID	930 7	89154 8	67712 8	5348 4	720 8	2913 4	424 8	1574 8	10304 7	3846 7	26292 4	27521 2	C 19619
Query	50.9	24.8	22.1	21.6	19.9	19.2	18.3	17.3	17.0	16.5	16.3	16.2	
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AC008259 Drosophil
X83571 S.cerevisia
Z49396 S.cerevisia
Z98979 S.pombe chr
X811199 Z.mays ZMMI
J04742 Human auton
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AC009805 Leishmani
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AC016779 Oryza sat
AF166527 Zea mays
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AC005694 Homo sapi
Y18000 Homo sapien
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AC004709 Plasmodiu
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AF047444 Oryza sat
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Direct Submission
Submitted (20-58P-1999) Institute of Forest Biology and Tree
Physiology, Am Flughafen 17, Freiburg im Breisgau 79085, Germany
Location/Qualifiers
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(Dases 1 to 930)

Kopriva,S., Koprivova,A. and Suss,K.H.
Identification, cloning, and properties of cytosolic D-ribulose-5-phosphate 3-epimerase from higher plants 20092904
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35. .721
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SCPOS18
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Busaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 89154)
Lin,X., Kaul,S., Town,C.D., Benito,M., Creasy,T.H., Haas,B.,
Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R., Barnstead,M.E.,
Bowman,C.L., White,O., Wierman,W.C. and Frasër,C.M.
Arabidopsis thaliana chromosome III BAC F2877 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr.
Rockville, MD 20850, USA
e-mail: xlin@tigr.org
BAC clone F2847 is from Arabidopsis chromosome III and is near the
molecular marker ILRN:
The orientation of the sequence is from SP6 to 77 end of the BAC
                                                                                                                                                                                    ó
QELIQSIKAKCMRPGYSLRPGTPVEEVFPLVEAENPVELVLVWTVEPGFGGOKFMPEM
MEKVRALRKKYPSLDIEVDGGLGPSTIDVAASAGANCIVAGSSIFGAAEPGEVISALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (21-0CT-1999) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA (bases 1 to 89154)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (23-SEP-1999) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA, xlin@tigr.org 3 (bases 1 to 89154)
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DEFINITION Arabidopsis thaliana chromosome III BAC F28J7 genomic sequence,
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Pred. No. 1.6e-41;
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AC010797.2 GI:6091712
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Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (available by anonymous ftp from arthur.epm.orn.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://www.cbs.dtudk/netpgene/Cbsnetpgene.html), searches of the complete sequence against a peptide database and the Arabidopsis Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity to other proteins are named similarity but with EST similarity, that are predicted by more annotated as 'hypothetical' proteins. Genes without protein or EST similarity, that are predicted by more annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (seas EdV). Simple repeats are identified by repeatmasker (Arian Smit, Pervin) Paring of identified by repeatmasker (Arian Smit, Pervin) Paring of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://ftp.genome.washington.edu/RM/RepeatMasker.html). Regions of genomic sequence that are not annotated as genes but have predicted exons by GRAIL are annotated as misc features.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DYSGYGGSTGKPSEHNTYADIEAVYKCLEETFGSKOEGYILYGGSVGSCPTLDLASRL
PQLRAVVLHSPILSGLRVMYSVKKTYWFDIYKNIDKIPYVDCPVLIIHGTSDEVVDCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HGKQLWELCKOKYEPLWYKGGNHCDLEHYPEYIRLALYYVERLPCPPLIHGYSDEVDCS
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HEKTRKSVDQIERGRKSVDRLDRVRSE"
3677. 4136
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PENSKHPLGCDWYPALNKPAAVVHWLHHTNIDAEYVVLLDADMILRGPITPWEFKAA
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SFTKLDHHEDNIVYDGNRLFPEPPYPREVKIMEPDPSKRRGLILSLECMNTLNBGLIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="exon predicted by xgrail, quality good" 10571. .10626
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                                                                                                                                                                                                                                                                                                                             complement(<4853. .>6434)
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Brassicales; Brassicaceae; Arabidopsis.

[1] (bases 1 to 67712)

Lin,X., Kaul,S., Town,C.D., Bantto,M., Creasy,T.H., Haas,B., Wu,D.,
Matit,R., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R.,
Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
Arabidopsis thaliana chromosome I BAC F9N12 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      denes were identified by a combination of three methods: Gene prediction programs including GRAIL (available by anonymous ftp from arthur.epm.orn.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/~chris/CENSCANW.html), and NetPlantGene http://gnomic.stanford.edu/~chris/Sensetpgene.html), searches of the complete sequence against a peptide database and the Arabidopsis EST database at TIGR (http://www.tlgr.org/tdb/at/at.html).
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (01-FEB-2000) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA, xlin@tigr.org 3 (bases 1 to 67712)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (18-FEB-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA on Feb 18, 2000 this sequence version replaced 91:6910594. Address all correspondence to:at@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAC clone F9N12 is from Arabidopsis chromosome I and is near the molecular marker mi353. The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45282 AGGIGGAIGGCGGCTITAGGCCCTICAACGAICGACACAGCGGCIGCAGCAGGCGCCAACI 45223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 45222 GTATTGTTGCTGGAAGTTCAGTGTTTGGAGCTCCGGAGCCAGGAGTGTCATCTCCCTTC 45163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 aggitgaiggigitctiaggiccticaaccaiagacgiggccgcaictgciggggccaait 106
                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATAC022355 67712 bp DNA PLN 18-FEB-2000
Arabidopsis thaliana chromosome I BAC F9N12 genomic sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 45162 TGAGGACCAGTGTTGAGAAAGCCCAACCCACCATGAGT 45123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 tgaggaagagcgtcgagggctctcagaacaaaaactgatt 206
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Lin, X. and Kaul, S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC022355.3 GI:6997182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                        Similarity
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JOURNAL
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JOURNAL
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SOURCE
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KVQDELAQKIGLIGODENTOKOK KOKGICLIYNILREKSEYLEPLDDINEKVDIALEIGVPD
PRITKKGRKLAFTTRSQEVCARMGVEHPMEVOCLERNVAFDLFOKKVGGTTLGSDFGIP
POLARIYAKKGCGLPLALVIGETMSKKRTIQENHAIHVLNSYAAEFIGMEDKVLPLL
KYSYDNILKGEDOKSZLLYCALYPEDAKILKEDINIEHMICEETIDGSBGIEKAEDKGYE
IIGCLVRASLLMEWDDGDGRRAVCMHDVYREMALMYARSLLGREYGSIRSOLKTISSEFFNC
MPKINNNYVRRASLENELPEETSOLNIVSLKYLNLLGKREYGSIRSOLKTISSEFFNC
MPKLAVLDLSHNKSLFELPEETSONIVSLKYLNLLYTEISHLFKGIOBEKKIIHLNLEY
TRKLESITGISSLHNLKKVLKLERSRLPWDLNTVKELETLEHLEILTTTIDPRAKGFE
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RRRFPSHGEVLAYLKDFAKEFGIEEMVRFETEVVKVSPAAEEGIGKWRIESTBEKKKY
RRDEIYDAVVCNGHYVEPRLAQIPGISSWPGKEMHSHNYR KT PEPFRKVLIFIDHNV
AVLIGNSSSAEDISKDIARVAKEVHVACSNPADTFIKQTGYNNLWTHSMIESVHEDG
SVYYQMGKTISVDI HHLCTGYKKHFPFLDTNGIVTVDDNRVGBLYKOVFPPAFAPWLS
FIGIPWOVLPFPMFELQSKWIAGVLSGRIPLPSKEDMMIEIKTFYSTLEVGIPKRYT
HRMGNIQFFYSNDIMASQCGCSETEEWRKEMCLANGVRKEAHPETYRDEWDDHHLVSEA
Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with ESF similarity are named as 'unknown' proteins. Genes without protein or ESF similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy. http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RW/RepeatMasker.html).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSKSLTRSYRYGKSYPIRLREYEKLKGEVFGVITEQASTSAFEERPLQPTIVGQDTML
DKAGKHLMEDGVGIMGMYGMGGVGKTTLLTQLXNMFNKDKCGFDIGIWVVVSQEFHVE
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/translation="MAPALSPIRSHHVAVIGAGPAGLVAARELRREGHSVVVFEKQKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="21552 nt beyond this point were not included in the submitted sequence due to an overlap with another bac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="contains similarity to NBS/LRR disease resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(3469. .4024,4432. .4526,4569. .4721,4795. .4877,
4969. .5104,5177. .5350,5443. .5622)
/gene="F9N12.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(3453 .4024,4432 .4526,4569 .4721,4795 .4877,4966 .5104,5177 .5350,5443 .>5622)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="contains similarity to Flavin-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="overlap with BAC clone F2K11
                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cultivar="Columbia"
                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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<6658.
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/gene="F9N12.2"
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/gene="F9N12.1"
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/gene="F9N12.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YODFSLYS"
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mRNA

CDS

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CSKSLTTSYPKGKSYPELKLERVEEVISDOASTSEVBEQOLQPTVQQETML
DNANNHLMEDGVGIMGLXGMGGVGKTTLLTQINNKFSKYMCGFDSVTWVSKEVNVE
NILDEIAQKVHISGEMOPTKKYQKGYYLYRELEKRYKFOKFUELDDIFFKWNLVSKEVNVE
NILDEIAQKVHISGEMOPTKKYQKGYYLYRELEKRYMFOKTUFLDDIFFKWNLVFIGVPF
PTIKNKCKVVFTTRSELDVGTSMGVRFRVOEMFVOCLADNDAYDLFQKKVGGITLGSDPEIR
KYSYDSLKGFDVAKCCGLPLALNVVSETMSCKRTVOEWRHAIYVLMSYAAKFSGMDDKILPL
KYSYDSLKGFDVAKCLLYCALFPEDAKIRKENLIEVWICCEIIDGSBGIDKAENQGYE
IIGSLVRASLLAMEVEVELDGANIVCLHDVVREMALWITASTIVANSYAGIRIGINEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(<14808. .15360,15864. .16003,16086. .16168,16272. .16407,
16498. .16560,16724. .>16945)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                monooxygenase"
join(14808 . 15360,15864. .16003,16086. .16168,16272. .16407,
14698. .16560,16724. .16945)
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                                  LVDVNIFNCEGLRELTFLIFAPKIRSLSVWHAKDLEDIINEEKACEGEESGILPFPEL
NFLTHDLPKLKKIYWRPLPFLCLEEINIRECPNLRKLPLDSTSGKQGENGCIIRNKD
SHRLLSHSRLLEIYGSSVSSLNRHLESLSVSTDKLREFQIKSCSISEIKMGGICNFLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLSGNYYLSELPNGISELVSLQYLNLSSTGIRHLPKGLQELKKLIHLYLERTSQLGSM
VGISCLHNLKVLKLSGSSXAWDLDTVKELEALEHLEVLTTTIDDCTLGTDQFLSSHRL
MSCIRFLKISNNSNRNRNSSRISLPVTMDRLQEFIIEHCHTSEIKMGRICSFSSLIEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKVENWNVVRRMSLMKNNIAHLDGRLDCMELTTLLLQSTHLEKISSEFFNSMPKLAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NLSNCRLRELTFLMFAPNLRRLHVVSSNQLEDIINKEKAHDGEKSGIVPFPKLNELH
LYNLRELKNIYWSPLPFPCLEKINVMGCPNLKKLPLDSKSGKHGGNGLIITHREMENI
TRVEWEDEATKTRFLANRSSFSSKLICFSNDLVSRDNUCFHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(17308. .18791,18891. .19026,19143. .19199))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MVPAVNPPTTSHHVAVIGAGAAGLVAARELRREGHSVVVFERGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QIGGVWAYTPNVEPDPLSIDPTRPVIHSSLYSSLRTIIPRECMGFTDFPFSTGPENKS
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KLSGYDNLWLHSNIETVREDGSVVFKNGKTVYADTIMHCTGYKYYFPFLDTKGEVTVE
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QCDYPRIEKWREQMFYRVFKRIQSQSSTYKDDWDDDHLIAEAYEDFVKFPSNYPSSLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RDPRRHPGHIEVLAYLKDFARKFKMDEMIRFETEVVRAEPAAENPKKWRVESRNSGDI
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VVTYSSLISCLCSYGRWSDASQLLSDMIEKKINPNLVTFNALIDAFVKEGKRVEAEKL
HDDMIKRSIDPDIFTYNSLINGFCMHDRLDKAKQMFEFWVSKDCFPDLDTYNTLIKGF
CKSKRVEDGTELFREMSHRGLVGDTVTYTTLIQGLFHDGDCDNAQKVFKQMVSDGVPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MYYHPRRRDCLFVGISWGKDLKLDDAIGLFGGMVKSRPLPSIFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FNKLLSAIAKMKKFDLVISLALLGKMMKLGYEPSIVTLSSLLNGYCHGKRISDAVALV
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                                                                                                                                                                                                                                                          /note-"similar to NBS/LRR disease resistance protein
GB:AAC26125 from [Arabidopsis thaliana]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to GB:AAD43616 from [Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="F9N12.4"
/note="contains similarity to Flavin-containing
                                                                                                SRWFEGVKWADEATKKRFLPSCQLISLK"
                                                                                                                                                                                                                                                                                                                                                                                            /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(<17308. .>19199)
/gene="F9N12.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAF34848.1"
/db_xref="G1:6997186"
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/db_xref="G1:6997187"
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                                                                                                                                                                                                .>13892
                                                                                                                                     <111196. .>13892
                                                                                                                                                                                                                                                                                                                                                          /gene="F9N12.3"
                                                                                                                                                                                                                           /gene="F9N12.3"
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                                                                                                                                                             /gene="F9N12.
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DIMTYSILLDGLCNNGKLEKALEVFDYMQKSEIKLDIYIYTTMIEGMCKAGKVDDGWD
LFCSLSLKGVKPNVVTYNTMISGLCSKRLLQEAYALLKKMKEDGPLPDSGTYNTLIRA
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1 (bases 1 to 5348)
de Vetten, N.C. and Ferl, R.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEERNLLSVAYKNVIGARRASWRIISSIEQKEEGRGNEDRYTLIKDYRGKIETELTKI
CDGILKLLETHLVPSSTAPESKVFYLKMKGDYYRYLAEFKTGAERKDAAENTWVAYKA
AQDIALAELAPTHPIRLGLALNFSVFYYEILNSPDRACSLAKQAFDEAISELDTLSEE
SYKDSTLIMQLLRDNLTLWTSDISEDPAEEIREAPKRDSSEGQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5//133 5148 bp DNA PLN 26-SEP-1995 GRFI=general regulatory factor [Zea mays, XL80, Genomic, 5348 nt].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Two genes encoding GF14 (14.3-3) proteins in Zea mays. Structure, expression, and potential regulation by the G-box binding complex Plant Physiol. 106 (4), 1593-1604 (1994)
                                                                                                                                                                                                                                                                                                                                                                                       577133 Centrol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="14-3-3 protein homolog; This sequence comes from
                                                                                                                                                                                                                                                                                                                                                            47 aggttgatggtgtctaggtccttcaaccatagacgtggccgcatctgctggggccaatt 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                107 gcatcgtcgctggaagctctatatttggcgctgcggacccaggagccatcatatctgtgc 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 164519] from the original journal article. This sequence comes from Fig. 1.
                                                                                                                                                                                                                                                                                                                                 0; Gaps
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|onn(2177. 2583,2671. 2749,2876. 2998,4387. 4503,
|4610. 4689|
|yene="GRF1"
                                           HLRDGDKAASAELIREMRSCRFVGDASTIGLVANMLHDGRLDKSFLDMLS*
join(<19198. .19534,19579. .>19943)
/gene="F9N12.6"
                                                                                                                                                'note-"similar to unknown protein GB: AAF18697 from
                                                                                                                                                                                                                                                                             22.1%; Score 69.8; DB 8; Length 67712; 67.6%; Pred. No. 1.7e-11;
                                                                                                                                                                                                                                                                                                                                 47; Indels
                                                                                                                                                                     [Arabidopsis thaliana]"
join(19198. 19534,19579. 19943)
                                                                                                                                                                                                                                      /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                          0; Mismatches
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/db_xref="GI:998430"
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join(1491. .2583,2671.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="GF14-6"
                                                                                                                                                                                                                  /gene="F9N12.6"
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/gene="GRF1"
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The cDNA library to be analyzed within the framework of this project was created using a Borrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant.
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Submitted (01-SE-1999) Phytopathologie, INRA, route de St Cyr, 78026 Versailles, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 aggicoticaaccatagacgiggccgcatcigciggggccaatigcatcgicggiaag 122
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                                                                                                                                          3 taaggtgcgcacactgagaaagaagtaccttcccttgacatagaggttgatggtggtct 62
                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                                                           CNS01918 720 bp mRNA PLN 02-SEP-199
Botrytis cinerea strain T4 cDNA library under conditions of
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Leotiales; Sclerotiniaceae; Botryotinia.
                                                                    Query Match 21.6%; Score 68.4; DB 45; Length 5348; Best Local Similarity 87.2%; Pred. No. 3.2e-11; Matches 75; Conservative 0; Mismatches 11; Indels 0;
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Pred. No. 1.3e-09;
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146 c 178 g 170 t
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     1651 t
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Botryotinia fuckeliana.
Botryotinia fuckeliana
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   1203 g
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       1169 c
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FAGKOLEDGRILADYNIQKESTLHLVLRLRGGMOIFWYTLTGKTITLEWESSDTIDNV KAKIOKEGIPPDOQRLIFAGKOLEDGRTLADYNIQKESTLHLVLRLRGGMOIFWYTL TGKTITLEWESSDTIDNWAKIQKEGIPPDOGRLIFAGKOLEFRKTLTLEWESSDTIDNWAKIQKEGIPPDOGREGARTADYNIQKESTLHLVLRLRGGMOIFWTLTGKTITLEWESSDTIDNWAKIODKEGIPPDOQRLIFAGK QLEDGRTLADYNIQKESTLHLVLRLRGGMOIFWTLTGKTITLEWESSDTIDNWAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="ubiquitin"
/protein_id="AAC49014.1"
/db_xref="E1:90586"
/tanslation="WQIFVKTLTGKTITLEVESSDTIDNVKARIODKEGIPPDQORLI
                                                                                                                                  Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
1 (bases 1 to 2913)
                                                                                                                                                                                                    Liu, L., Maillet, D.S., Frappier, J.R., Walden, D.B. and Atkinson, B.G. characterization, chromosomal mapping, and expression of different polyubiquitin genes in tissues from control and heat-shocked maize seedlings
                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (14-JUN-1995) J. Roger H. Frappier, Zoology, University
of Western Ontario, University of Western Ontario, Rm 340 B&G
Bldg., London, Ontario N6A 2T2, Canada
Location/Qualifiers
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            20-JUL-1995
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ZMU29162 2913 bp DNA PLN Sea mays clone MubG9 ubiquitin gene, complete cds. U29162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="radicle"
/dev_stage="5-day-old radicles"
1025. .1034
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1909. .2136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /map="4L position 186"
/chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:4577"
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/strain="Oh43"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                G37533 424 bp DNA STS genomic, sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prepared with primer pairs derived from W80360 -- Unigene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 degrees C for 30 seconds
60 degrees C for 30 seconds
72 degrees C for 23 seconds
30
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Initial incubation: 95 degrees C for 10 minutes
                                                                                                                                                                                                                                                                                                            Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 18.3%; Score 57.8; DB 89; Length 424; Best Local Similarity 50.0%; Pred. No. 6e-08; Matches 137; Conservative 0; Mismatches 137; Indels 0
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each 200 uM
Ampliraq Gold Polymerase: 0.07 units/ul
Total Vol:
5 ul
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each 1 uM
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/db_xref="taxon:9606"
/map="5"
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50 mM
10 mM
8.3
                                                                                                                                                                                                                                                                                                                                                                                  Email: myers@shgc.stanford.edu
Primer A: CATGAACAGGAACACTGGGC
Primer B: TTGAGGACCCAGTTCCCATC
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75 g
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                /clone_lib="Human"
132. .363
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288 gatattcgagaatggagggagta 310
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103 c 75
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Unpublished (1997)
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PCR Profile:
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Best Local Similarity
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/translation="ESTRKQLGQDPFFDMHMNVSKPEOWVKPWAVAGANQYTFHLEAT
ENPGALIKDIRENGMKVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGQKFWEDM
MPKVHWLRTQFPSLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIMRSEDPRSVINLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (12-FEB-1998) Stanchi F., CRIBI Biotechnology Centre,
Universita' di Padova, Via G. Colombo 3, 35121, ITALY
2 (bases I to 1574)
Stanchi,F., Bertocco,E., Simionati,B., Zimbello,R. and Valle,G.
Finding homologues between human and yeast
                                                                                    184 ggctctcagaacaaaaactgattttggtgtttctgctgtaaagtactcctccgtttttt 243
                                                                                                                                                                                                                                                                              375 AAGGTTCACTGGTTGAGGACCCAGTTCCCATCTTTGGATATAGAGGTCGATGGTGGTG 316
                                                64 ggtccttcaaccatagacgtggccgcatctgctggggccaattgcatcgtcgctggaagc 123
                                                                                                                                                124 tctatatttggcgctgcggacccaggagccatcatatctgtgctgaggaagagcgtcgag 183
                                                                                                                                                                                            255 GCTATINIGNGGNGTGAAGACCCCAGATCTGTGATCAATCTATAAGAAATGTTTGCTCA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSAJ4326 1574 bp mRNA PRI 27-FEB-1998
Homo sapiens mRNA for putative ribulose-5-phosphate-epimerase,
partial cds.
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Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 1574)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE clone 206790"
/clone_lib="Soares fetal liver spleen INFLS"
/dev_stage="20 week post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/tissue_type="spleen"
/tissue_type="liver"
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/protein_id="CAA11895.1"
/db_xref="G1:2894532"
                                                                                                                                                                                                                                                                                                                                            244 tttattcgtcgcgttttagttcaaacatgaacta 277
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/db_xref="taxon:9606"
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Ribulose-5-phosphate-epimerase.
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3508. .3601,4052. .4154,4273. .4324,4401. .4441,4605. .4684,
5226. .5669,8502. .9085,9174. .10295)
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MEMQERGKIDINKLSDKPQAMDTKKAAGLVNSNPSAMPISPHTŞAAQPVDSSPSTSK
OSTDPOPDRTEISGGLKLNIGSKNNYLKKLOCKYKAMOI PRAWIDEBSWSVGAGDNSK
ELEVOTORNRREKETFYTSQVPMNPKDPPADLEMDEDDSJTPEVPIDQVPDVDAMET
BSVGAARSAVAPVKROIESASSTSGAVADDEBANTDYELLTVLLRNPELVFALTSNK
GENMPNEOTIALLDTIKQTGLESISEVNRLGNNGGLEKEPEPEPEPIPSDF
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LPAQIOANAPPSLPLLAVSVNPPVQHVSPVNNLLNRASVHQHGQQQYALLSDPVATPL
HQQAAGSKPRVVAHPSLPEPRASSHTAFPWOSNAADMTHAGRANATADWAAARAANSY
STASASTVPSANONAVGDGGKQGAY SSYGFSAASSRPVVPGHGHDRNGYSRSALIVEYP
WDGHHQRHSRSPDPGVNBDYDTDYGGAGGYSQOPLTOWSAGKVQQQGYNPEPSRQWSS
SQAHQGGYAPAEPSRQWSSSQAHQSYAPELPRQWSSERRGYDDAEPSRTWSSGQONPE
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IPPDIEAQAEVIEPLRILEPVVLQSFLQPTCVPQISSOSMELQOSDLQHMEYFONSLQ
OAEAGHNIAPTUMESCAMYMOPTDAR IS SDSVQKREVKGEGVHSGVASEDKRFLESIFA
LMQKEFFFSGQVKLMEWILQINNYTVLSRFYYMGGITINSTYLSOAAIEEOTSYIHVI
FKVLLHIPLHRALPVHNSVVLQTINKIRFYRTQDISSRARNILSRLSKVLVRIQALKK
PQKDLICKQRISEILRDESWKSEVDITEEVLALTDGAMESRREPFRET
                                                                                                                                                                                                                                                                                                                                                                       /translation="MELVLVKPAAGALVEVGSGSVAGAGSIPAMVAAQQEILHEQVDQ
LQRLVVAQCRLTGVNPLAQEMAAGALSIKIGKRPRDLLNPKAVKCMQSLFALKDILGK
                                                                      TUKKESYOTKEKOKKKVLLVEQPUKKATWKNANSVRNTSTNUSRPLSADDIOKAKMRA
MFMQEKRGKIDINKLSDKPOAMDTKKAAGLVNSNPSAMPISPHTSAAQPVDPSPSTSK
                                                                                                                      QSTDPQPDNTE1SGGLKLNIGSKNNVIKKLDCKKVLWQIPPGIFLLCAPQFAILLNVE
LMQKEETFSGQVKLMEWILQINNVTVLSRFVTMGGLTIMSTWLSQAAIEEQTSVIHVI
                          FKÜLLHLPLHKALPVHKALVVLQTINKLRFYRTQDISSRARNLLSRLSKVLVRIQALKK
PQKDLICKQRISEILRDESWKSEVDITEEVLALTDGANESRKPEPRKTPMLLTASAIE
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                                                                                                                                                                                                                                                                                             /product="flowering-time protein isoform alpha"
/protein_id="AAD51942.1"
/db_xref="GI:5805319"
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/replace="c"
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/product="flowering-time protein isoform beta"
join(580: 918,1604. 1631,1924. 2054,2692. 3251,3334. 3427,
3508. 3601,4052. 4154,4273. 4324,4401. 4441,4605. 4684,
5226. 5669,8502. 9085,9174. 10304)
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join(724. 918,1604. 1631,1924. .2054,2692. .325,3334. .3427,
508. .3601,4052. .4154,4273. .4324,4401. .4441,4605. .4684,
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3601,4052. 4154,4273. 4324,4401. 4441,4605. 4684,
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KETREISLLCCYTVTQVREFFVVQRSRVRKFVRLSQEKALRIETPKEODNSYSINTEO
IPPDIEAQAEVIEPLRTLEPVVLQSFLQPTCVPQISSQSMELQOSDLQHMEVFQNSLQ
QAEAQHNIAAPIMPSGAMVMQPTDAKISSDSVQKEVKQEGVHSGVASEDKKFLESIFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               van Nocker, S. and Amasino, R.M. Characterization of a gene from Zea mays related to the Arabidopsis flowering-time gene LUMINIDEPENDENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
1 (bases 1 to 10304)
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van Nocker, S. and Amasino, R.M.
Direct Submission
Submitted (07-UL-1999) Horticulture, Michigan State University,
390 Plant and Soil Science Building, East Lansing, MI 48824, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          zea mays flowering-time protein isoforms alpha and beta (ZmLD) gene, alternatively spliced products, complete cds.
               124 tctatatttggcgctgcggacccaggagccatcatatctgtgctgaggaagagcgtcgag 183
                                                                                                                                     434 GCTATTATGAGGAGTGAAGACCCCAGATCTGTGATCAATCTATTAAGAAATGTTTGCTCA 493
                                                                                                                                                                                          494 GAAGCTGCTCAGAAACGTTCTCTTGATCGGTGAAACCATAAGGAGCCCAGTGTTCCTGTT 553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="alpha transcript"
/product="flowering-time protein isoform alpha"
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                                                                                                                                                                                                                                                                                                                                             554 CATGAAATCTCCCTTTTACTGGAAAACAGGAATA 587
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/chromosome="3"
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184 ggctctcagaacaaaactgatttt 208
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HTG; HTGS_PHASE2.
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                                                                                                                                                                                                                                                                                                                                                                                           Genomic organization and transcriptional regulation of maize ZMRRI and ZMRR2 encoding cytokinin-inducible response regulators
Blochim. Blochis. Acta 1492, 216-220 (2000)
2 (bases 1 to 3846)
Sakakibara, H., Deji,A. and Sugiyama,T.
Direct Submission
Submitted (10-AuG-1999) to the DDBJ/EMBL/GenBank databases. Hitoshi Sakakibara, Nagoya University, Graduate School of Bloagricultural Sciences: Furo-cho, Chikusa, Nagoya, Aichi 464-8601, Japan (E-mail:sakaki@ara, nagoya. a.c.ip, Tel:81-52-789-4105,
                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
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DEFINITION Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
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                                                                                                                                                                                                                                                                                                                                                             Deji,A., Sakakibara,H., Ishida,Y., Yamada,S., Komari,T., Kubo,T. and Sugiyama,T.
238 ttttttttttttgtcgccgttttagttcaaacatgaactagcggacgactgttttcgag 297
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/db_xref="taxon:4577"
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/protein_id="BAA85113.1"
/db_xref="GI:6009897"
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/gene="ZmRR2"
/note="cytokinin-inducible"
/codon_start=1
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                                                      283 cgactgatattcgagaatggaggagtactt 313
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Zea mays ZmRR2 gene for
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"Ison. R., Ainscough, R., Anderson, K., Baynes, C., Berks, M.,
Bonfeld, J., Button, J., Connell, M., Copsey, T., Cooper, J.,
Coulson, A., Craxton, M., Dans, S., Durbin, R., Favello, A.,
Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M.,
Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N.,
Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B.,
O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A.,
Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E.,
Staden, R., Sulston, J., Thierry Mieg, J., Thomas, K., Vaudin, M.,
Vaughan, K., Waterston, R., Watson, A., Weinstock, L.,
Wilkinson-Sproat, J. and Wohldman, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 24474 AAGGTCAAGTGGCTGCGCGAAAACTACCCCAACCTGGACATCGAGGTGGACGGAGGTGTG 24533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24594 GCCGFGGTGGGCGCCTCCGATCAGTCGCAGGTCATCAAGGAGTTGCGCGGATGTGGTGCAC 24653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24534 GGACCCAAGACTATACACTGCTGTGCCGAGGCCGGAGCCAACATGATCGTCTCGGGAACC 24593
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

I (bases 1 to 26292)
Adams,M. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 ggtccttcaaccatagacgtggccgcatctgctggggccaattgcatcgtcgctggaagc 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 tctatatttggcgctgcggacccaggagccatcatatctgtgctgaggaagagcgtcgag 183
                                                                                                                                                                                                                                                                                                    This sequence was identified as CDM:10211468 by the submitter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 aaggtgcgcacactgagaaagaagtacccttcccttgacatagaggttgatggtggtcta 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-1995
                                                                                                                                                                                                                                                                                                                                      For more information on this record e-mail to fly@celera.com.
                                                                                                                                                                                        Direct Submission
Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
                                                                                                                                                                                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 26292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans strain-Bristol N2.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
a 6111 c 5943 g 7116 t
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53.2%; Pred. No. 1.5e-05;
1ve 0; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CELF08F8 27521 bp DNA
Caenorhabditis elegans cosmid F08F8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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AUTHORS TITLE JOURNAL REFERENCE AUTHORS

JOURNAL MEDLINE REFERENCE TITLE JOURNAL

COMMENT

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join(20193. .20236,20314. .20426,20522. .20618,20711. .20916,

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22725. .22878)

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22725. .22878)
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SVVRSTLASGNQNINWADKRKLLDFLQSCDISDEASRKIENFICENYDOKEKEKKPL
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FRAVRLIRRGGARSREESRFPARQAIPIRRFINKKFENLPYLGYDYTLATECCCENV
IGYTPVPVGVAGPLTLNGTSEIYVPMATTEGALIASTNRGMNVIRAAGGVETSIENSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MTRAPYVKFPPTARDAYSMKRALEHPENQDRARQEFQSCSRFAKLKSIDITIDGNLAYL
RFDAHTGDAMGMMISKSCDSTMRFLMENFFEMTVLALSGNLCVDKKRAAKNWTEGRG
RSVVABCLLIPREVYRKTLRTPPEQLAYLTTKLHIGSRRAGAVGGSNAHAANIVPAIF
IATGQDAAQVYSSSMCSTRMEVTADKNLXVSCTLPCVEVGTVGGGTLLAPQRACLESL
GCAGPWREQPEQNABELLAEVIAATVLAGELSLAMALTYNELVSSHMKLANRSKQQLYAD
DSGKATHFEKEVEKAGSLLSGKSGNIKLKRLPQDVVQCSNIL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAASHYYGQRVERKKRLGGELARRQGRVYEEVSSPGFLKRSADQSRAGSIQPABGPSR
KQRRNNKWOYTVNAEDISDDEEBHANSETWEALRKARSTENSIDVKLYSLKLYA
SSHGGFDIDBYRYGSRQTSFKTVTTEIEGI. EQLININDDMIDYAGAGSSASMANDPA
IQHTLRRHREILIRDYGSEYRRARDINVDQVLQREILLISSSNENRNNYILINNRARGYDMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IKTRKQKNTLILAAVISSIOMTLRPEVCPSILNADLASLASECKKLLAAGADMLHLDV
MDGHFVPNLITEGHPVVESLRKSLGAEPFFDVHLMVSNPGQWVEPMAKAGASQFTFHYE
AVDGDVAVSELIEKIRKSGMKVGLSVKPGTSVEHILKHANHLDNALIMTVEPGFEGGQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMENMMEKVRTIRSKYPNLTIQVDGGVTPENIEISAQAGANAIVSGTGIIKAADQSVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RCPKRKVLDDDATDDNITANGPFKKLFNEHMKKINEELGYCDEKNDLWSPEKRIFLVL
SVREERMLIGGILVIEKISRAWTNVGKMEVTDNNDINDWIVGVDRIWVDSHCRMKGVA
NSLLDAATTQDRQMEFRSRRLRIAFCDPTDDGIKLARRFIEQQKNLNSYICRILETGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERQLDGKYYLEEEAKLTPIEEKAKNNYVRRMTVHNPRFLKLTEKIQKNRTFRLRKVWL
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complement(join(6985. .7182,7232. .7319,7372. .7671,
8071. .8175,8664. .8751,9101. .9233,9285. .9369,9416. .956
9608. .9717,10088. .10199,10440. .10528,10903. .10965,
11548. .11750,12334. .31134,13515. .13882,14444. .14561,
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15979. .16159,17067. .17684,17731. .18062,18111. .18261,
18957. .19168,19216. .19415,19855. .19947,19993. .20089))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MKDPGLPKNSLKKSKLDDYFKKVERNTEENLOEQSTSADVQKSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="coded for by C. elegans cDNA cmllo3; coded for by C. elegans cDNA yk34f3.5; similar to hydroxymethylglutaryl-coA reductase (NADPH)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="coded for by C. elegans cDNA cm21c7"
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/db_xref="GI:861367"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAA68385.1"
/db_xref="G1:861366"
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/gene="F08F8.5"
                                                                                                                                                                                                                                                                                                                                                                                                         /gene="F08F8.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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                            CDS
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/ GOTOL_STAIT=1
/ GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_GOTOL_
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6071. 8175,8664. 8751,9101. 9233,9286. 9369,9416. 9564,

9608. 9717,10088. 10199,10440. 10528,10903. 10965,

11548. 11750,12334. 13134,13515. 13882,14444. 14551,

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15979. 16159,17067. 17684,17731. 18062,18111. 12251,

18957. 19168,19216. 19415,19855. 19947,19993. 20089))
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1676. .1814,1861. .1948,2079. .2433,2784. .3002,3089. .3213,
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HPUHLGSVUVNY STNGQKQETKPGKKDNRYPEDVTFPPSDIERVYDTMGDEDTRKSKT
MTLGTIEEPARKSAMLSLQKTPKESETDLKKTLPRSPPPIPURKQPSREIMLTPKQST
KTANAGGRSKEPSLAWTAMSQEAGNIEPRKTPSKDTIGSTGVLPSNQDKKTPSKEKESV
KNTPAPTFKLGTAEPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coding sequences below are predicted from computer analysis, using the program Genefinder (P. Green and L. Hillier, ms in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5' cosmid is F56C9, 2904 bp overlap; 3' cosmid is T29B12, 1500 bp overlap. The actual start is at base position 23860 of CELF56C9; actual end is at base position 7908 of CELF20B12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Sequencing Center
Department of Genetics, Washington University,
St. Louis, MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CBIO, IRQ, England
e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk

    .27521
    /organism="Caenorhabditis elegans"
    /strain="Bristol N2"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (12-JUN-1995) Robert Waterston
                                                                                                                                                                                                                                                                            The sequence of C. elegans cosmid F08F8 Unpublished (1995) 3 (bases 1 to 27521) Waterston, R.
                                             Nature 368 (6466), 32-38 (1994)
94150718
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/map="III"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted by:
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                                                                                                                                                                                            (bases 1 to 27521)
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. .26249,26492. .26554,26921. .27018,27105. .27222,
                                                                                                                                                                                                                                                                            join(25631. .26249,26492. .26554,26921. .27018,27105. .27222,
                                                                                       /translation="MKTTTATNSILFKLYFAPGATEQISIEYYNLQQLIEKLELKLGE
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                                                                                                                                                                              RFQESHGHPEFKRRHCFGGRRARSASPIGRRPCREGEEFKRHPLGSFGTPCGREEFEG
                                                                                                                                                                                                               PTGGFGRPFGRRGMDHHGFNFHRHHPPFGAFHGFGGHHHGFFGHGFFGHHGFKRQHPFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RHCGRRDRSRSRGFDRSRSRSRSRFHDHHKRHOMKKLMMKRPQESHGHPEFKRRHC
FGGRRARSASPIGRRPCREGEEFKRHPLGSFGTPCGREEFEGPTGGFGRPFGRROMDH
HGFNRTHHHPFGAFHGFGGHHHGFGHGFGHHGFKRQHPFERRFGRLTFCIFTSNNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRLLIFKLKLAMPWNTNNRNSVKNSFISPPSMPBYEÖLPNFONVQPFNASETSBIIRF
LRIQFPINDLTCGLLENLSDYRKPISMNQVTTLRFCQTIEFCVENSVFVLVTRYIEIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MANRDSASIFVIADSDSSDSSDSSDSGDEDVIIADAPEVAPHR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7186 TCAGGITCGCACAATCCGTTCAAAATATCCCAAATCTGACTATTCAAGTTGACGGAGGAGT 7127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7126 AACACCTGAAAATATTGAAATCTCTGCTCAAGCTGGAGCCAATGCGATGGTGAAGTGGAAC 7067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7066 IGGAAICAICAAAGCIGCAGAICAATCIGICGCCAIGACAACAATCAGAAAIGCAGIIGA 7007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 aggteetteaaceatagaegtggeegeatetgetgggggeeaattgeategtegetggaag 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 ctctatattttggcgctgcggacccaggagccatcatatctgtgctgaggaagagcgtcga 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 taaggtgcgcacactgagaaagaagtacccttcccttgacatagaggttgatggtggtct 62
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16.3%; Score 51.4; DB 30; Length 27521;
Best Local Similarity 52.6%; Pred. No. 1.5e-05;
Matches 112; Conservative 0; Mismatches 101; Indels 0;
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/evidence=not_experimental
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/db_xref="GI:861368"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAA68388.1"
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                                                                                                                                                                                                                                                                                                          27271. .27431)
/gene="F08F8.1"
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Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
Pl library location: 36-94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /map="43D1-43D7"
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/clone="Pl DS03454 (D399)"
/note="DS03454 (D399) is a partial bridge clone containing
the minimal sequence necessary to overlap its proximal
neighbor (DS01142) D148 and extending to pl end."
Zieran, L.L. and Rubin, G.M.
Sequencing of Drosophila chromosome 2R, region 43D1-43D7
Upublished (1998)
2 (bases 1 to 50089)
2 (chanker, S.E., George, R.A., Galle, R., Svirskas, R.R., Hoskins, R.A., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Chavez, C., Chew, M., Doyle, C.M., Farfan, D. B., Flanagan, J., Houston, K.A., Hummasti, S.R., Karrak, K., Kearney, L., Kim, S.H., Lee, B., Lomotan, M.A., Mak, J., Mazda, P., Mok, M.S., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Feiffer, B., Punch, E., Shir, E., Twomey, B., Wan, K.H., Whitelaw, K.R., Yee, A., Zhang, R.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                     Submitted (10-SEP-1998) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA On Nov 26, 1998 this sequence version replaced gi:3893005.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45542 AAGGTCAAGTGGCTGCGCGAAAACTACCCCAACCTGGACATCGAGGTGGACGGAGGTGTG 45483
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    .50089
    /organism="Drosophila melanogaster"
    /strain="y2; cn bw sp"
    /db_xref="taxon:7227"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence submitted by:
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HTG; HTGS_PHASE1.
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                                                               JOURNAL
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                                 TITLE
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REFERENCE AUTHORS

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f unknown length
g of 2210 bp in length
f unknown length
g of 2239 bp in length
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                                                                                                                                                                                                                                                                                                         Upubblished

[Lases 1 to 125150]

[Celniker, S.E., George, R. A., Galle, R., Svirskas, R.R., Hoskins, R.A., ArGaina, T.T., Baxter, E., Blazej, R.G., Chavez, C., Chew, M., Doyle, C.M., Farfan, D.E., Flanagan, J., Houston, K.A., Humasti, S.R., Karra, K., Kearney, E., Kim, S.H., Lee, B., Lomotan, M.A., Mak, J., Mazda, P., Mok, M.S., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Punch, E., Shir, E., Twomey, B., Wan, K.H., Whitelaw, R.R., Yee, A., Zhang, R., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (14-A0G-1998) Drosophila Genome Center, Lawrence Berkeley Laboratory MS 64-121, Berkeley, CA 94720, USA On Jul 30, 1999 this sequence version replaced gi:5597051.

For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases. Pl library location:
              Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Drosophila; Dr
    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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of 652 bp in length
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unknown length
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unknown length
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TITLE JOURNAL

COMMENT

TITLE JOURNAL

REFERENCE AUTHORS

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                                                ORIGIN
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ACO08258 131899 bp DNA HTG 31-JAN-2000 Drosophila melanogaster chromosome 2 clone BACR04G20 (D921) RPCI-98 04.62.20 map 43C-43C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ACO08258 ö 26389 AAGSTCAAGTGGCTGCGCGAAAACTACCCCAACCTGGACATCGAGGTGGACGTGTG 26330 26329 GGACCCAAGACTATACACTGCTGTGCCGAGGCCGGAGCCAACATGATCGTCTCGGGAACC 26270 26269 GCCGTGGTGGCGCCTCCGATCAGTCGCAGGTCATCAAGGAGTTGCGCGATGTGGTGCAC 26210 64 ggtccttcaaccatagacgtggccgcatctgctggggccaattgcatcgtcgctggaagc 123 124 tetatatttggegetgeggaeceaggageeateatatetgtgetgaggaagagetegag 183 Gaps 4 aaggtgcgcacactgagaaagaagtaccettccettgacatagaggttgatggtggtcta 63 DB 27; Length 125150; ô Score 51.4; DB 27; Length Pred. No. 2e-05; 0; Mismatches 96; Indels Db 26209 AGCTACCTCAAATAGAGATTCATTT 26185 184 ggctctcagaacaaaaactgatttt 208 16.3%; 53.2%; Matches 109; Conservative Best Local Similarity Query Match q ò Qγ ð g δ

Submitted (30-JUL-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA On 131, 2000 this sequence version replaced gi:5670394.

For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.frultfly.org/sequence/) or send email to bdgp@frultfly.org/sequence/) or send email the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence. It currently consists of 119 contigs. The true order of the pleces Updates 1 to 131899)
Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Cleniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Celliker, S. C., Agagyali, A., Arcaina, T.T., Baxter, E., Blazej, R.G. Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D. E., Galle, R., George, R.A., Harris, M. L., Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karray, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A., Monner, M., Moshrefi, M., Richards, S., Sethi, H., Sylrskas, R.R., Wan, K.H., Webster, D., Rolley, P., Yang, S., Yee, M., Yu, C. and Rubin, G.M. Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila. 1 (bases 1 to 131899) iruit fly. Drosophila melanogaster AC008258.3 GI:6838455 HTG; HTGS_PHASE1. Direct Submission Unpublished Rubin, G.M. fruit fly AC008258/c DEFINITION ORGANISM ACCESSION REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS JOURNAL KEYWORDS VERSION TITLE TITLE RESULT SOURCE LOCUS

COMMENT

arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. not known and their order in this sequence record is octing of 1192 bp in length is gap of unknown length is contig of 1086 bp in length is gap of unknown length is gap of unknown length contig of 885 bp in length is gap of unknown length is contig of 790 bp in length is contig of 1088 bp in length is contig of 1188 bp in length is gap of unknown length is contig of 1175 bp in length is gap of unknown length is gap of unknown length is gap of unknown length is contig of 1132 bp in length is gap of unknown length gap of unknown length contig of 727 bp in length contig of 783 bp in length gap of unknown length gap of unknown length contig of 979 bp in length gap of unknown length contig of 828 bp in length gap of unknown length contig of 866 bp in length gap of unknown length contig of 1005 bp in length gap of unknown length contig of 999 bp in length f unknown length g of 1009 bp in length f unknown length g of 1275 bp in length of 1005 bp in length unknown length of 1175 bp in length unknown length contig of 1023 bp in length gap of unknown length of 783 bp in length of 1235 bp in length contig of 1006 bp in length gap of unknown length contig of 1260 bp in length of 739 bp in length of 819 bp in length unknown length of 644 bp in length unknown length of 896 bp in length unknown length of 647 bp in length length length unknown length of 772 bp in length 689 bp in length of 841 bp in length unknown length of 981 bp in length 822 bp in length unknown length g of 790 bp in len unknown length unknown length length unknown length unknown length unknown length unknown length of 689 bp in unknown oţ contig gap of contig gap of contig gap of contig gap of gap of contig contig gap of contig gap of gap of gap of contig contig contig contig contig contig gap of gap of gap of contig qap of contig gap of gap of gap of contig gap of 3492: 4400: 2894: 2433: 6198: .0391: 390: 2814: 32990: 34250: 4480 5299 6137 784 864 1591 10392 10472 11560 111640 1128915 114027 14107 14973 115053 116058 4481 5220 5300 6119 6199 671 2434 3493 8557 8637 9522 9602 19926 20006 21281 21361 221361 22920 23000 23647 23727 7391 17861 17941 18837 8917 24982 25671 25751 26523 26603 27626 7471 22231 24902 28627 29608 29688 30923 31003 31825 31905 32911 28547

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OM nucleic - nucleic search, using sw model

Run on:

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US-09-300-482-619

Perfect score:
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Scoring table:
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Searched:
480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters:
960044

Minimum DB seq length: 0

Maximum Match 100%
Listing first 45 summaries

Database:
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N_Geneseq_36:*

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Human insulin-resp Human FLAME-1 CDNA Human MACH related I-FLICE-1 coding s Human CLARP coding Human CLARP coding Human insulin-resp Gsurpin-alpha poly Homo sapiens B258 Human CFLIP-L DNA. Human FLICE-like i Human FILCE-like i Human FILCE-like i Human FILCE-like i Human FILCE-like i Human FILCE-like i	Sequence of human Polynucleotide seq Human iduronate-2-Human IDS cDNA. HUMAN IDS CDNA. HUMAN iduronate-2-Human IDS gene. HUMAN iduronate-2-Human IDS gene. HDNA encoding iduronate-2-Human IDS gene. HDNA encoding iduronate iduro	eponema pallidum. lia infection; animal; terisation, prevention ularly syphilis
	N90338 X20665 V52836 X818181 V52837 V52837 V522975 V522975 V52294 V52199 V52199 V52199 V52199 V52199 X56946 V18275 Z22914 X35267	ALIGNMENTS BP. the genome of Tr syphilis; Borre dum nucleic acids diagnosis, charac figerions, partic figerions, partic p; English.
22222	12923 10 12923 10 12924 19 12297 19 12297 19 1428 19 1418 19 1418 19 1618 19	firs sec idum ion, jour jour jour jour jour jour jour jour
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	#	1 20527 standi 20527; 5-MAY-1999 0lynucleotic reponema pal 12yme produc reponema pal 12yme produc reponema pal 12yme produc reponema pal 12yme produc reponema pal 12yme produc reponema pal 12yme produc reponema pal 13yme produc reponema pal 14yme produc 14yme produ
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                                 Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrelia infections in animals, and for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2718 CITCAGACCACGCTITITATITITGGTATCAAAGACTGGTACGACGCTTGAAACACTCAGT 2659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 ggtctactagaagtacagaaagccttcagagatgcgggggctgcaattctcgaaacagggt 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 ctggcaactactcttgtaattgtcatttctaagagcggaggcacacctgaaacccgcaat 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of
X20500-21243 represent polynucleotide sequences from the genome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 10820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                      Sequence 10820 BP; 2418 A; 2982 C; 2962 G; 2450 T; 8 other;
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                                                                                                                                                                                                                                                                  production of biosynthetic products such as enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2598 GIGGCAGITACCAGCGAGACCAGICCACTIGCAAATAATCC 2558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 gttgcaattactcaagaaaattctctgttggataacactgc 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36.2; DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fannon MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0.068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 1752-1753; 3271pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.1%;
51.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361..420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are intelly to encode antigens have been identified and these polypeptides can be obtained. Specifically, sequences which are be used in a vaccine composition against S.aureus in a sample. S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, ostcomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypetides. The new DNA sequences can be used cand their fragments) are useful as primers or probes for isolating the production of the S.aureus DNA sequences contained on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 aattgotcaactaggacctgaactggcaactactcttgtaattgtcatttctaagagcgg 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207 AATTGTACTIGTGCAACTAGGACTAACAAATTCTGTAGTAGCAATCATTATTATTGCCAG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 aggcacacctgaaacccgcaatggtctactagaagtacagaaagccttcagagatgcggg 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 AGAATTTGCCGTAACTGGTTTACGTTTACTACAAATTGAACAAGGATTCGTAAGTGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterococcus faecalis, contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence 543 BP; 178 A; 100 C; 53 G; 152 T; 60 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterococcus faecalis genome contig SEQ ID NO:399.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 32.4; D. Pred. No. 0.37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 gctgcaattctcgaaacagggtgttgcaattact 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 IGGICAATTAGGIAAAATTAAAACAGCAGTTACT 54
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97US-0044031.
97US-0046655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.8%;
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                                                                                                                                                                                                                                                                                                                                                      computer readable medium.
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Matches 78; Conservative
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16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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A computer readable medium has been developed which has recorded on it $1298 nucleotide sequences isolated from the Enterococcus faecalis genome. $12938 to $1399 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system commercial importance. The products can be used to detect the presence diagnosing Enterococcus faecalis in samples. They can also be used for products can be used to detect the presence diagnosing Enterococcul infection in an animal and monitoring progression of disease, and for identifying agents which can be used to another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                 4906 aattcatcaatttcatattaagttttttgtagatgggaataaacgcagaacagcaaatca 4965
                                                                                                                                                                                                                                                                                                                                                                                                            52 taggacctgaactggcaactactcttgtaattgtcatttctaagagcggaggcacacctg 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 aaacccgcaatggtctactagaagtacagaaagccttcagagatgcgggggtgcaattct 171
                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phosphatidylglycerophosphate synthase; pgsA gene; infection; diagnosis; therapy; vaccine; antibacterial; antibiotic; screening;
                                                                                                                                                                                                                                                                                                                                                        Length 32768;
                                                                                                                                                                                                                                                                                              Sequence 32768 BP; 10797 A; 5960 C; 7083 G; 8921 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New synthase polypeptide useful to treat conditions requiring synthase and to screen for antibacterial compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S. aureus phosphatidylglycerophosphate synthase pgsA gene.
                                                                                                                                                                                                                                                                                                                                                                                      69; Indels
                                                                                                                                                                                                                                                                                                                                                        DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Warren RL;
                                                                                                                                                                                                                                                                                                                                              ch 10.5%; Score 31.6; Di Similarity 51.4%; Pred. No. 3.3; 73; Conservative 0; Mismatches
                            Claim 1; Page 1592-1609; 2084pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4966 aggtcgtggttgttccatctcc 4987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 cgaaacagggtgttgcaattac 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X87836 standard; DNA; 579 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0026017.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Petit CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-518603/43.
                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9942562-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-AUG-1999.
infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Holmes DJ,
                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X87836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                Matches
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The present sequence represents a claimed polynucleotide coding for the phosphatidylglycerophosphate synthase (pgsA, see Y31662) of staphylococcus aureus WGCH29 (NCIMB 40771). The gene can be isolated from chromosomal DNA of WGUH29 using a hybridisation proble. The invention provides pgsA polynucleotides and antagonists. The polypeptides can be administered therapeutically, especially by expressing encoding polynucleotides, to treat an individual in need of pgsA polypeptide (claimed). Polynucleotides and can can be used to produce probes for detecting or isolating sequences useful for recombinant production of pgsA polypeptides, and can also be used to produce probes for detecting or isolating sequences relating pgsA or similar sequences e.g. to diagnose diseases relating to polypeptide expression or activity (claimed) and to for gene mapping. Computer readable forms of the present sequence may be used to perform homology identification, by comparing the sequence with at least one polynucleotide/polypeptide sequence to sequence and a second polynucleotide sequence (claimed). The computer and a second polynucleotide sequence (claimed) or a least one overlapping region between the present sequence and a second polynucleotide sequence (claimed). The polynucleotides can mammal is incoulated with a nucleic acid vector dispersion of the nucleic acid vector dispersion of the nucleic acid vector dispersion of the nucleic acid vector dispersion of the nucleic acid vector dispersion of the near an immunological disperiment in vivo avarragation of the near and nucleic acid vector dispersion of the near and a second polynucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 aattgctcaactaggacctgaactggcaactactcttgtaattgtcatttctaagagcgg 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     270 aattgtacttgtgcaactaggactaacaaattctgtagtagcaatcattattgccag 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 aggcacacctgaaacccgcaatggtctactagaagtacagaaagccttcagagatgcggg 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           330 agaatttgccgtaactggtttacgtttactacaaattgaacaaggatttgtaagtgcagc 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               directing in vivo expression of the pgsA polypeptide or fragment/variant, in order to produce antibody and/or T cell immune responses to protect the animal from disease (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterococcus faecalis; contig; detection; Enterococcal infection; Vaccine; attenuation; computer readable medium; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.3%; Score 30.8; DB 20; Length 579; 50.0%; Pred, No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 579 BP; 176 A; 62 C; 115 G; 226 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterococcus faecalis genome contig SEQ ID NO:542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 gctgcaattctcgaaacagggtgttgcaattact 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   390 tggtcaattaggtaaaattaaaacagcagttact 423
  Claim 6; Page 42; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X13479 standard; DNA; 1004 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-US08985.
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Best Local Similarity 50.08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterococcus faecalis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-NOV-1997;
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16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-NOV-1998
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A compute reduction has been considered from the Enterococcus faccalis genome. X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as configs. The computer-based system commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcual infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcus!
                                                                                                                                                                                                                          A computer readable medium has been developed which has recorded on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 gcacacctgaaacccgcaatggtctactagaagtacagaaagccttcagagatgcggggc 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                788 getegeaagacacccacacgcacactgtacgtatgcaacgccacttattttattgtngte 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 tgcaattctcgaaacagggtgttgcaattactcaagaaaattctctgttggataacactg 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 ctagaatagagggatggttagctcggtttcctatgtttgattgggttggtggtaggactt 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        848 yttaatcactgcaccetggtagttaaattycttcataaaattctccatcatcgtaataat 907
                                                                                                 New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae, antigen; vaccine; infection; diagnosis; detection; pneumonia; otitis media; meningitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1004 BP; 304 A; 188 C; 187 G; 316 T; 9 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.3%; Sco...
47.0%; Pred. No. 1...
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "no stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae SP0075 nucleotide.
                                                                                                                                                                                           Claim 1; Page 1797-1798; 2084pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "SP0075"
                                    Dillon PJ, Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V27386 standard; DNA; 1051 BP.
(HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                       WPI; 1999-045171/04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86;
                                      Barash SC,
                                                                                                                                                                 infection
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The present sequence encodes a protein from Streptococcus pneumoniae.
The nucleic acid sequence encoding the Streptococcus pneumoniae protein
Streptococcus pneumoniae, for inducing protective antibodies against
Streptococcus pneumoniae, for treatment or prevention of infection e.g.
The nucleic acid sequence encoding protective antibodies against
The streptococcus infection (by usual hybridisation or are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific antibodies in standard immunoassays, especially for diagnosing or antibodies in standard immunoassays, especially for diagnosing or antibodies in standard immunoassays, to purify the protein and for passive detect corresponding antigans, to purify the protein and for passive immunisation (optionally coupled to a toxin). Vaccines are administered, e.g. by injection, orally or through the skin, typically at 0.01-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   677 AATCCCACTCCCCTTCTGGCATGACAACAGGGTAATCTTCCATGTCTTGGGCAAGCTGAT 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 aacaccgatcctgctgggattgatcatcaaattgctcaactaggacctgaactggcaact 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S. pneumoniae; genome; diagnosis; assay; vaccine; pharmaceutical composition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 actottgtaattgtcatttctaagagcggaggcacacctgaaacccgcaatggtcta 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ,0,
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                                                                                                                                                                                                                                                                               Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae genome fragment SEQ ID NO:33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1051 BP; 283 A; 225 C; 263 G; 280 T; 0 other;
                                                                                                                                                                                     Johnson LS, Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 75-76; 118pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V52166 standard; DNA; 13206 BP.
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                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae; computer readable medium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 53.8%
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae
                                                                                                                                                                                           Choi GH, Hromockyj A,
                                                                                                                                                                                                                                 WPI; 1998-272224/24
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                                                                                                                 31-OCT-1996;
WO9818930-A2
                                                                           30-0CT-1997;
                                       07-MAY-1998.
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V52166
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Gaps

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96US-0029960
31-OCT-1996;
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(HUMA-) HUMAN GENOME SCI INC

Fannon Dougherty BA, Dillon PJ, Rosen CA; Cho1 GH, Barash SC, Kunsch CA,

WPI; 1998-272225/24.

Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus oneumoniae

Claim 1; Page 332-339; 1409pp; English

The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (V22134 to V55524) recorded to nit, or a representative fragment or a sequence at least 95% identical to SED ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391 (V52134 to V52524) are genomic fragments from Streptococcus collecule encoding a homologue of any of the fragments of the S. pneumoniae of pneumoniae are present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S. pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a process comprising: (a) screening a genomic DNA library using as a process comprising: (b) screening a genomic DNA library using a process comprising of the library which contain sequences to 391, identifying members of the library which contain sequences from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the computer-based system for identifying fragments of the solution encounter of the sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome or computers from the present convention can be never invention can be neved in a computer-based system for identifying fragments of the subminiar genome or commercial importance, or expression modulating invention can be neved in diagraphy to the second or expression modulating invention can be neved in diagraphy to the second organizating the amplification primer according to the second organizating the amplification when the present invention can be neved in diagraphy and second organizating the amplification in the present invention can be neved to the second organizating the second organizating the second organizating the second organizating the second organizating the second organizating the second or used in diagnosis kits and assays, and pharmaceutical vaccines for S. pneumoniae. compositions and

Sequence 13206 BP; 4016 A; 2929 C; 2473 G; 3786 T; 2 other;

ö Gaps 10.2%; Score 30.6; DB 19; Length 13206; 53.8%; Pred. No. 4.8; ative 0; Mismatches 54; Indels 0; Conservative Query Match Best Local Similarity 63; Best Loca Matches

9898 aateccattcccttctggcatgacaacagggtaatcttccatgtcttgggcaagctgat 9957 12 aacaccgatcctgctgggattgatcatcaaattgctcaactaggacctgaactggcaact 71 g

RESULT V74475

δ

V74475 standard; DNA; 22243 BP

(first entry) 16-MAR-1999 Staphylococcus aureus contig SEQ ID #164.

Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds

Staphylococcus aureus

(ev

Location/Qualifiers

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/*tag= c //*tag= c //*tag= c //*tag= c //*tag= c //*tag= c //*tote= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
                                                  the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence. /*tag= b //note= "these bases represent a line of missing text in
                                                                                                                                      "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence."
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /note- "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"...10920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
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                                     /note= "these bases represent a line of missing text in
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/*tag= f
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                   /*tag= a
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                                                                                                    misc_feature
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of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or requilatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used
                               the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents one of 5191 Staphylococcus aureus DNA sequences
"these bases represent a line of missing text in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20692 attititagicaattacggcttictgctaatatggaagttatcattgcgaatacattaaatga 20751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 actggcaactactcttgtaattgtcatttctaagagcggaggcacacctgaaacccgcaa 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 atttattgacaacaccgatcctgctgggattgatcatcaaattgctcaactaggacctga 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of anti-S.aureus vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.2%; Score 30.6; DB 18; Length 22243; 50.7%; Pred. No. 5.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Choi GH, Dillon PJ, Fannon MR, Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 800-813; 3271pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 20812 tggttgcatggaagaattaaaa 20833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 tggtctactagaagtacagaaa 143
                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239041 standard; cDNA; 1062
                                                                                                                                                                                                                                                                                                       97EP-0100117.
                                                                                                                                                                                                                                                                                                                                                                          96US-0009861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               computer readable medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-374922/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                           07-JAN-1997;
                                                                                                                                                                            EP786519-A2
                                                                                                                                                                                                                                           30-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z39041;
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The present sequence encodes human FLICE-like inhibitory protein short form, designated FLIP-S. The present invention describes a new treatment of a condition characterised by vascular wall inflammation in a subject comprising administering a FLIP molecule to inhibit Fas ligand-mediated apoptosis of vascular endothelial cells in the subject. The method can be used to treat atherosclerosis, transplant arteriosclerosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 acccgcaatggtctactagaagtacagaaagccttcagagatgcgggggctgcaattctcg 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 ggacctgaactggcaactactcttgtaattgtcatttctaagagcggaggcacacctgaa 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246 ggagctgtactgcaagacccttgtgagcttccctagtctaagagtaggatgtctgctgaa 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                 /product= "FLICE-like inhibitory protein short form" /note= "FLIP-S; apoptosis inhibitor"
          Human FLICE-like inhibitory protein short form nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          306 gtcatccatcaggttgaagaagcacttgatacagatgagaaggagatgctgctttttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating conditions characterized by vascular wall inflammation
                                         Human; FLICE-like inhibitory protein long form; FLIP-L; FLIP-S; FLICE-like inhibitory protein short form; apoptosis inhibitor; arteriosclerosis; vascular wall inflammation; vascular injury; Fas ligand-mediated apoptosis; atherosclerosis; transplant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1062 BP; 328 A; 212 C; 246 G; 276 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                         (SELI-) ST ELIZABETH'S MEDICAL CENT BOSTON INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                Location/Qualifiers
294..959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 71; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 9.9%;
Local Similarity 51.1%;
hes 70; Conservative
                                                                                                                                                                                                                                                                                                                                       99WO-US03558
                                                                                                                                                                                                                                                                                                                                                                         98US-0075471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V61936 standard; DNA; 1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 aaacagggtgttgcaat 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tgccgggatgttgctat 382
                                                                                                                                                                                                      /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-527469/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human CFLIP-S DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vascular injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; Y57455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-JUL-1999
                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                      W09942570-A1
                                                                                                                                                                                                                                                                                                                                                                           20-FEB-1998;
                                                                                                                                                                                                                                                                                                                                         19-FEB-1999;
                                                                                                                                                                                                                                                                                                        26-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Walsh K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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V61936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 acccgcaatggtctactagaagtacagaaagccttcagagatgcggggggtgcaattctcg 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         346 ggagcigtactgcaagacccttgtgagcttccctagtctaagagtaggatgtctgctgaa 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          406 gtcatccatcaggttgaagaagcacttgatacagatgagaaggagatgctgctctttttg 465
                                                                                                                                                                                                                                                                                                                                                                                                          New DNA encoding for anti-apoptotic gene product - used to treat HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MRIT beta 1; MACH related inducer of toxicity; human; apoptosis; pro-apoptotic; cancer; autoimmune disease; infection; anglogenesis; atherosclerosis; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; retinitis pigmentosa; stroke; AIDS; aplastic anaemia; myocardial infarction; therapy; ss.
 domain; human; murine; anti-apoptotic; treatment; autoimmune disease; FLIP protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.9%; Score 29.8; DB 19; Length 1190;
51.1%; Pred. No. 3.5;
ive 0; Mismatches 67; Indels 0;
                                                                                                                                                                                                                                                                                                             rench EL, Hahne M, Hoffmann K;
Schneider P, Schroeter M, Steiner V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human MACH related inducer of toxicity MRIT beta 1 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1190 BP; 360 A; 250 C; 280 G; 298 T; 2 other;
                                                                         Location/Qualifiers
394..1059
                                                                                                                  /product= "CFLIP-S"
                                                                                                                                                                                                                                                                                                                                                                                                                             infections and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                       Hofmann K;
                                                                                                                                                                                                                                                                                                            French EL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; Fig 4A; 45pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X25510 standard; DNA; 1308 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.1%;
                                                                                                                                                                                                        97DE-1013393
                                                                                                                                                                                                                                    97DE-1013393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            466 tgccgggatgttgctat 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70; Conservative
                                                                                                                                                                                                                                                                                                                         Rimoldi D,
                                                                                                                                                                                                                                                                                                                                       Tschopp J,
                                                                                                                                                                                                                                                                                                          Bodmer J, Burns K,
Irmler M, Rimoldi D
                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-532710/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                               (TSCH/) TSCHOPP J. (APOT-) APOTECH SA.
Death effector
                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; W76630.
               HIV infection;
                                                                                                                                              DE19713393-A1
                                             Homo sapiens.
                                                                                                                                                                                                       01-APR-1997;
                                                                                                                                                                                                                                    01-APR-1997;
                                                                                                                                                                         08-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-AUG-1999
                                                                                                                                                                                                                                                                                                                                       rhome M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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The present sequence represents DNA coding for MACH-related inducer CO f toxicity (MRIT) isoform MRIT beta 1 (see Y05789), a CED-4 homologue that has pro-apoptotic activity. An EST sequence having chomology to the p20 domain of human ICB-like protease MACHJ/FLICE was isolated from an EST database. Several overlapping EST clones were sequenced to deduce the sequence of the full-length MRIT alpha 1 clone (see X25508) and 2 isoforms, alpha 2 (see X25509) and beta 1. The MRIT gene was localised to the human chromosome 2q32.33 cepton. MRIT alpha 1. Selective enhancers and inhibitors of MRIT appa 1. Selective enhancers and inhibitors of MRIT appa 1. Selective enhancers and inhibitors of MRIT appatal. Selective of programmed cell death or proliferation. In addition, nucleic acid molecules encoding proliferation. In addition, nucleic acid molecules encoding programmed cell death. A cell accumulation disorder such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         selectively enhances MRIT apoptotic activity, thereby inducing apoptosis in a subject. A disorder of cell loss, such as a neurodegenerative disorder, including Alzheimer's disease, Parkinson's disease, retinitis pigmentosa, stroke, aplastic anaemia, myocardial infarction or AIDS can be treated by administering an agent that selectively inhibits MRIT apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer, autoimmune disease, viral infection, angiogenesis and atherosclerosis is treated by administering an agent that
                                                                                                                                                                                                                                                                                                                                                                                                             Identifying regulators of MACH-related inducer of toxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1308 BP; 367 A; 275 C; 330 G; 334 T; 2 other;
                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Fig 1H; 78pp; English.
                                                                                                                                                                                                                                            97US-0946226.
                                                                                                                                                                                                       98WO-US21132.
                                                                                             /*tag- a
                                                                                                                                                                                                                                                                                  (UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-277275/23
                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; Y05789
                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                   Chaudhary PM;
                                                                                                                             WO9918230-A2
                                                                                                                                                                                                       07-OCT-1998;
                                                                                                                                                                                                                                          07-OCT-1997;
                                                                                                                                                                    15-APR-1999
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Gaps

67; Indels , 0;

> 셤 à g à 셤

RESULT V52969

Query Match
9.9%; Score 29.8; DB 20; Length 1308;
Best Local Similarity 51.1%; Pred. No. 3.6;
Matches 70; Conservative 0; Mismatches 67; Indels 0;

us-09-300-482-619.rng

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Gl protein; CASH-beta; human; caspase homologue; Fas receptor; modulator; apoptosis; cell death; inflammation; tumour; HIV;
                               Human G1 protein isoform beta (CASH-beta) cDNA.
                                                                        Location/Qualifiers
482..1137
V52969 standard; cDNA; 1373 BP.
                                                                                                                                           (YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                 97IL-0120367.
                                                                                                                 98WO-IL00098.
                                                                                                                            97IL-0120759
                     11-JAN-1999 (first entry)
                                                                                   /*tag= a
                                                                                                                                                                     WPI; 1998-495842/42.
                                                                                                                                                                          P-PSDB; W78904.
                                                                                                                                                      Brodianski V,
                                                               Homo sapiens
                                                                                                                  26-FEB-1998;
                                                                                                                            01-MAY-1997;
                                                                                                                                  03-MAR-1997;
                                                     therapy; ss.
                                                                                             WO9839435-A1
                                                                                                                                                                                                                                                                                                                                                                     expression.
                                                                                                                                                           Wallach D;
           V52969;
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this cups a seqence coues for the beta isolaid (incord) man of 1 protein. It was isolated from a human skin fibroblast connected and a longer isolated from a human skin fibroblast connected and a longer isoform, G1-alpha (see WA8903), represent 2 splice and a longer isoform, G1-alpha (see WA8903), represent 2 splice cand a longer isoform, G1-alpha (see WA8903), represent 2 splice and a longer isoform, G1-alpha (see WA8903), represent 2 splice converted the G1 protein. These G1 proteins are capable of casp-8), and thereby of binding to the intracellular domain of the p55 tumour necrosis factor (TMF) intracellular domain of the p55 tumour necrosis factor (TMF) creceptor, to which MORT-1 binds, or of binding to the creceptor, to which PRADD binds and to which TRADD protein MORT-1 binds, they are considered as mediators or modulators of py the binding of FAS ligand to FAS-R, and also having a role in e.g. the signalling process that is initiated by the binding of TMF to p55-R.

C5 FAS-R having a role in e.g. the signalling process that is initiated by the binding of TMF to p55-R.

C6 I DNA (1) and polypeptide (II), vectors and fragments are used to regulate cell death, and its inhibitors augment, end and the simplificors and a specific cell scarrying an FAS-R or p55-R. Tumour, HIV-infected or other considerated using a viral vector encoding (II), which binds a specific cell surface protein, which binds a specific cell. Surface protein, which binds a specific cell. Surface ceptor, blook the capuated using a vector encoding a ribozyme of fetted son also be regulated using a vector encoding a ribozyme that interacts with a cellular mRNA encoding (II), and allows (II) expression of (II) and can also regulate the above effects. This cDNA segence codes for the beta isoform (see W78904) of novel New DNA encoding isoforms of G1 protein which bind MORT-1 - and regulate the effects of FAS and tumour necrosis factor receptors, useful for killing of cells e.g. HIV and cancer cells Goltsev Y, Kovalenko A, Varfolomeev E; Claim 4; Fig 2; 132pp; English.

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Sequence 1373 BP; 417 A; 283 C; 335 G; 338 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insulin-responsive amino peptidase-binding protein; IRAP-BP; IRAP-BP-1; insulin responsive amino peptidase; IRAP; glucose transporter; GLUT4; insulin-responsive translocation; insulin resistance; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes a human insulin-responsive amino peptidase-binding protein (IRAP-BP) polypeptide, designated IRAP-BP-1. The polypeptide amino peptidase (IRAP) polypeptide, and is a regulator of insulin-responsive translocation of glucose transporter, GUDT4. The polypeptide is useful in treating disorders associated with aberrant activity or expression of IRAP-BP by administration of IRAP-BP modulators. Disorders associated with insulin resistance or diabetes. The protein is also useful for the treatment of respiratory disorders e.g. asthma and as immunogens for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a /product= "insulin-responsive amino peptidase-binding
                                                                                                                                   54 ggacctgaactggcaactactcttgtaattgtcatttctaagagcggaggcacacctgaa 113
                                                                                                                                                                                                     434 ggagctgtactgcaagacccttgtgagcttccctagtctaagagtaggatgtctgctgaa 493
                                                                                                                                                                                                                                                                    114 accogcaatggtctactagaagtacagaaagccttcagagatgcggggctgcaattctcg 173
                                                                                                                                                                                                                                                                                                                           494 gtcatccatcaggttgaagaagcacttgatacagatgagaaggagatgctgctcttttg 553
                                                                     0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human insulin-responsive amino peptidase-binding protein cDNA.
   Length 1373;
                                                                     Indels
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Score 29.8; DB 19;
Pred. No. 3.7;
0; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 114-116; 118pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          respiratory disorder; asthma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Z99543 standard; cDNA; 1683 BP.
      9.9%;
51.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                           174 aaacagggtgttgcaat 190
                                                                                                                                                                                                                                                                                                                                                                                                                                          Pilch PF, Tojo H, Lin B;
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                                                                        70; Conservative
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                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; Y69411.
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          Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z99543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X E X X B X X X E E E E E E E X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X 
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                                                                                                                                                                                        Gaps
 producing anti-IRAP-BP antibodies, to purify IRAP-BP ligands and in screening assays to identify molecules which inhibit the interaction of IRAP-BP with an IRAP-BP ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This cDNA sequence codes for human FLAME-1 (see W90107), or FADD-like apoptotic/anti-apoptotic molecule 1. FLAME-1 is a novel anti-apoptotic protein that interacts specifically with FADD, McD4, McD5 and FLAME-2. It is recruited to the Fas receptor complex and Ras/TNF-induced apoptosis upon expression in FaS/TNF-induced apoptosis upon expression in can abrogate Fas/TNF-induced apoptosis upon expression in chromosome 2933-34. The full-length FLAME-1 cDNA was isolated from a Jurkat cDNA library using a partial FLAME-1 cDNA probe that had itself been generated from the Jurkat library using primers (see 184139-42) based on an isolated EST tlone. Host cells, recombinant ectors, and methods of using FLAME-1 to identify substrates, activators or inhibitors of FLAME-1 are provided. FLAME-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated FADD-like anti-apoptotic molecules - used to develop apoptotic and anti-apoptotic agents for treating, e.g. HIV infection, Alzheimer's disease or neoplastic conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLAME-1; FADD-like apoptotic/anti-apoptotic molecule; human; apoptosis; HIV; infection; Alzheimer's disease; cancer; therapy;
                                                                                                                                            ó
                                                                                                                                                                                                                                9.9%; Score 29.8; DB 21; Length 1683; 54.0%; Pred. No. 4;
                                                                                                                                            Indels
                                                           Sequence 1683 BP; 544 A; 345 C; 375 G; 419 T; 0 other;
                                                                                                                                            52;
                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 413..1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; Page 36-38; 68pp; English.
                                                                                                                                                                                                                                                                                                                                               ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                           V74136 standard; cDNA; 1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US10200.
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                                                                                                                                                                                                                                                                                                                                                                                                     12-APR-1999 (first entry)
                                                                                                                                          Conservative
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                                                                                                                         Local Similarity
Hes 61; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human FLAME-1 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; W90107.
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                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                           V74136;
                                                                                                                                                                                                                                                                                                               RESULT 14
                                                                                                                                      Matches
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SSSSXS
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54 ggacctgaactggcaactactcttgtaattgtcatttctaagagcggaggcacacctgaa 113
                                                                                                                                                                                                                                       365 ggagctgtactgcaagacccttgtgagcttccctagtctaagagtaggatgtctgctgaa 424
                                                                                                                                                                                                                                                                      114 acccgcaatggtctactagaagtacagaaagccttcagagatgcgggggtgcaattctcg 173
                                                                                                                                                                                                                                                                                             Gaps
FLAME-2 (see W90108) and agonists can be used to inhibit apoptosis, e.g. for treating HIV infection or Alzheimer's disease. Inhibitors of the polypeptides can be used as apoptotic agents. FLAME nucleic acid molecules can be used for gene therapy, e.g. antisense oligonucleotides can be used in vivo for antineoplastic purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MRIT alpha 1; MACH related inducer of toxicity; human; apoptosis; pro-apoptotic; cancer; autoimmune disease; infection; anglogenesis; atherosclerosis; neurodegenerative disease; Alzhelmer's disease; Parkinson's disease; rettinitis pigmentosa; stroke; AlDS; aplastic anaemia; myocardial infarction; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents DNA coding for MACH-related inducer of toxicity (MRIT) isoform MRIT alpha 1 (see Y05787), a CED-4 homologue that interacts simultaneously with caspases and Bcl-2 family polypeptides, and which has pro-apoptotic activity. An EST sequence having homology to the p20 domain of human ICE-like protease MACHI/FLICE was isolated from an EST database. Several
                                                                                                                                                                               ;
0
                                                                                                                                                  Length 1750;
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                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human MACH related inducer of toxicity MRIT alpha 1 DNA.
                                                                                               Sequence 1750 BP; 465 A; 400 C; 476 G; 409 T; 0 other;
                                                                                                                                                                              67;
                                                                                                                                                DB 20;
                                                                                                                                                                              0; Mismatches
                                                                                                                                                               Pred. No. 4;
                                                                                                                                                Score 29.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig 1F; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                             9.9%;
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                                                                                                                                                                                                                                                                                                                                     174 aaacagggtgttgcaat 190
                                                                                                                                                                                                                                                                                                                                                                                                                                              X25508 standard; DNA; 1996
                                                                                                                                                                                                                                                                                                                                                        | || || || || || || || 485 tgccgggatgttgctat 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                            70; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UNIW ) UNIV WASHINGTON
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P-PSDB; Y05787.
                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09918230-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-0CT-1997;
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                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X25508;
                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
                                                                                                                                                                          Matches
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coverlapping EST clones were sequenced to deduce the sequence of the full-length MRIT alpha 1 clone and 2 isoforms, alpha 2 (see X25510). The MRIT gene was localised to the human chromosome 2432-33 region. MRIT alpha 1 includes an N-terminal death effector domain and a C-terminal caspase homology commin, but is not a cysteine protease. Selective enhancers and inhibitors of MRIT appottotic activity can be identified and used to treat diseases mediated by the dysfunction of programmed cell death or proliferation. In addition, nucleic acid molecules encoding pro-appotentic isoforms of MRIT can also be used as inducers of programmed cell death. A cell accumulation disorder such as cancer, autoimmune disease, viral infection, angiogenesis and anterosciencosis is treated by administering an agent that selectively enhances MRIT apoptotic activity, thereby inducing apoptosis in a subject. A disorder of cell loss, such as a neurodegenerative disorder, including Alzheimer's disease, retinitis pigmentosa, stroke, aplastic anamia, myocardial infarction or ALDS can be treated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1996 BP; 543 A; 461 C; 540 G; 451 T; 1 other;
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0; Gaps Ouery Match 9.9%; Score 29.8; DB 20; Length 1996; Best Local Similarity 51.1%; Pred. No. 4.2; Matches 70; Conservative 0; Mismatches 67; Indels 0;

; 0

54 ggacctgaactggcaactactcttgtaattgtcatttctaagagcggaggcacacctgaa 113 387 ggagetgtactgcaagaccettgtgagettccctagtctaagagtaggatgtetgetgaa 446 174 aaacagggtgttgcaat 190 g δ Db ò

Search completed: November 4, 2000, 13:45:55 Job time: 16482 sec

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November 4, 2000, 13:34:22; Search time 189.35 Seconds (without alignments) 239.622 Million cell updates/sec
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Sequence 1, Appli
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                                                                                                                                                           1 gatttattgacaacaccgat.....ttcagaaatgtctgctgtgg 300
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Sequence 102, App
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/5C_COMB.seq:*
/cgn2_6/ptodata/2/ina/5C_COMB.seq:*
/cgn2_6/ptodata/2/ina/6_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-345-212-1

US-08-484-493-6

US-08-484-494-6

US-08-742-212-6

US-08-714-918-97

US-08-892-403A-2

US-08-487-810-1

US-08-469-537A-102

US-08-469-537A-102
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US-08-980-060-1
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                                                                                                                                                                                                                              262060 seqs, 75620727 residues
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US-08-618-464-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                OM nucleic - nucleic search, using sw model
                                                                                                                                                                                      IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                 Issued_Patents_NA:*
                                                                                                                                    US-09-300-482-619
300
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Maximum DB seq length: 2000000000
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1932
15225
1146
3906
4165
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1055
1055
2441
3705
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Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 1, Appli
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Appl
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                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Alnemi, Emad S.
APPLICANT: Alnemi, Emad S.
TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
NUMBER OF SEQUENCES: 17
                                                    Sequence 2, M
Sequence 2, M
Sequence 5, M
Sequence 1, M
Sequence 3, M
Sequence 3, M
Sequence 35, M
Sequence 27, M
                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6037461ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
       Sequence 16,
Sequence 18,
                               Sequence 1,
                                                                                                                                                                                                      Sequence
                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                     Seguence
                                                                                                                                                                                                                               Sequence
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           US-08-645.193B.18
US-08-445.193B.18
US-08-459-415.2
US-08-480-604A-5
US-08-480-604A-5
US-08-490-604A-5
US-08-490-6496A-5
US-08-405-496A-5
US-08-446-345-33
US-08-446-345-35
US-08-609-049A-27
US-08-609-049A-27
US-08-477-451-1
US-08-477-451-5
US-08-477-451-5
US-08-477-451-1
US-08-477-451-1
US-08-477-451-1
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US-08-477-451-1
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,167
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY.

ZIP: 19103
COMPTTER READBLE FORM:
MEDIUM TYPE: Floppy disk

~~VEHTER: IBM PC COMPATIBLE

~~VEHTER: IMP PC COMPATIBLE

~~VEHTER: IMP PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08859167
Patent No. 6037461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION UNDBER: 33,229
REFRENCE/DOCKET UNDBER: TJU-
TELECOMMUNICATION INFORMATION:
TELEFAX: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.9%;
51.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1750 base pairs
                         111832
3881
3881
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8133
8135
878
3825
4080
6831
10299
19932
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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Best Local Similarity
 TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
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US-08-859-167-1
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227
229
330
331
332
333
334
44
44
45
45
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1505 ATTGCCTATAGCCAGTATCCCCGGCCTTCAGACATCCCTCAGTGGAATTCTGACAAGCCG 1564
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9.7%; Score 29; DB 2; Length 2297;
Best Local Similarity 53.0%; Pred. No. 1.8;
Matches 62; Conservative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,493
FILING DATE: U7-JUN-1995
CLASSIFICATION 7424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Did(3)140, Frank S
REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 34162
RECISTRATION NUMBER: 94162
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION STATE 1846
TELEFRANCE/DOCKET NUMBER: 94162
TELECOMMUNICATION STATE 1846
TELEFRANCE/DOCKET NUMBER: 94162
TELEFRANCE/DOS SED 1D NO: 1:
INFORMATION FOR SED 1D NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 400 Garden City Plaza
CITY: Garden City Plaza
STATE: New York
COUNTRY: nc.
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Occhiodoro, Teresa
APPLICANT: Bielicki, Julie
APPLICANT: Elenicki, Julie
APPLICANT: Clements, Peter R
APPLICANT: Hopwood, John J
TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
TITLE OF INVENTION: IDURONATE 2-SULFATASE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                 ; Sequence 1, Application US/08484493 ; Patent No. 5728381
                                                                                                                                                                                                                                                                                                                  APPLICANT: Wilson, Peter J
APPLICANT: Morris, Charles P
APPLICANT: Anson, Donald S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2297 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                               174 aaacagggtgttgcaat 190
                                                                                                                      485 TGCCGGGATGTTGCTAT 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
125..1774
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         365 GGAGCTGTACTGCAAGACCCTTGTGAGGACTAGAGAAGAAGAAGAAGATGTCTGTGAAA 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Alnemri, Emad S.
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: GAND THE SAME, AND COMPOSITIONS FOR AND METHODS
TITLE OF INVENTION: Of MAKING THE SAME
TOTALE OF INVENTION: OF MAKING THE SAME
CORRESPONDENCE JOURNESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6063760ris
STREET: One Liberty Place, 46th floor
                                                            54 ggacctgaactggcaactactcttgtaattgtcatttctaagagcggaggcacacctgaa 113
                                                                                                                                                  114 accegeaatggtetactagaagtacagaaagcetteagagatgeggggetgeaatteteg 173
                                                                                                 365 GGAGCTGTACTGCAAGACCCTTGTGAGCTTCCCTAGTCTAAGAGTAGGATGTCTGCTGAA 424
                                                                                                                                                                                       425 GICAICCAICAGGITGAAGAAGCACTIGATACAGAIGAGAAGGAGAIGCIGCICTITIIG 484
                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 51.1%; Pred. No. 0.85;
Matches 70; Conservative 0; Mismatches 67; Indels 0
                    67; Indels
                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/109,273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: DeLuca, Mark
REGLSTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TUU-
TELECOMMUNICATION INFORMATION:
TELEPPAN: (215) 568-3100
TELEPRAX: (215) 568-3439
INPORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,167
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09109273 Patent No. 6063760 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: WINDOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1750 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                             174 aaacagggtgttgcaat 190
                                                                                                                                                                                                                                                                      485 TGCCGGGATGTTGCTAT 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: WordPerfect
CURRENT APPLICATION DATA
                         70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               413..1750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: 413
US-09-109-273-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                             US-09-109-273-1
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                           Matches
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US-08-345-212-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 atggtctactagaagtacagaaagccttcagagatgcggggctgcaattctcgaaacagg 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
1565 AGTITAAAAGATATAAAGATCATGGCTATTCCATACGCACCATAGACTATAGGTAT 1621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 9.7%; Score 29; DB 2; Length 2297; Best Local Similarity 53.0%; Pred. No. 1.8; Matches 62; Conservative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NOBER: US/08/484,494
FILIG DATE: 07-91N-1995
CLASSIFICATION: 435
                                                                                                                                                                                                       APPLICANT: Morris, Charles P
APPLICANT: Morris, Charles P
APPLICANT: Anson, Donald's
APPLICANT: Occhiodoro, Teresa
APPLICANT: Clements, Peter R
APPLICANT: Clements, Peter R
APPLICANT: HOPWOOG, John J
TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
TITLE OF INVENTION: IDURONATE 2-SULFATASE
NUMBER OF ESQUENCES: 15
CORRESSPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 991,973
FILLING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: DIG19110, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8416Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2237 DASE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                             US-08-484-494-1
; Sequence 1, Application US/08484494
; Patent No. 5798239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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STRANDEDNESS: double
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MEDIUM TYPE: Floppy
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125..1774
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; LOCATION:
US-08-484-494-1
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Sequence 1, Application US/08345212
Patent No. 593221
GENERAL INFORMATION:
APPLICANT: Wilson, Peter J
APPLICANT: Morris, Charles P
APPLICANT: Anson, Donald S
APPLICANT: Occhiodoro, Teresa
APPLICANT: Clements, Peter R
APPLICANT: Clements, Peter R
APPLICANT: Hopwood, John J
TITLE OF INVENTION: IDURONATE 2-SULFATASE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: FIDEPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentur Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/345,212
                                                                                                                                                                                                                                                                            ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 29; DB 4
Pred. No. 1.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 84162
TELECOMMUNICATION INFORMATION:
TELEPAN: 516-742-4346
TELEFAX: 516-742-4366
TELEFAX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Disiglio, Trank S
REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-484-493-6
Sequence 6, Application US/08484493
Patent No. 5728381
Patent No. FARSHINGEMENT NO. Peter J
APPLICANT: Wilson, Peter J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 9.7%;
Best Local Similarity 53.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 2297 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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125..1774
                                                                                                                                                                                                                                                                                                                     CITY: Garden City
STATE: New York
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                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                             ZIP: 11530
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US-08-345-212-1
                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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FEATURE:

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COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,493
FILING DATE: U7-JUN 1995
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 91,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGILO, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/POCKET NUMBER: 31,346
REFERENCE/POCKET NUMBER: 31,346
RELEPAX: 516-742-4366
TELEFAX: 516-742-4366
TE
APPLICANT: Morris, Charles P
APPLICANT: Anson, Donald S
APPLICANT: Occhiodoro, Teresa
APPLICANT: Bielicki, Julie
APPLICANT: Bielicki, Julie
APPLICANT: Bielicki, Julie
APPLICANT: Hopwood, John J
TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
TITLE OF INVENTION: 1DURONATE 2-SULFATASE
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                 E: Scully, Scott, Murphy & Presser 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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1841..2041
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1044..1221
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1350..1351
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1716..1717
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                                                                                                                                                                                                                                                                                                                                                 STREET: 400 cm.
CITY: Garden City
STATE: New York
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332..434
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536..537
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693..829
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962..963
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ZIP: 11530
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LOCATION:
FEATURE:
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LOCATION:
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LOCATION:
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FEATURE:
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3636 ATTGCCTATAGCCAGTATCCCCGGCCTTCAGACTCCCTCAGTGGAATTCTGACAGCCG 3695
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 29; DB 2; Length 4428; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTYARE: Patentin Release #1.0, Version #1.25
SURREWI APPLICATION DATA:
APPLICATION NUMBER: US/08/484,494
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGILO, Frank S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Morris, Charles P
APPLICANT: Morris, Charles P
APPLICANT: Anson, Donald S
APPLICANT: Occhlodoro, Teresa
APPLICANT: Clements, Peter R
APPLICANT: Clements, Peter R
APPLICANT: Clements, Peter R
APPLICANT: Hopwood, John J
TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
TITLE OF INVENTION: IDURONATE 2-SULFATASE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 9.7%; Score 29; DB 2
Best Local Similarity 53.0%; Pred. No. 2.5;
Matches 62; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 6, Application US/08484494
; Patent No. 5798239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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3033..3206
                                                                                                                                                                           intron
2904..2905
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                     2294..2464
                                                                             2585..2586
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3435..3908
                                                             intron
                                                                                                                                                                                                                                                                                               intron
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APPLICANT: Wilson,
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ZIP: 11530
NAME/KEY:
LOCATION:
FEATURE:
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US-08-484-493-6
                                                                                                                   NAME/KEY:
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US-08-484-494-6
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REFERENCE/DOCKET NUMBER: 84162
TELECOMONULACATION INFORMATION:
TELEFRAX: 516-742-4364
TELEFAX: 516-742-4366
TELEFAX: 530 901 SANS UR
TELEFIX: 230 901 SANS UR
SEQUENCE CHARACTERISTICS:
LENGTH: 4428 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
REGISTRATION NUMBER: 31,346
                                                                                                                                MOLECULE TYPE: DNA (genomic)
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1841..2041
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3435..3908
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1716..1717
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2585..2586
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1044..1221
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1480..1569
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1350..1351
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2294..2464
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2904..2905
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962..963
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536..537
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693..829
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LOCATION:
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LOCATION:
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LOCATION:
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LOCATION:
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US-08-484-494-6
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3636 ATTGCCTATAGCCAGTATCCCCGGCCTTCAGACATCCCTCAGTGGAATTCTGACAAGCCG 3695
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                                                                                181 gtgttgcaattactcaagaaaattctctgttggataacactgctagaatagagggat 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Morris, Charles P
APPLICANT: Morris, Charles P
APPLICANT: Anson, Donald's
APPLICANT: Occhiodoro, Teresa
APPLICANT: Clements, Peter R
APPLICANT: Clements, Peter R
APPLICANT: Hopwood, John J
TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
TITLE OF INVENTION: IDGRONATE 2-SULFATASE
NUMBER OF SEQUENCES: 15
CORRESSPONDENCES ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/345,212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City Plaza STATE: New York COUNTRY: USA
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CLASSIFICATION: 435
FILOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: D161910. Frank S
REFERENCE/DOCKET NUMBER: 84162
TELECOMMONICATION INFORMATION:
TELEPROME 516-742-434
TELEPROME: 516-742-436
TELEFAX: 516-742-436
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TELEFE S 516
                                                                                                                                                                                                                                                                                                                     US-08-345-212-6; Sequence 6, Application US/08345212; Patent No. 5932211
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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1044..1221
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332..434
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693..829
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LOCATION:
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NAME/KEY:
LOCATION:
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LOCATION:
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FEATURE:
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FEATURE: NAME/KEY:

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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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                                              OPERATING SYSTEM:
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US-08-714-918-97
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Patent No. 6037123
GENERAL INFORMATION:
GENERAL INFORMATION:
BENTON: Benton, Bret
APPLICANT: Malouin, Francois
APPLICANT: Malouin, Francois
APPLICANT: Schmid, Molly B.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: TARGET GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
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3435..3908
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2206..2207
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2294..2464
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1716..1717
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2684..2810
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CORRESPONDENCE ADDRESS:
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          1350..1351
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STATE: California
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FEATURE:
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FEATURE:
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GENERAL INFORMATION:
APPLICANT: Murphy, Brian R.
APPLICANT: Collins, Peter L.
APPLICANT: Whitehead, Stephen S.
APPLICANT: Whitehead, Stephen S.
APPLICANT: Juhasz, Katalin
TITLE OF INVENTION: PRODUCTION OF ATTENDATED RESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS VACCINES FROM CLONED NUCLEOTIDE SEQUENCES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       775 AATTGTACTTGTGCAACTAGGACTAACAAATTCTGTAGTAGCAATCATTATTATTGCCAG 834
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Townsend and Townsend and Crew LLP Two Embarcadero Center, 8th Floor
                                                                               CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,918
FILING DATE: September 13, 1996
CLASSIFFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
FILING DATE: DECEMBER: 60/003,798
                                                                                                                                                                                                                                                                                                           FILING DATE: September 15, 1995
ATTORNEY AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 2, Application US/08892403A
; Patent No. 5993824
                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE TO THE STATE OF THE STATE OF TELECOMMUNICATION INFORMATION:
TELECHONE: (213) 498-1600
TELEFAX: (213) 955-0440
TELEX: (67-3510
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 1932 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
IBM Compatible
SYSTEM: IBM P.C.
Word Perfect 5.1
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187 caattactcaagaaaattctctgttggataacactgctagaatagagggatggt 240
                                                                                                                                                                                             APPLICANT: Maisonpierre, et al.
TITLE OF INVENTION: EHK AND ROR TYROSINE
TITLE OF INVENTION: KINASES
OF INVENTION: KINASES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILLING DATE: O. O. O. D. C. CLASSIFICCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/406,247
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: USSN 08/144,992
FILING DATE: 28-OCT-1993
APPLICATION NUMBER: USSN 07/736,559
FILING DATE: 26-JUL-1991
ATTORNEY AGENT INFORMATION:
NAME: Kempler, Ph.D., Gail M
REGISTRATION NUMBER: 32,143
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,537A
FILING DATE: 06-JUN-1995
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                                                                                                 RESULT 12
US-08-469-537A-102/c
; Sequence 102, Application US/08469537A
; Patent No. 5843749
; GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
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Best Local Similarity 60.8<sup>3</sup>
Matches 45; Conservative
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LOCATION: 476..3493
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US-08-469-537A-102
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Pred. No. 3.9;
0; Mismatches 54; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 28; DB 4; Length 15225;
Pred. No. 10;
0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-CDS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,810
INFORMATION FED IN NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                            NAME: Parmelee, Steven W.
RECISTRATION NUMBER: 31990
REFERENCATION NUMBER: 17634-000510
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 15225 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/047,634
FILING DATE: 23-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/046,141
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,403A
FILING DATE: 15-JUL-1997
                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/021,773
FILING DATE: 15-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-487-810-1; Sequence 1, Application US/08487810; Patent No. 5618695; GENERAL INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 71.29
Matches 37; Conservative
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Best Local Similarity 52.68
Matches 60; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-487-810-1
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Score 27.6; DB 3; Length 3906;
Pred. No. 7.2;
0; Mismatches 29; Indels 0
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Pred. No. 7.5;
0; Mismatches 29; Indels 0
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Patent No. 579848

GENERAL INFORMATION

APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
Sequence 1, Application US/08442248
Patent No. 5759863
GENERAL INFORMATION:
APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                         COMPUTER TRADABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: patin (Generated)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,248
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                          ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330128
FILING DATE: 27-0CT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 920C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415,725-8674
TELEFAX: 415,952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
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Best Local Similarity 60.8%;
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LENGTH: 4165 bases
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STRANDEDNESS: single
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928 TAAAATTCTGGAA 915
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US-08-440-815-1/C
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IMMUNE PROTECTION AGAINST ARTHR
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Pred. No. 7.5;
0; Mismatches 29; Indels 0:
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THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,464
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS COFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: FISH & RICHARDSON P.C. STREET: 4225 Executive Square, Suite 1400 CITY: La JOLIA STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/042001
                                                                                                    APPLICATION NUMBER: US/08/440,815
FILING DATE: 15-MAY-1995
CLASSIFECATION: 435
PAION APPLICATION DATA:
APPLICATION NUMBER: 08/330128
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                     NAME: TOTCHIA, TIMOCHY E.
REGISTRATION NUMBER: 36,700
REFRENCE/DOCKET NUMBER: 920C;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 1, Application US/08618464
; Patent No. 5773570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: CARSON, DENNIS A.
APPLICANT: ALBANI, SALVATORE
TITLE OF INVENTION: UACCINE COM
TITLE OF INVENTION: INVOLVED IN
TITLE OF INVENTION: THE PATHOGE
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4165 bases
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Best Local Similarity 60.88
Matches 45; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
US-08-440-815-1
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US-08-618-464-1/c
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November 4, 2000, 13:37:55; Search time 4075.18 Seconds (without alignments) 412.624 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                            OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                            US-09-300-482-356
385
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Maximum DB seq length: 2000000000
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gb_ox:*
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em_bu3:*

em_bu4:*

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gb_htg7:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	+ 00 00000 CVSCOUR	V15701 Capaigns or	746646 C mlontocin	552265 Company 1	ABO72000 Sequence 1	alloco sequence	75000 CLINA ENCOGI	230039 S. Luberosum	746647 C.prantagin	17654 Crimest	At 162205 Perchasol	AJ249787 Cvanophor	TOTAL
	ID	AP002542	CAY15781	СРТКТЗ	A52295	AR072009	E13696	STIKETMR .	CPTKT7	CPTKT10	SPITER	ATT4C21	CPA249787	
	Query Match Length DB	01441 8	2319 8	1802 8	2629 5	2629 5	2629 5	2447 4	2232 8	2207 8	2519 45	107865 8	2595 8	
æ		64.4 101441	48.8	46.2	44.3	44.3	44.3	43.4	43.0	42.5	42.2			
	Score	247.8	187.8	177.8	170.4	170.4	170.4	167	165.4	163.8	162.4	162.2	155.6	
	Result No.	c 1	7	m	4	2	9	7	80	6	10	11	12	

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Submitted (21-30W-2000) to the DDBJ/EMBL/GenBank databases. Takuji Submitted (21-30W-2000) to the DDBJ/EMBL/GenBank databases. Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program: Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mall:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
Tel:81-298-310-0f the sequence is from T7 to SP6 of the PAC clone. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.
1 (bases 1 to 101441)
                                                                                                                                                                  Z95844 Mycobacteri
AE004133 Vibrio ch
AF015445 Bacillus
AE000755 Aquifex a
X68025 E.coli tkt
AE000376 Escherich
U28377 Escherichia
                                                                                                                                                                                                                                                                          AE000333 Escherich
D90875 E.coli geno
Z73234 B.subtilis
Z99113 Bacillus su
       AF069299 Arabidops
AL161471 Arabidops
AF246362 Acidithio
AL096839 Streptomy
AC004708 CLC5B11.1
AL031107 Streptomy
                                                                                                                                                                                                                                                                                                                            U32783 Haemophilus
                                                                                                                                                                                                                                                    AC073770 Mus muscu
                                                                                  U00013 Mycobacteri
                                                                                                                                                                                                                                                                                                                                      AE002495 Neisseria
                                                                                                                                                                                                                                                                                                                                                           AF211846 Sinorhizo
AL162756 Neisseria
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AE004013 Xylella f
                                                                                                                              AE004392 Vibrío ch
D90905 Synechocyst
                                                                                                                                                                                                                                                                D12473 Escherichia
                                                                                                          AB023377 Corynebac
                                                                                                                                                      M68904 Alcaligenes
                                                                                             299125 Mycobacteri
                                                                                                                   M68905 Alcaligenes
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AC002387 Arabidops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
clone:P0679C08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AP002542 101441 bp DNA PLN 23-JUN-20
Oryza sativa genomic DNA, chromosome 6, PAC clone:P0679C08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (cultivar:Nipponbare) DNA, clone:P0679C08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published Only in DataBase (2000) In press
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Direct Submission
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/cultivar="Nipponbare"
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AC073770
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BSUB0010
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AF211846
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AE000755
                        ATCHRIV1
AF246362
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AC004708
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                                                                                                                                                                                 AE004133
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             F6N15
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40.3 122871
35.2 95643
28.4 17119
28.4 17119
26.0 167234
26.0 167234
25.7 36281
25.7 3628
24.4 2722
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/db_xref="SPTREMBL:078327"
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NSGHPGLPMGCAPLGHILYDELMRYNENDYWFNRDRFVLSAGHGGMLQYALLHLAGY
DAVREEDLKSFRQWGSKTPGHPENFETPGVEVTTGPLGGGLANAVGLALSEKHLAARF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotta, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryotta, Viridiplantae; Spermatophyta; Magnoliophyta; eudicotyledons; Asteridae; Solananae; Solanales; Solanaceae; Capsicum.

1 (bases 1 to 2319)

1 (bases 1 to 2319)

1 (bases 1 to 2119)

1 (bases 2 to 2319)

1 (bases 3 to 2319)

1 (bases 3 to 2319)

1 (bases 4 (Alarlingue, A., Suire, C., Backhaus, R.A. and Camara, B.)

1 (bedicated roles of plastid transketolases during the early onset of isoprenoid biogenesis in pepper fruits!

1 (4), 1423-1431 (1998)
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                                                                                                                                                                                                                                                                                                       181 teacagegaggateageategaggeegggteeacteteggetggeagaagtaegteggag 240
                                                                                                                                                                                                                                                                                                                                                       121 cctgggaactctttgatgagcagtcggatgagtacaaggagagcgtcctccctgccgacg 180
                                                                                                                                         07-SEP-1998
                                   0; Gaps
                                                                       1 caaccggcaccaagcctgacatcattgggttgggcaccggctccgagctggagatcgcgg
Length 101441;
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Capsicum annuum mRNA for plastid transketolase 1.
 DB 8;
 64.4%; Score 247.8; DB 80.2%; Pred. No. 2.6e-37; ive 0; Mismatches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Capsicum annuum"
/db_xref="taxon:4072"
/note="plastid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="transketolase 1"
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/db_xref="GI:3559814"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA
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Capsicum annuum
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LPGFLGGSADLASSNWTLMKMFGDFOKNTPEERNLRFGVREHGMGALONGIALHSPGL
IPYCATFFYTDYMRAAIRISALSESRYIYYWHDDSIGLGEBGFTHOPIEHLASFRAM
PNYLMIRRADGWETAAKYOYLIKSKTPSIIALSROKLPOLAGTSIEGTAKGGYTSD
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PAAVIARYSIEBAGSTFGWEKIVGSKGRAIGIDRFGASAPAGKIYKESYL
PAAVIARYSIEBAGSTFGWEKIVGSKGRAIGIDRFGASAPAGKIYKEYGIABA
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NKANSYSVHGSALGAKEVEATRONLGWPYEPFHVPEDVKSHWSRHVPEGAALEAGWNT
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Bernacchia,G., Schwall,G., Lottspeich,F., Salamini,F. and
                                                                                                                                                                                                                                                                                                                                                                                                2084 CIGCIAGAGITAGCAITGAAGCIGGATCCACATITGGGIGGGAGAAGAICGICGGAICCA 2143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 aaggcaaggccattggcatcgacaagttcggcgcgagtgctcctgccgggacgatctaca 303
                                                                                                                                                                                                                                                                                                                                                                        4 coggoaccaagctgacatcattgggttgggcaccggctccgagctggagatcgcgggca 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (10-NOV-1994) Bartels D., Max-Planck-Institut fuer Zuechtungsforschung, Pflanzenzuechtung und Ertragsphysiologie, Carl-von-Linne-Weg 10, Cologne, NRW, Germany, 50829 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-FEB-1995
                                                                                                                                                                                                                                                                                      48.8%; Score 187.8; DB 8; Length 2319; 71.7%; Pred. No. 9.3e-26; Live 0; Mismatches 97; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The transketolase gene family of the resurrection plant
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C.plantagineum tkt3 gene for transketolase.
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Craterostigma plantagineum.
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ITTSRRRTPSSAAAAAVRSPAIRASAATETIEKTETALVDKSVNTIRFLAIDAVERO
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KPDAEIVDHYTYVILGDGCQMEGISQEACSLAGHWGLGKLIAFYDDNHISIDGDTEIA
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Pred. No. 1.5e-22;
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                                                                                                                       /note="unnamed protein product"
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                                                                         /organism="Nicotiana tabacum"/db_xref="taxon:4097"
               Other publication CA 2167768 960724 Other publication DE 19501906 960725.
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                                                                                                                                                 /protein_id="CAA03393.1"
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Rarufuumihiyaeru,S., Maaku,S. and Uubue,Z...
PROTEIN HAVIG TRANSKETOLASE ACTIVITY, NUCLEIC ACID CODING THE
PROTEIN HAVIG TRANSKETOLASE ACTIVITY, NUCLEIC ACID CODING THE
BEBICIDAL ACTION SUBSTANCE, TEST SYSTEM FOR IDENTIFYING *
TRANSKETOLASE-INHIBITING SUBSTANCE, HERBICIDAL ACTION SUBSTANCE AND
PACHOL: JP 1997224678-A 1 02-SEP-1997;
BASF AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2176 AGGGGAAGGCCATCGGAATTGACAGATGGGGTGCCCAGTGCCCTGCTGGAAAATATACA 2235
                                                                                                                                                                                                                                                                                                                                                                                                                                    1996 AGGCTGCTGATGAACTCAGGAAAGAAGGAAAAGCAGTGAGAGTTGTTTCTTTGTTTTGTT 2055
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                                                                                                                                                                                                                                                                                                                    4 ccggcaccaagcctgacatcattgggttgggcaccggctccgagctggagatcgcgggca 63
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0
                                                                                                                                             Score 170.4; DB 5; Length 2629;
Pred. No. 1.5e-22;
0; Mismatches 116; Indels 0;
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CDNA encoding plant transketolase from tobacco.
El3696
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/clone='TK-23'
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Location/Qualifiers
1. .2629
                                            /organism="unknown"
595 c 620 g
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02-SEP-1997
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c topology: Linear;
c hypothetical: No;
                                                                                                                                                     44.38;
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Matches 240; Conservative
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euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
Asteridae; Solananae; Solanales; Solanaceae; Solanum; Potatoe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (12-JUL-1995) Teige M., Institute of Plant Genetics and
Crop Plant Research, Mol. Cell Biology, Prot. Biochem. Group,
Correnssirasse 3, Gatersleben, Sachsen-Anhalt, Federal Republic of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (08-OCT-1996) Teige M., Institute of Plant Genetics and Crop Plant Research, Mol. Cell Biology, Prot. Biochem. Group, Corrensstrasse 3, Gatersleben, Sachsen-Anhalt, Federal Republic of
/product='Plant transketolase from tobacco' 290. .2291
/product='Plant transketolase from tobacco' 2292. .2629.
                                                                                                                                                                                                                                                                                                                                                                            1936 CTGGCAACAAACCTGATGTCATTTTGATTGGTACTGGCTCAGAGTTAGAAATTGCTGTCA 1995
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Teige,M., Kopriva,S., Bauwe,H. and Suess,K.H.
Primary Structure of Chloroplast Transketolase from Potato RACession No. 250099)(PGR96-121)
Plant Physiol. In press
2 (bases 1 to 2447)
                                                                                                                                                                                                                                                                DB 5; Length 2629;
                                                                                                                                                                                                                                                       Match 44.3%; Score 170.4; DB 5; Length; Local Similarity 67.4%; Pred. No. 1.5e-22; les 240; Conservative 0; Mismatches 116; Indels
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S.tuberosum mRNA for transketolase.
250099

    .2629
/organism="unidentified"

                                                                                                                                                         /db_xref="taxon:32644"
595 c 621 g
                                                                                          Location/Qualifiers
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CATFFVFTDYMRGAMRISALSEAGVIYVWTHDSIGLGEDGPTHQPIEHLASFRAMPNI
LMFRPADGNETAGAYKVAVLKRKTPSILALSRQKLPQLAGTSIEGAAKGGYIYSDNSS
GNKPDYILIGTGSELEIAVKAAEELKKEGKTVRVVSFVCWELYDEQSAEYKESVLPSS
VTARVSIEAGSTFGWQKFVGDKGKAIGIDGFCASAFADKIYKEFGITAEAVVAAARQV
                                                                                                                                                                                                                                                                                                                                                /db_xref="SWISS-PROT:043848"
/translation="MASSSSLTLSOVIFSPSLPRHGSSSSSSPSLSFSTFSGLKSTPF
TSSHRRILPSTTVTKQQFSVRASAAVETLEKTDAAIVEKSVNTIRFLAIDAVEKANSG
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                                                                                                                                                                                                                                                                                                                                                                                                                              HPGLPMGCAPMGHILYDEVMKYNPKNPYWFNRDRFVLSAGHGCMLQYALLHLAGYDSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 teacagegagateageategaggeegggteeacteteggetggeagaagtaegteggag 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 gcaatgcggccgacgagctgaggaaggagggaagacggtccgcgtcgtctcgttct 120
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Germany, 06466
On Nov 5, 1996 this sequence version replaced gi:902740.
Location/Qualifiers
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 120; Indels
                                                                                                                                                                                                                                                                               /product="transketolase precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.plantagineum tkt7 gene for transketolase.
246648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.4%; Score 167; DB 45;
66.6%; Pred. No. 6.4e-22;
                                                                                                     /organism="Solanum tuberosum"
                                                                                                                                                                                                                                                                                                      /protein_id="CAA90427.1"
/db_xref="GI:1658322"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="transketolase"
                                                                                                                                               /db_xref="taxon:4113"
/tissue_type="leaf"
28. .2253
                                                                                                                                                                                                   28. .2253 /
/EC_number="2.2.1.1"
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                                                                                                                             /cultivar="Desire'
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Craterostigma plantagineum.
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                                                                         1. .2447
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LGWHVIWVKNGNDGCDEIRAAIEEAKSVKDRPTWIKVTTTIGYGAPSKANITGVGNA
LGWERATTRILGWPYEPFHYPDDVKKHWSHITAEGAALESWNAKRFAEFEVKFPEE
AADLKSIITGELPTNWEST PPTYTPENGLPTRTLSHOILNGLGDVLPGLLGGSADLT
LSNMAFIKNSOPDGKRSPGERRVKFGAREHAMGSICNGLALHSPGLLPYCATYFVFTD
YMRAAMRISALSKARVLXIMTHDSIGLGEDGPTHQPVEHLASFRAMFNILTLRRADGN
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PMGHVLYDEFWRFNPKNPYWFNRDRFVLSAGHGCMLQYALLHLSGYDSVKEEDLKSLR
QWGSRTPAHPENFETPGVEVTTGPLGQGIASAVGLAVAEKHLAARYNKPGFEIYDHYT
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LIGTGSELEIAARAGDELRKEGKKVRVVSLVCWELFAEQSEKYRETVLPSGVTARVSV
EAGSTFGWERFIGPKGKAVGIDRFGASAPAERLFKEFGITVEAVVAAAKEIC"
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              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphylophytes; Spermatophyta; Magnollophyta; eudicotyledons;
Asteridae; Gentiananae; Lamiales; Scrophulariaceae; Craterostigma.
(bases 1 to 2232)
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                                                                                                                                                                                                                                                                                               The transketolase gene family of the resurrection plant
Craterostigma plantagineum: differential expression during the
rehydration phase
                                                                                                                                                        Submitted (10-NOV-1994) Bartels D., Max-Planck-Institut fuer Zuechtungsforschung, Pflanzenzuechtung und Ertragsphysiologie, Carl-von-Linne-Weg 10, Cologne, NRW, Germany, 50829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 aagcctgacatcattgggttgggcaccggctccgagctggagatcgcgggcaatgcggcc 71
                                                                                                                                                                                                                                                 Bernacchia, G., Schwall, G., Lottspeich, F., Salamini, F. and
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/clone="Cpl-tkt7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAA86609.1"
/db_xref="G1:664903"
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95163594
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Craterostigma plantagineum
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29, 2050
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/db_xref="SMISS="PROT: 042675"
//db_xref="SMISS="PROT: 042675"
//translation="MAKTTBSSPSAAAABELVVKSVNTIRFLAIDAVENVKSGHPGMP
AKCAPKGHPEPEPEMKPNPWFNNDFRFVLSAGHGAMLLYGLLHLAGYDSVKVFDL
KGLROWGSKTPAHPERFETPGYPSTTGPLGGGYGSAVGLALAEKHLGARXNKPDFENV
DHYTYMILGDGCQMEGISNEASSLAAHWGLGKLIALYDDNHTTIDGTPLAFTBDVGK
REPALGMHVLTVANGNGDYDEIREAITKVARSYTBYDFTLIKYTTIGGFGSPNRANTYGY
HGNALGPREABARNGWPETFHYPDDVKKHWSRHISEGARLESANNAKFABYEK
YPKEAAELKSIITGELPLGWEKALPTYTPESPGNPTTIGGGS
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PUTDYMRAAIRIAALSKARWYINTHDSIGLGEBDFPHQPVBHASFFRMPNITULRP
ADGNETAGAYKVAVENAGRESILSSRQKLPQLPGTSVEGVGRGGYVISDNSKOGEKP
EVILMOTGSELBIAARAGEELKREGKKVRVVSLVSWELFGEQSKEYKEMVLFSEVTAR
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
eukaryota; Spermatophyta; Magnoliophyta; eudicotyledons;
Asteridae; Gentiananae; Lamiales; Scrophulariaceae; Craterostigma.
1 (bases 1 to 2207)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The transketolase gene family of the resurrection plant Craterostigma plantagineum: differential expression during the
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Carl-von-Linne-Weg 10, Cologne, NRW, Germany, 50829
2 (bases 1 to 2207)
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/db_xref="taxon:4153"
/clone="Cpl-tkt10"
2012 GGGATAACCGTCGAAGCAGTCGTCGCGGCGGCGAAGAGTTT 2054
                                                                                                                            CPTKT10 2207 bp mRNA PLN
C.plantagineum tkt10 gene for transketolase.
Z46647
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Pred. No. 2.6e-21;
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/protein_id="CAA86608.1"
/db_xref="GI:664899"
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/EC_number="2.2.1.1"
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Best Local Similarity 68.1%;
Matches 228; Conservative
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LEEDLKTFROWGSRIPGHPBENFETPVVBYTFGFLGGGTANAVGTALLARKHLAARFNKP
DAETVÜHYTYVI LGGCGQMEGIAGRACSLAGHWGLGKLIAFYDDNH SIDGDRALAF
ESVDLRFEALGWHVIWVKNGNTGYDEIRAAIKEAKTYTDKPTLIKVTTTIGFGSBNKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLGGSADLASSNMTLLKMFGDFRRTHRKKETFRFGVREHGMGAICNGICLHSPGFVPY
CATFFVFTDYMRGAMRISALSEAGVIYVMTHDSIGLGEDGPTHQPIEALSKFPAMPNI
LMLRPADGNETAGSYKVAVENRKTPSILALSRKKLPNLPGTSIEGVEKGGYTITDNSS
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VTARVSIEAGSTFGWHKIVGSKGKAIGIDKFGASAPAGKIYQEYGITVEAVVEAAKSV
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LLKSTSSSRRLRVGSASAVVRAAAVEALESTDIDQLVEKSVNTIRFLAIDAVEKANSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Flechner, A., Dressen, U., Westhoff, P., Henze, K., Schnarrenberger, C. and Martin, W. Molecular characterization of transketolase (EC 2.2.1.1) active in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Processing site of transit peptide determined experimentally by M. Teige (Dissertation, Univ. of Hannover). See also accession number 250099; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPITRAN 2519 bp mRNA PLN 29-JAN-1999
Spinacia oleracea transketolase mRNA, chloroplast gene encoding
1875 GITAGCGTGGAGGCGGCTCGACGTTCGGGTGGGAGAGGTTCGTCGGGTTGAAGGGTCGG 1934
                                                                                                                                                                                                                                                                                                                                                                                         1935 GCCGTGGGGATCGATCGGTTCGGGCGAGCGCATCGGCGGAGAGGCTTTATAAGGAGTTC 1994
                                                                                                                                                                                                                251
                                                                                                                                                                                                                                                                                                                                    gccattggcatcgacaagttcggcgcgagtgctcctgccgggacgatctacaaggagtac 311
                                                                                             tttgatgagcagtcggatgagtacaaggagagcgtcctccctgccgacgtcacagcgagg
                                                                                                                                                  1815 TTCGGCGAGCAGTCGAAAGAGTACAAAGAGATGGTTTTGCCCTCGGAGGTTACGGCTAGG
                                                                                                                                                                                                                atcagcatcgaggccgggtccactctcggctggcagaagtacgtcggaggccaaggcaag
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/organelle="plastid:chloroplast"
/db_xref="taxon:3562"
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1 (bases 1 to 2519)
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Plant Mol. Biol. 32 (3), 475-484 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1995 GGTATTACTGTTGAAGCCGTTGTTGCTGCCGCTAA 2029
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/note="putative"
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thale cress.
Arabidopsis thaliana
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Brassicales;
Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.genoscope.cns.fr
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2111 CTGCAAGAGTAAGTATTGAAGCAGGATCAACCTTTGGATGGCATAAGATTGTGGGGGTCAA 2170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2171 AGGGGAAAGCCATTGGTATTGACAAGTTTGGAGCAAGTGCACCAGCAGGAAAGATTTACC 2230
                                                                                                                                                                                                                                                                                                                                                                                 1931 CAGGTAACAAACCTGATGTTATTCTTATTGGAACTGGTTCAGAACTGGAAATTGCTGCAA 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1991 AGGCTGGTGATGACTTAAGAAAGAAGGAAAAGCTGTTAGGGTTGTATCATTTGTTTCTT 2050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gggaactetttgatgagcagteggatgagtacaaggagagagegteeteeetgeegaegtea 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 cagogaaggatcagcatcgaggccgggtccactctcggctggcagaagtacgtcggagccc 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aaggcaaggccattggcatcgacaagttcggcgcgagtgctcctgccgggacgatćtaca 303
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Cholsne,N., Robert,C., Brottier,P., Wincker,P., Cattolico,L.,
Artiquenave,F., Saurin,W., Weissenbach,J., Mewes,H.W., Rudd,S.
Lemcke,K., Mayer,K.F.X., Quetier,F. and Salanoubat,M.
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Arabidopsis thaliana DNA chromosome 3, BAC clone T4C21.
                                                                                                                                                                                                                                              Score 162.4; DB 45;
Pred. No. 4.5e-21;
0; Mismatches 121;
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EU Arabidopsis sequencing, project.
                                                                                    /product="transketolase"
2287. .2519
                                          /EC_number="2.2.1.1"
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                                                                                    ...ad/. .2519
/note="putative"
538 c
                                                                   /note="putative
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66.0%;
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                                                                                                                                                        684
                     mat_peptide
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/organism="Arabidopsis thaliana"

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Sat Nov

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VTASTTKGSALPEDMGSIAPNLSAIVGSAVAKLMGTAGGLSALAKMPACNVQVLGHK
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STHGSLEYGCTLDCFWFKLGGLFAPVLNTGIGTSRWPTILGGGAHWYGGTALAILSFC
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STIAFGVLNFFGSVFGDLTESMIKRDAGVKDSGSLIFGHGGILDRVDSYIFTGALAS
                                                                                                                                                                                                                                                                                                                                                          TLNYDDLDSVSKLQKTQRYDDIMHKVEBALGKDSDDHEYKLIVDCNKLSVDIEDEIVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synechocystis sp., PIR:S77254
Contains Phosphatidate cytidylyltransferase signature
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for analysis and annotation"
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EMBL:NPL251365"
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                                                                                      misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyanophora paradoxa mRNA for putative transketolase precursor (tktC
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
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thaliana, EMBL:AF036303"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thesis (1999) University of Vienna, Institute of Biochemistry and
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Submitted (10-OCT-1999) Ma Y., Institute of Biochemistry and
Molecular Cell Biology, University of Vienna, Dr. Bohrgasse 9/5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 aaggcaaggccattggcatcgacaagttcggcgcgagtgctcctgccgggacgatctaca 303
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1 (bases 1 to 2595)
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                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 42.1%; Score 162.2; DB 8; Length Best Local Similarity 66.4%; Pred. No. 1.8e-21; Matches 233; Conservative 0; Mismatches 118; Indels
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2 (bases 1 to 2595)
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Best Local Similarity
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VYDPATDAGDATRILTGNTLNAIADAVPTFLGGSÄDLASSNMTLLKKYADFOKTSPEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RDRFVLSAGHGCMLQYALLYLTGYDSVGIEDIKTFRQMESECPGHPENFVTKGIEVTT
GPLGQGIAQAVGLAMGEAHLAARFNKPDVKLIDHYTYVIMGDGCNMEGVAAEAASLAG
HYGLGNLIALYDDNEISIDGNTDISFTEDVTKRYQSYGWHTVVVEDGNTDINAIRKAI
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PEEAMNKWREAIPKGKSAEDEWNKKFAEYKAKYPQEAADFFKYVMKKELPANWEKCLP
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922 c 731 g 441 t
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25. .23.
A-1030 Vienna, AUSTRIA
                                                                                                                                                                                                      25. .2340
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RESULT

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Bukaryota; Viridialantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicoryledons; core endicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

( bases 1 to 122871)
Lin,X., Kaul,S., Rounsley,S.D., Shea,T.P., Benito,M.-I., Town,C.D., Fujil,C.Y., Mason,T.M., Bowmap,C.L., Barnstead,M.E., Town,C.D., Feldblyum,T.V. Buell,C.R., Ketchim,K.A., Lee,J.J., Ronning,C.M., Koo,H., Moffat,K.S., Cronin,L.A., Shen,M., VanAken,S.E., Umayam,L., Tallon,L.J., Gill,L.E., Adams,M.D., Carrera,A.J., Crassy,T.H., Goodman,H.M., Somerville,C.R., Copenhaver,G.P., Preuss,D., Nierman,W.C., White,O., Eisen,J.A., Salzberg,S.L., Fraser,C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
On Dec 17, 1999 this sequence version replaced gi:2583106.
The sequence and annotation of chromosome 2 were merged from those of the individual chones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site (http://www.tigr.org/tdb/at/at.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence and analysis of chromosome 2 of the plant Arabidopsis
   05-APR-2000
               complete sequence. Sequence from clones T14P1, F4L23. AC002387 AE002093
AC002387.2 GI:6598365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 402 (6763), 761-768 (1999)
   DNA
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122871 bp
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Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (ftp://arthur.epm.orn.jgov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/GENSCANW.html), and NetPlantGene (http://gnomic.stanford.edu/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu-dk/services/NetGenes/), searches of the complete sequence against a peptide database and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes without significant peptide similarity but with EST similarity to other proteins are named similarity but with EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRRAscan-SE (sean Eddy, their length are predicted by tRRAscan-SE (sean Eddy, Simple repeats were identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are numbered from the top to bottom of the chromosome.
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We thank the CSHL/WashU/ABI consortium for sequencing BAC clones F6P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Deterson, Michael Holmes, and Delwood Richardson for software and database support.

This work was supported by the National Science Foundation, Department of Energy and the US Department of Agriculture.

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Address all correspondence to: at@tigr.org.
Location/Qualifiers
1. 122871
/r. 122871
/cryaniam="Arabidopsis thaliana"
/cultivar="Columbia"
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source

FEATURES

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53354 TATCAGCTAGAGTTAGTATCGAAGCTGGATCGACTTTTGGATGGGGAAAGATCGTCGGAG 53413

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53414 GAAAAGGGAAATCGATTGGAATTGATACGTTTGGAGCAAGTGCACCAGCAGGAAAGCTTT 53473

301 acaaggagtacggcatcaccgtggagagcatcattgcaactgccaag 347

qq

241 cccaaggcaaggccattggcatcgacaagttcggcgcgagtgctcctgccgggacgatct 300

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n complement(17986.18864)
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                                                                                                                                                                                                                                                                                                                                                   /gene="At2g45210"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MAFRAYIINFVILCILVASTVSGYNQKDVKAWCSQTPNPKPCEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MRKIIGFRIGRRVSRWIFRKTRIQRSGYNRIHSTQQACMLMRPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKLKSWGORLKQSFRRRSTRRSAYIPVDHKKADPVPRCHLAIYVGQKDGDCHRVLVPI
VYENHPLFGELLREAEKEYGFCHEGGITIPCLYSDFERVKTRIASGSSSRVFPWGRHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IHNSRVTAASDLRPVLGSTKTYLGRPWRQYSRTVFMKTSLDSLIDPRGWLEWDGNFAL
KTLFYAEFQNTGPGASTSGRVTWPGFRVLGSASEASKFTVGTFLAGGSWIPSSVPFTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53174 CAACCGGTAACAAACCCGATGTGATCTTGATCGGAACTGGATCAGAGCTAGAGATTGCTG 53233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53234 CTCAAGCTGCAGAAGTTAAGGGAACAAGGCAAAAGTGTGAGAGTTGTTTCCTTTGTAT 53293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 tcacagcgaggatcagcatcgaggccgggtccactctcggctggcagaagtacgtcggag 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 caaccggcaccaagcctgacatcattgggttģggcaccggctccgagctggagatcgcgg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(<22224. .22909,23488. .>24334))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 122871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(22224. .22909,23488. .24334))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 40.3%; Score 155; DB 7; Length 12 Best Local Similarity 65.4%; Pred. No. 3.7e-20; Matches 227; Conservative 0; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="putative pectinesterase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="GI:2583132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="(TA)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="At2q45220"
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                                                                                                                                                                                                                       repeat_region
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                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                          mRNA
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Direct Submission
Submitted (29-MAY-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
Submitted by:
                                                                                                                                                                                                                         Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coding sequences below are predicted from computer analysis, using the program Genefinder(P. Green and L. Hillier, ms in preparation). Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cosmid is F5110, 1300 bp overlap. Actual start of this is at base position 1 of F6N15; actual end is at 1950 F5110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAPPING: Clones were assigned to the YAC map by hybridization by M. Lodhi, Cold Spring Harbor Laboratories, and fingerprinted by M. Marra, WashU, to pick the best candidates for sequencing.
                                                           09-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Genetics, Washington University, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 95643)
Washington University Genome Sequencing Center.
                                                              PLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEIGHBORING COSMID INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   The A. thaliana Genome Sequencing Project
Unpublished (1997)
2 (bases 1 to 95643)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e-mail: rwilson@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                   Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence from more than one subclone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ryan, E., Edwards, J. and Pape, K. The sequence of A. thallana F6N15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Sequencing Center
                                                  F6N15 95643 bp DNA Arabidopsis thaliana BAC F6N15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neighboring submissions.
                                                                                                                                            AF069299.1 GI:3193311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1998)
3 (bases 1 to 95643)
                                                                                                                                                                                                 thale cress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waterston, R.
                                                                                                                 AF069299
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                                                                                   DEFINITION
14
                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
RESULT 1
F6N15/c
                                                                                                                                                                    KEYWORDS
                                                                                                                                            VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                                                                                                                                                                    SOURCE
                                                        LOCUS
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/organism="Arabidopsis thaliana"

source

FEATURES

Page 12

gene

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join(15299. .15951,16806. .17061,17136. .17246,17320. .19104, 19156. .19234,19332. .19628,19799. .20001,20363. .20614, 20746. .20892) /gene="F6N15.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YPKLCVRSMSRYVRSRAVQNPRDLARFALKASLYRAKYTKAFLLKEVKNLETTLRPQY
YASVHDCLDQIRDSVNQLSLAIAELDRVSRRQGKSQGDLHWHINNLQTWTSTALTDAE
TCVSQFPGRRMSKLKATIKGKVKNVEETTSNALAFIEHYAAARYRARRP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YFILMMNTGLYIFVLGASLIIPYMVLFFLICGCSGHVYYEIPIMLVVEVPCDLICSI
OSPKIGPDCITVDQDSNGNFRWVGFEDSAAANSLPNWTGNLAIAKSYRLDISFKTPSH
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Complement (23234 . 252288)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MSLLSEENFFLFDLNEIPEKTVYSDDGDEFLFDLNKIPPREETV
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GLRMDTDPYQELRMDTDHMTYEQLLQLCNNMGYENSGVKASNIDRCLRNTKPSEFQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSSDLPSLCFKKSRGLISRVSESNESERFVFDSTRLFGSGEGERAQDCSCSVNSLDSV
WABERLITUNDRFVETWDVLSDGAFLKRGESDUSLGSNWFELEWIAKAKTSTSMEAFVANS
SMGTITTLVDCILERIGGELMY ISIDSVKSELLDDNTHKCSPSSSSNOKLGSTRRKOK
GKTRNMKKPTPEAKSDKNVNLSTKNGKKDQAKLEFNKSREAIECKKVPTASTMINDPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASAATMEVVPGLVARKGRTKKKRKEKNKSKKCTSLENNGEVNKSVVNSSALVKASKCD
SSCTSANQHPQEYINAQIIEEHGSFSCERNRSGTCASVNGAANCEYSGEEESHSKAET
HVISSDLSSVDPAGGPSCENVNPQKSCCRGDRKEKLTMPNERSRTLDEGESHRIHHQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REAGYGFASSSSEFVSYEWPAVAPMYFSHVSSHLPTATDRLHLDVGHNLHPYVRQPFV
STVQHARNPSIEGSHKQVLSRPMPNDSHOGLTTAFTCNYDSGILVDIPEQ
KNKHELGNECENNWMLEEDFEVHTVSGVDYNQYFGGGVMYWNPSDHLGTGFSRPPSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGNET STKILQAPPTTIEGAGEEEVSGTLASLSGDVEGNSGDSLPYPILRPIIIPNMS
KSEYRRSYDTKSPNVPPTRREHPRIKRPPSPVVLCVPRAPRPPPPSPVSNSRARRGFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIAMSQLGRDQEHVSNVFDIYPDVAFPLQPPELLNCPMQGESLSLIHENYMSIFEVCI
YFSWDGVSSNPLNYILLAKVAAENMARKPYINWAIKRVTRSLQVLWPRSRTNIFGSSA
TGLSLPSSDVDLVVCLPPVRNLVSKPKIIPHLVLKIYISLLLKWVVYVYNQDSVLKFYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDDSSWAWHEAEMKRSVDDMVAFSSYSANGLDSPTAASFCSPFHPLGPPNQPLGYVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVRSGSSSPRHWGMRGWFHDGVNWEEPRGAEIVLPWRNKSLAVRPIIQPLPGALLQDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MAANNKLFFVLLSLFPLIIFSATATSSKDYDTKAYVHSWCRTTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(23534. .23629,23711. .23845,23934. .23999
24049. .24092.24457. .24490,24753. .24823,25132. .25288))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="contains similarity to Lotus japonicus RING-finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 accaagcctgacatcattgggttgggcaccggctccgagctggagatcgcggggcaatgcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 95643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="contains similarity to pectinesterases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADKICCICQDGFQKRAGVGKLNCGHNFHVNCVKPWILTKK".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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/note="codon recognized: AAG; Lys"
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28096. .30456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 135.6; DB 8;
Pred. No. 1.5e-16;
); Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
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/db_xref="G1:3193325"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAC19316.1"
/db_xref="GI:3193334"
                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="GI:3193327"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein (GB:Z36750)"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26808. .27437
/gene="F6N15.9"
26808. .27437
/gene="F6N15.9"
                                                                                                 15299. .20892
/gene="F6N15.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Matches 221;
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                                                                                                                                                                                                       complement(join(829. .942,1006. .1086,1156. .1237,1315. .1500, 1574. .1675,1776. .1809,1863. .2001,2106. .2230,2325. .3299, 3548. .3709,3844. .3987,4073. .4226))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(11756. .11816,11897. .12294,12667. .12732,13158. .13535,
13624. .13710)
/gene="F6N15.11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAC19299.1"
/db_xref="G1:3193317"
/translation="MLVSARVEKQKRVAYQGKATVLALGKALPSNVVSQENLVEEYLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EIKCDNLSIKDKLOHLCKSTTVKTRYTVMSRETLHKYPELATEGSPTIKORLEIANDA
VVOMAYEASLVCIKEWGRAVEDITHLVYVSSSEFRLPGGDLYLSAQLGLSNEVORVML
YFLGCYGGLSGLRVAKDIAENNPGSRVLLTTSETTVLGFRPPNKARPYNLVGAALFGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNVEEFCKKLVAKAGSGALELNDLFWAVHPGGPAILSGLETKLKLKPEKLECSRRALM
VSKYSSNITFYIMDKVRDELEKKGFEGEEWGLGLAFGPGITFEGFLMRNL"
11756. 13710
/gene="F6N15.11"
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TASSTKYSTGAGGTLESIVDQATRLPNPKPTDELVPWFHHRSSRAAMAMDALVPCSNL
VHEQOSKPGGVGSTRVGSCSDGRTWGGGKRARVAPEWSGGSQRLTMDTYDKRRDKIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MSTWQLFPDSSGDGFRWEVAGRILQSVSDSTPTKALESTAPLPS
MADLLLQGCSKLIAREEAMPGEIPWFRTGLGKSVVLKESSIAKAKSILAEKVTYSDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EALKRARNLLGDPELGSFFDDVAGGDQFFTPEKDERLSDIAINNGSANRGYIAHEEKT
SNKHTPNSFVSPLMSSSKQFSSVNLENLASGGNLIKKFDAAVDETDCALNATHGLSNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKVCDRSFEACMWIVWKLAČYDĨYYPAKCRGNFĽTITNVLEELKYRYEREVNHGHCSA
IKRILSGDAPASSMMVLCISAINPKTDNDSQEAHCSDSCSNVKVELTDGWYSMNAALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVLTKOLNAGKLFVGQKLRHAYVLISYLKILGAGLSGWATPTSPLESFIQPNFQAVIS
STICLLLNINGTYRAHWADRLGFCK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEEDRGLRTQKDPKKRDEIVNAIESMTVIGRSSITTDDSLSATWRLLWTTEKEQLFII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKAGLFGTTAGDVLQVIDVNKRILNNVITFPPDGVFFVRSDIDIASPQRVNFRFNSAV
LRGKNWELPLPPFGKGWFENVYMDGEIRVAKDIRGDYLIVDRAPYNWTESFV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAALIIGADPTESESPFWELHCAMQQFLPQTQGVIDGRLSEEGITFKLGRDLPQKIE
                                                                                                                                                                                                                                                                                                                                                                    'note="contains similarity to breast cancer susceptibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NTNCSIPQMRQVDTAETLPMFRTASGKSVPLKESSIAKAMSILGSDKIIDSDNVLPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGFGVSNSLFQTASNKKVNVSSAGLARAKALLGLEEDDLNGFNHVNQSSSSSQQHGWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DFFGMHPTATTRTMSEESNQVMQINMYSVMSLLQTRLELKLFFKCWLSLVLPYNMHPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MALALSLSACSPPLRRTRRAGFRTSCSIFANPAQRAKRKLLELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSLASDMAVNNSKVNGFIPRGRQPGRPADQPLVDITNRRDTAYAYNKQDSTQKKRLGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IVSVSPFKRPRISSFKTPSKKHALQASSGLSVVSCDTLTSKKVLSTRYPEKSPRVYIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLKTHEEFDATVVKHHSGTPGQYEDYVSGKRSEVLNPSLKVPPTKFQTAGGKSLSVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="contains similarity to transcriptional activators such as Ra-like and myc-like regulatory R proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to plant chalcone and stilbene synthases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  jóin(7427. .7890,7976. .8041,8120. .8228)
/gene="F6N15.13"
/note="coded for by A. thaliana cDNA W43412"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(8515. ..8695,8783. .9759)
/gene="F6N15.12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence=not_experimental
/protein_id="AAC19315.1"
/db_xref="G1:3193333"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAC19310.1"
/db_xref="G1:3193328"
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                                                                                                                                                                complement(829. .4226)
/gene="F6N15.14"
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                                  /db_xref="taxon:3702"
   /cultivar="Columbia"
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/gene="F6N15.12"
                                                                                                 /chromosome="IV"
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/gene="F6N15.13"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                              /clone="F6N15'
                                                                                                                                    /map="unknown"
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gene

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Arabidopsis thaliana
Bukaryota; Viridiplantae: Embryophyta; Tracheophyta; Spermatophyta;
Bukaryota; Viridiplantae: Embryophyta; Tracheophyta; Budicotyledons; Rosidae; eurosids II; Brassicales;
Brassicacea; Arabidopsis;
1 (Bases 5139 to 100781; 99482 to 197119)
Wilson, R., Lamar, B., Stoneking, T., Stumpf, J., Mewes, H.W., Lemcke, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (10-MAR.2000) MIPS, at the Max-Planck-Institut fuer Blochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mips.blochem.mpg.de.mayer@mips.blochem.mpg.de.mayer@mips.blochem.mpg.de.mayer@mips.blochem.mpg.de.mayer@mips.blochem.mpg.de.mayer@mips.blochem.mpg.de.mayer.mpg.de.mayer.mpg.de.mayer.cam.uk
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
and 5 can be viewed at: http://www.mips.blochem.mpg.de/proj/thal/
this fragment has an overlap with ATCHRIV2 at the 3' end.
35013 GGAGAGAAGCTAAGAAAGAAAGAAAGCAGTGAGAGTAGTGTCATTGGTGAGTTGGGAG 34954
                                                                                                                                                                                                                              Zhong,J., Ma,P., Parnell,L.D., Chen,C.N., Chen,E.Y., Mewes,H.W.
Lemcke,K. and Mayer,K.F.X.
Unpublished
                                                               gocgacgagctgaggaaggagggaaggacggtccgcgtctcgtctcgtctcctgggaa 128
                                                                                                                                                  ctctttgatgagcagtcggatgagtacaaggagagcgtcctccctgccgacgtcacagcg 188
                                                                                                                                                                                                                                                                                                                 249 aaggocattggcatcgacaagttcggcgcgagtgctcctgccgggacgatctacaaggag 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCHRIV1 197119 bp DNA PLN 16-MAR-2000
Arabidopsis thaliana DNA chromosome 4, contig fragment No. 1.
AL161471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(3199. .3438,3545. .3749,3977. .4119,
4406. .4588,4657. .4908))
3199. -4908
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/note="homology to fragments of putative reverse
                                                                                                                                                                                                                                                                                                                                                                                                                         309 tacggcatcaccgtggagagcatcattgcaactgccaagagctttt 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .197119
/organism="Arabidopsis thallana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 (bases 1 to 197119)
EU Arabidopsis sequencing, project.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /variety="Columbia"
/db_xxef="taxon:3702"
/chromosome="4"
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/gene="AT4g00010"
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DEFINITION
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AUTHORS
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SOURCE
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5139. 6001

/note="overlap to BAC F6N15; please refer to GB:AF069299

for analysis and annotation"

complement(join(5967. 6080,6144. 6224,6294. 6375,

6453. 65436,6712. 6813,6914. 6947,7001. 7139,7244. 7368,

7463. 8437,8686. 8847,8982. .9125,9211. .9364))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(5967. .6080,6144. .6224,6294. .6375,
6453. .6638,6712. .6813,6914. .6947,7001. .7139,7244. .7368,
7463. .8437,8686. .8847,8982. .9125,9211. .9364))
/gene="AT4g00020"
                                                                                                                                                                                                                                                                            VPINSDSEILYLHARGSSSRWOPLSPRDSENPHEFDTAAYVYVGNATTDVLOKKOWV
FVTDGSAQHSGEISNSLLAISFSTSFWDDSSVSHISHNLVGSVVGFCNLIKRRKDVTN
EIWVAEAAENSVYFINAEAAYSSHLKTSSAHIQTWAKLSSSKSVRSRRLPLSIIIRFK
                                                                                                                                                                                                                          SEEGAKIFKLLETAAEPEFLMAEMSPEQLRSFTTYKAKFEAAQOMRKEKSVAETLEDA
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63.9%; Pred. No. 1.3e-16;
tive 0; Mismatches 124;
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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dР	Query	Match		44.3	20.9	20.8	16.4	74.5			13.4	11.4	11.4	11.0		11.2	11.2	
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ALIGNMENTS

d; cDNA; 2629 BP.		(first entry)	Sequence encoding tobacco transketolase.	herbicide; Nicotiana tabacum; identification;	um.	Location/Qualifiers 602291 /*tag= a /product= Transketolase.			96EP-0100458.	95DE-4001906.	ж.	Sonnewald U, Stitt M;	
T35903 standard; cDNA;	T35903;	29-JAN-1997 (first	equence encoding t	Transketolase; herk screening; ss.	Nicotiana tabacum.	Key Loc CDS 60.	EP723017-A2.	24-JUL-1996.	13-JAN-1996; 96ЕР	23-JAN-1995; 95DE	(SCHM/) SCHMIDT R. (BADI) BASF AG.	Schmidt R, Sonnewa	WPI: 1996-335478734

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 aaggcaaggccattggcatcgacaagttcggcggagtgctcctgccgggacgatctaca 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 gggaactctttgatgagcagtcggatgagtacaaggagagcgtcctccctgccgacgtca 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 ccggcaccaagcctgacatcattgggttgggcaccggctccgagctggagatcgcgggca 63
                                                                                                                                                                          The transketolase from tobacco is useful for identifying herbloides for their ability to inhibit the transketolase. The transketolase can be produced in pure form by cloning the gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S. pneumoniae; genome; diagnosis; assay; vaccine; pharmaceutical composition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 aggagtacggcatcaccgtggagagcatcattgcaactgccaagagcttttaagag 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Computer-readable medium with recorded Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                    Score 170.4; DB 17; Length 2629; Pred. No. 4e-34;
                 New trans:ketolase from tobacco and related DNA - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 116; Indels
                                            screening for inhibitors which are potential herbicides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae genome fragment SEQ ID NO:49.
                                                                                                                                                                                                                                                                                                           Sequence 2629 BP; 686 A; 595 C; 620 G; 728 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dougherty BA,
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                                                                                                                   Claim 5; Page 9-12; 26pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V52182 standard; DNA; 11443 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                  similarity 67.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Best Local S
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The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID No:1 to 391 (V52134 to V52524) recorded to nit, or a representative fragment or a sequence at least 95% identical co SEQ ID No: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 prosent invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae CC molecule encoding a homologue of any of the fragments of the S.pneumoniae CC genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a crose target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members of the library which contain sequences conformable in amplifying nucleic acid molecules whose nucleotide conforms and organism, amplifying nucleic acid molecules whose nucleotide conforms to the sequence of commercial importance, or expression and isolating the amplification primers derived from the conjuter-based system for identifying fragments of the S. pneumoniae genome of commercial importance, or expression modulating craments of the S. pneumoniae genome. Products from the present computerion and vaccines for S. pneumoniae, or expression modulating compositions and vaccines for S. pneumoniae.
polynucleotide sequences – useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                Claim 1; Page 445-451; 1409pp; English.
                                                                             pneumoniae
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Gaps

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0; Gaps Length 11443; Sequence 11443 BP; 3350 A; 2057 C; 2533 G; 3502 T; 1 other; Indels Query Match
20.9%; Score 80.6; DB 19;
Best Local Similarity 51.9%; Pred. No. 1.9e-11;
Matches 182; Conservative 0; Mismatches 169;

257 tggcatcgacaagttcggcgcgagtgctcctgccgggacgatctacaaggagtacggcat 316 셤 g δ

10303 tacggtagagaatatcgttgctcaagttaagtccctatagaaaccaattac 10353 317 caccgtggagagcatcattgcaactgccaagagcttttaagagctaacaac 367 V74685 standard; DNA; 1953 BP (first entry) 16-MAR-1999 V74685; RESULT V74685 ŏ

Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; Staphylococcus aureus contig SEQ ID #374.

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Fannon

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skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
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Staphylococcus aureus.

Location/Qualifiers 961..1020 /*tag= a misc_feature

"these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence" /note=

EP786519-A2

30-JUL-1997

97EP-0100117. 07-JAN-1997;

96US-0009861. 05-JAN-1996;

(HUMA-) HUMAN GENOME SCI INC

Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA; Rosen CA;

WPI; 1997-374922/35.

Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of anti-S.aureus vaccines

Claim 1; Page 1267-1268; 3271pp; English.

This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access the S.aureus DNA sequences allows putative functions to be assigned to find protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are be used in a vaccine composition against S.aureus infection. The polypeptides can polypeptides can be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelld infections, food poisoning, osteomyelitis, syndrome, etc. Organisms transformes at the bus syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences homologues of any of the S.aureus DNA sequences computer readable medium.

Sequence 1953 BP; 658 A; 259 C; 353 G; 618 T; 65 other;

Query Match

ö 367 ccagaattcctattattagcttcaggttcagaagttagtcttgcagttgaagctgctaaa 426 427 gatottgaaaaacaaggtaaatcagtacgtgttgtttcaatgcotaactggaatgcattt 486 Gaps 15 octgacatcattgggttgggcaccggctccgagctggagatcgcgggcaatgcggccgac 74 ó Y Match 20.8%; Score 80; DB 18; Length 1953; Local Similarity 52.0%; Pred. No. 1.9e-11; hes 179; Conservative 0; Mismatches 165; Indels (Matches 179; g ð ò g

probable transketolase, and represents a DNA sequence of the invention. The DNA sequences were isolated from Streptococcus pneumoniae strain of the DNA sequences were isolated from Streptococcus pneumoniae strain of 1000993 (WILMB 40794). The Streptococcus pneumoniae strain of 1000993 (WILMB 40794). The Streptococcus pneumoniae proteins of the invention can be used to identify compounds which interact with and used to treat diseases caused by S. pneumoniae proteins. Antagonists can be used to treat diseases caused by S. pneumoniae proteins, through genetic immunisation. They can also be used to induce an immunological response in a mammal by inoculation with the S. pneumoniae proteins or delivery and/or T cell immune responses to protect the animal from disease. The proteins can also be used to identify antimicrobial compounds which are proteins can also be used to prevent adhesion of bacteria to mammalian capable of inhibiting their bioactivity. In particular the proteins of the invention can be used to prevent adhesion of bacteria to mammalian extracellular matrix proteins on in-dwelling devices or in wounds, to block protein-mediated mammalian cell invasion, and to block the normal

This sequence encodes a Streptococcus pneumoniae protein that is a

Claim 4; Page 106; 483pp; English.

487 gaacaacaatctgaagaatataaagaatcagttattccatcaagcgtaacaaaacgtgtt 546 195 agcatcgaggccgggtccactctcggctggcagaagtacgtcggagcccaaggcaaggcc 254 g ò

135 gatgagcagtcggatgagtacaaggagagcgtcctccctgccgacgtcacagcgaggatc 194

δŏ

607 attgctattgacggctttggcgcaagtgcacctggcgatttagtagttgaaaaatatgga 666 255 attggcatcgacaagttcggcgcgagtgctcctgccgggacgatctacaaggagtacggc 314 Streptococcus pneumoniae protein; genetic immunisation; antagonist; immunological response; inoculation; antibody production; inhibitor; T cell immune response; antimicrobial compound; bacterial adhesion; extracellular matrix protein; protein-mediated cell invasion; wound; Novel Streptococcus pneumoniae proteins and related DNA - useful for diagnosing anti-microbial agents for treatment of bacterial 667 tttacaaaagaaaatatcttaaaccaagttatgagcttataaga 710 315 atcaccgtggagagcatcattgcaactgccaagagcttttaaga 358 DNA encoding a S. pneumoniae probable transketolase. Hodgson JE, Knowles DJC, Nicholas RO; complement (895..1350) Location/Qualifiers (SMIK) SMITHKLINE BEECHAM CORP. T98569 standard; DNA; 1738 BP 97WO-US07950. 96US-0017670. 06-NOV-1998 (first entry) /*tag= a Streptococcus pneumoniae. WPI; 1998-008793/01. pathogenesis; ss. P-PSDB; W38502. 14-MAY-1997; 14-MAY-1996; WO9743303-A1 20-NOV-1997. Stodola RK; infections Black MT, T98569; RESULT 198569, g ò ò

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tgagcagtcggatgagtacaaggaggggtcctccctgccgacgtcacagcgaggatcag 196
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progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or other surgical techniques.
                                                                                                                                                                                                                                                                                                                                    212 ATTGGTTTTACAAGGTGGTAAAGTACGTGTGGTATCTATGCCCTCAACCGAACTATTTGA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 CATTGAAATGGCAGCGACCCAAAGTTGGTACAAGTATGTTGGTTTGGATGGCGCGGNCAT 33
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                              17 tgacatcattgggttggggcaccggctccgagctggagatcgcggcaatgcggccgacga 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 IGCTCAAGATGCTACCTACAAGGAAGACATTTTACCATCTAAGACTCGTCGTCTGTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.
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                                                                                                                                                                          Query Match 16.4%; Score 63; DB 19; Length 1738; Best Local Similarity 51.8%; Pred. No. 3.4e-07; Matches 141; Conservative 0; Mismatches 131; Indels (
                                                                                           Sequence 1738 BP; 493 A; 410 C; 365 G; 469 T; 1 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X13233 standard; DNA; 3225 BP
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can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1685 tetgetgaatataaagaaagtgtgttacetaaagetgtgacaaaacgtgtggegattgaa 1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1745 gctgcaagcaagctttggttgggaacgctatgtagggacggaaggcaaaacaattacaatt 1804
                                                                                                                                                                                                                                                                                                                                                                                                                                1565 attttaattgcgactggttctgaagtaaatctagcggtggaagcacaagcgaaattagcg 1624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 gccgggtccactctcggctggcagaagtacgtcggaggcccaaggccattggcatc 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 teggatgagtacaaggaggagggteeteetgeegaegteacagegaggateageategag 203
                                                                                                                                                                                                                                                                                                                                                                                                84 aaggagggaagacggtccgctcgtctcgttcgtctcctgggaactctttgatgagcag 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                          24 attgggttgggcaccggctccgagctggagatcgcggcaatgcggccgacgacgagctgagg 83
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay; computer readable medium; vaccine; pharmaceutical composition; ds.
                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                    Score 55.8; DB 20; Length 3225;
Pred. No. 2.5e-05;
0; Mismatches 127; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fannon M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae genome fragment SEQ ID NO:239.
                                                                                                                                                                                                Sequence 3225 BP; 1059 A; 613 C; 695 G; 856 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dougherty BA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1805 gatcacttcggcgcttctg 1823
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                                                                                                                                                                                                                                                          14.5%;
51.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                              Matches 132; Conservative
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Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-272225/24.
                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kunsch CA,
                                                                                                                                                                       infection
                                                                                                                                                                                                                                                              Query Match
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pneumoniae

Claim 1; Page 1259-1260; 1409pp; English.

The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (V22134 to V52524) recorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391 (V52134 to V52524) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae of SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) sercenhing a genomic DNA library using as a process comprising: (a) sercenhing a genomic DNA library using as a process comprising: (a) sercenhing a genomic DNA library using as a process comprising to a sercenhing a genomic DNA library using as a process comprising to a process comprising the library which contain sequences in that hybridise to the target sequence and isolating men produced from the members; or (b) isolating men organism, amplifying nucleic acid molecules whose nucleotide contain and organism, amplifying nucleic acid molecules whose nucleotide fragment of the S. pneumoniae genome to prime the amplification and consultar based system for infantifying fragments of the computer readable medium can be consultar and none or an anomal organism and consultar and a computer and the computer readable medium can be consultant and anomal organism and consultant and computer and the computer readable medium can be consultant and anomal organism and S. pneumoniae genome of commercial importance, or expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines for S. pneumoniae.

Sequence 946 BP; 272 A; 189 C; 218 G; 267 T; 0 other;

Ĥ 491 ccgactttgataccatcttgattgcgacaggttcagaggttaatcttgctgctgctcagctg 550 551 ctaaagaattggctagtcaaggcgaaaaatccgcgtagtcagcatgccatctacagatg 610 130 totttgatgagcagtcggatgagtacaaggagagcgtcctccctgccgacgtcacagcga 189 611 tctttgataaacaagatgcagcttacaaggaagaaatcttccaaatgcagtccgccgtc 670 190 ggatcagcatcgaggccgggtccactctcggctggcagaagtacgtcggagcccaaggca 249 671 gigitgcagicgaaaigggigcaagicaaaaciggiacaaaiaigtiggicicgaiggig 730 250 aggccattggcatcgacaagttcggcgcgagtgctcctgccgggacgatctacaaggagt 309 731 ccgttctaggtattga-tacttcggagcctctgccccagcaccaaaagtattggcagaat 789 1; Gaps 10 ccaagcctgacatcattgggttgggcaccggctccgagctggagatcgcgggcaatgcgg 69 14.0%; Score 53.8; DB 19; Length 946; 49.0%; Pred. No. 6.1e-05; tive 0; Mismatches 177; Indels 1 310 acggcatcaccgtggagagcatcattgcaactgccaagagcttttaaga 358 790 atggetttaetgtagaaaatettgtaaaagttgttegaaaettgaaata 838 Matches 171; Conservative Best Local Similarity Query Match g q QΩ ŏ ŏ ò δ g ò

P. aeruginosa detection probe #2. T28491 standard; DNA; 1872 BP 01-APR-1997 (first entry) RESULT T2849.

Detection; probe; amplification primer; bacterial pathogen; pneumonia; Escherichia coli; Klebsiella pneumoniae; Pseudomonas aeruginosa; Proteus mirabilis; Streptococcus pneumoniae; Staphylococcus aureus; Staphylococcus epidermidis; Enterococcus faecalis; respiratory tract; Staphylococcus saprophyticus; Streptococcus pyogenes; urinary tract;

The sequences given in T28490-503 represent probes which were used in the method of the invention for the detection of P. aeruginosa in a sample. The method comprises using probes and/or amplification primers which are specific, ubiquitous and sensitive for determining the presence and/or amount of nucleic acids from selected bacterial species in any sample, where the bacterial nucleic acid comprises a selected target region hybridisable with the probes or primers. The method comprises contacting the sample with the probes or primers and detecting the presence and/or amount of hybridised primers or amplification products as and indication of the presence and/or amount of parts of the presence and/or amount of hybridised primers or amplification products Haemophilus influenzae; Moraxella catarrhalis; septicaemia; meningitis; infection; intra-abdominal infection; skin infection; bacterial resistance; beta-lactam antibiotic; ds. Species. This method may be used to detect commonly encountered bacterial pathogens, e.g. Escherichia coli, Klebsiella pneumoniae, Steudomonsa aeruginosa, Proteus mirabilis, Streptococcus pneumoniae, Staphylococcus aureus, Staphylococcus spidermidis, Enterococcus faecalis, Staphylococcus saprophyticus, Streptococcus pyogenes, Haemophilus influenzae and Moraxella catarrhalis. These bacterial species are associated with approx. 90% of urinary tract infections and with a high percentage of other severe infections including septicaemia, meningitis, pneumonia, intra-abdominal infections, skin infections and other severe respiratory tract infections. The method may also be used to evaluate a bacterial resistance to beta-lactam Method for the detection of bacterial species using probes and primers - allows detection and quantification of antiblotic resistant bacteria in patients, the environment and food Sequence 1872 BP; 402 A; 651 C; 555 G; 264 T; 0 other; Claim 34; Page 71-72; 216pp; English. 95WO-CA00528. 94US-0304732 Bergeron MG, Ouellette M, (BERG/) BERGERON M G. WPI; 1996-179953/18. OUELLETTE M. (ROYP/) ROY P H. 12-SEP-1994; 12-SEP-1995; WO9608582-A2 21-MAR-1996. Synthetic.

4 ccggcaccaagcctgacatcattgggttgggcaccggctccgagctggagatcgcgggca 63 Ouery Match
Best Local Similarity 47.3%; Pred. No. 0.00025;
Matches 156; Conservative 0; Mismatches 174; Indels 0;

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1093 ggggagatgatgettegetacetgggetggaacgaggeggeggegteateateagggec 1152
                         183 acagcgaggatcagcatcgaggccgggtccactctcggctggcagaagtacgtcggagcc
                                                                                                                                                                                                                                 257439;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA of a structural gene coding a heat-resistant isocitrate dehydrogenase - useful as a reagent for research in medical chemistry, biochemistry, agricultural chemistry and pharmacology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 tgggaactctttgatgagcagtcggatgagtacaaggagaggggcgtcctcctgccgacgtc 182
                              244 aaggcaaggccattggcatcgacaagttcggcggagtgctcctgccgggacgatctaca 303
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Pred. No. 0.019;
0; Mismatches 165; Indels (
                                                                                                                                                                                                                                             Heat-resistant; isocitrate dehydrogenase; ICD; thermostable; medical chemistry; agricultural; pharmacology; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 1284 BP; 266 A; 424 C; 407 G; 187 T; 0 other;
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                                                                                                                                                                                                                        Heat-resistant isocitrate dehydrogenase encoding DNA.
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                                                                                        1016 cctcccacgagcaccccgagttcatcgtca 1045
                                                                 304 aggagtacggcatcaccgtggagagcatca 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 17-20; 22pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                 (MIYA/) MIYAZAKI K.
(ORIY ) ORIENTAL YEAST CO LTD.
                                                                                                                                                  Z46836 standard; DNA; 1284 BP
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11.4%;
Best Local Similarity 46.4%;
Matches 143; Conservative
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                                                                                                                                                                                                                                                                                   Thermus aquaticus
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                                                                                                                                                                                                                                                                                                         JP11346780-A.
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                                                                                                                                                                            246836;
                                                                                                                              RESULT
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973 atcgcccccggggccaacatcaactacaagacgggccacgccgtctttgaggccaccac 1032
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                                                                                                                            1213 gagggcaagccggccacgcttcttaagaccagcgagttcggccaggccctgatccagcac 1272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heat resistant; isocitrate dehydrogenase; ICD; ammonia; determination;
3 accggcaccaagcctgacatcattgggttgggcaccggctccgagctggagatcgcgggc 62
                                                                            243 caaggcaaggccattggcatcgacaagttcggcgcgagtgctcctgccgggacgatctac 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "heat resistant isocitrate dehydrogenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heat resistant isocitrate dehydrogenase encoding DNA SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a solution type reagent for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A liquid reagent for the elimination of ammonia determination of biosubstances in a sample
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 10; Page 23-26; 28pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                 Z57439 standard; DNA; 1284 BP.
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Best Local Similarity
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                                                                                                                                                                                                                                                1273 atggacta 1280
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isocitrate dehydrogense (ICD) starting from initiation codon and ending at terminating codon of the 2872 base sequence (24684), where the second codon GCC from the initiation codon ATG is replaced by GCT, GCA or GCG, useful as a reagent for researches in medical chemistry, biochemistry, biochemistry, agricultural chemistry and pharmacology. The method can prepare a heatresistant ICD in large amount at low cost. The present sequence represents a DNA encoding the heat-resistant ICD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention provides a DNA of a structural gene coding a heat-resistant
                              1033 ggcaccgccccaagtacgctggccaggacaaggtgaaccccagcagcgtcatcctctcc 1092
                                                                                               1153 atggagaggaccatcagcaagggcctggtcacctacgacttccaccgcctcctggtggcc 1212
                                                                                                                                                                                                                                 1213 gagggcaagccgccacgcttcttaagaccagcgagttcggccaggcctgatccagcac 1272
123 tgggaactetttgatgageagteggatgagtacaaggagagagegteeteeetgeegaegte 182
                                                                                                                                 183 acagogaggatcagcatcgaggccgggtccactctcggctggcagaagtacgtcggagcc 242
                                                                                                                                                                                                  243 caaggcaaggccattggcatcgacagttcggcgcgagtgctcctgccgggacgatctac 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dehydrogenase - useful as a reagent for research in medical chemistry, blochemistry, agricultural chemistry and pharmacology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heat-resistant; isocitrate dehydrogenase; ICD; thermostable; medical chemistry; agricultural; pharmacology; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA of a structural gene coding a heat-resistant isocitrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heat-resistant isocitrate dehydrogenase encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1281 BP; 264 A; 424 C; 407 G; 186 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                     Z46835 standard; DNA; 1281 BP.
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                                                                                                                                                                                                                                                                                                  1273 atggacta 1280
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Length 1281;

Score 43; DB 21; Pred. No. 0.033;

11.2%;

Query Match Best Local Similarity

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1033 ggcaccgccccaagtacgctggccaggacaaggtgaaccccagcagcgtcatcctctcc 1092
                                                                                                                                                                                      1093 ggggagatgatgcttcgctacctgggctggaacgaggcggcggacctcatcatcagggcc 1152
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                                                                                            63 aatgoggoogaogagtgaggaaggagggaagacgtoogogtogtototogtoto 122
                                                                                                                                                        123 tgggaactctttgatgagcagtcggatgagtacaaggagagagcgtcctgccgacgtc 182
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                                                                                                                                                                                                                                                                                  243 caaggcaatggcattggcatcgacaagttcggcgcgggtgtgtctgccgggacgatctac 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heat resistant; isocitrate dehydrogenase; ICD; ammonia; determination;
        Gaps
                              3 accggcaccaagcctgacatcattgggttgggcaccggctccgagctggagatcgcgggc 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dehydrogenase (ICD) showing a heat-resistant isocitrate dehydrogenase (ICD) showing a high stability at an alkaline pH and responding to both NADP+ and NAD-. The reagent is used for the determination of biosubstances in a sample. The reagent can eliminate ammonia in a very short period. The present sequence encodes ICD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= "heat resistant isocitrate dehydrogenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heat resistant isocitrate dehydrogenase encoding DNA SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A liquid reagent for the elimination of ammonia \, - useful for the determination of biosubstances in a sample
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a solution type reagent for the
   0; Mismatches 165; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Z57438 standard; DNA; 1281 BP.
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(ORIY ) ORIENTAL YEAST CO LTD.
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Matches 142; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 acagogaggatcagcatcgaggccgggtccactctcggctggcagaagtacgtcggagcc 242
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                                                                                                                                                                                                                                                                                                                       63 aatgeggeeggaegaggaggaaggggaagaeggteeggtegteteettee 122 | 122 | 122 | 123 | 123 | 124 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 125 | 
                                                                                                                                                                                                                        3 accggcaccaagcctgacatcattgggttgggcaccggctccgagctggagatcgcgggc 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (socitrate dehydrogenase; heat-resistant; thermostable; recombinant;
                                                                                                                                                                               Gaps
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                                                                                                                                                                               ö
                                                                                                                   Score 43; DB 21; Length 1281;
Pred. No. 0.033;
                                                                                                                                                                               0; Mismatches 165; Indels
                                                   Sequence 1281 BP; 264 A; 425 C; 406 G; 186 T; 0 other;
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       isolated from Thermus aquaticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V35659 standard; DNA; 1480 BP.
                                                                                                                                11.2%;
46.3%;
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                                                                                                                                                                                 Matches 142; Conservative
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                                                                                                                                                       Similarity
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                                                                                                                                Query Match
                                                                                                                                                               Best Local
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V35659
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DNA of a structural gene coding a heat-resistant isocitrate dehydrogenase - useful as a reagent for research in medical chemistry, biochemistry, agricultural chemistry and pharmacology
This DNA encodes a heat-resistant (thermostable) isocitrate dehydrogenase. A host transformed with a recombinant vector comprising the thermostable isocitrate dehydrogenase encoding DNA can be used to produce the protein recombinantly. The method can prepare the heat-resistant isocitrate dehydrogenase efficiently.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1392 gagggcaagcccgccacgcttttaagaccagcgagttcggccaggccctgatccagcac 1451
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                                                                                                                                                                                                                                                                                       11.2%; Score 43; DB 19; Length 1480; 46.3%; Pred. No. 0.034; tive 0; Mismatches 165; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heat-resistant; isocitrate dehydrogenase; ICD; thermostable;
                                                                                                                                                                                               Sequence 1480 BP; 298 A; 508 C; 459 G; 215 T; 0 other;
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(ORIY ) ORIENTAL YEAST CO LTD.
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            The invention provides a DNA of a structural gene coding a heat-resistant isocitrate dehydrogenase (ICD) starting from initiation codon and ending at terminating codon of the 2872 base sequence (246834), where the second codon GCC from the initiation codon ATG is replaced by GCT, GCA or GCG, and/or the ninth codon CCC is replaced by CCT, CCA or CCG. The ICD is useful as a reagent for researches in medical chemistry, biochemistry, agricultural chemistry and pharmacology. The method can prepare a heat-resistant ICD in large amount at low cost. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1212 ggcaccgccccaagtacgctggccaggacaaggtgaaccccagcagcgtcatcctctcc 1271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1272 ggggagatgatgcttcgctacctgggctggaacgaggcggcggacctcatcatcagggcc 1331
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                                                                                                                                                                                                                                                                                                                                                                   63 aatgcggccgacgagtgaggaaggaggaggaagacggtccgcgtctcgtctcgtctcc 122
                                                                                                                                                                                                                                                                                                                                                                                                                                      123 tgggaactctttgatgagcagtcggatgagtacaaggagagcgtcctccctgccgacgtc 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 acagegaggatcageategaggeegggteeacteteggetggeagaagtaegteggagee 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 caaggcaaggccattggcatcgacaagttcggcgcgagtgctcctgccgggacgatctac 302
                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                 3 accggcaccaagcctgacatcattgggttgggcaccggctccgagctggagatcgcgggc 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "heat resistant isocitrate dehydrogenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heat resistant isocitrate dehydrogenase encoding DNA SEQ ID NO:2
                                                                                                                                                                                                                                  11.2%; Score 43; DB 21; Length 2872; 46.3%; Pred No. 0.039;
                                                                                                                                                                                                                                                 Pred. No. 0.039;
0; Mismatches 165; Indels
                                                                                                                                                                                 Sequence 2872 BP; 519 A; 988 C; 966 G; 399 T; 0 other;
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Matches 142; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a solution type reagent for the elimination of ammonia containing a heat-resistant isocitrate dehydrogenase (ICD) showing a high stability at an alkaline pH and responding to both NADP+ and NAD-. The reagent is used for the determination of blosubstances in a sample. The reagent can eliminate ammonia in a very short period. The present sequence encodes ICD isolated from Thermus aquaticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1212 ggcaccgccccaagtacgctggccaggacaaggtgaaccccagcagcgtcatcctcc 1271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLT4; receptor tyrosine kinase; probe; metastasis; lymphoma; lymphangioma; immunological disease; cancer; diagnosis; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acagogaggatcagcatcgaggccgggtccactctcggctggcagaagtacgtcggagcc
                                                                                  - useful for the
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                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 165;
                                                                               A liquid reagent for the elimination of ammonia determination of biosubstances in a sample
                                                                                                                                                                                                                                                                                                                                               DB 21;
                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 0.039;
                                                                                                                                                                                                                                                                                                                                               11.2%; Score 43; 46.3%; Pred. No.
                                                                                                                               Claim 5; Page 15-18; 28pp; Japanese.
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(ORIY ) ORIENTAL YEAST CO LID.
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Best Local Similarity 46.33
Matches 142; Conservative
                              WPI; 2000-109696/10.
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                                              P-PSDB; X67969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 cctgccgacgtcacagcgaggatcagcatcgaggccgggtccactctcggctggcagaag 230
                                                                                                                                                                                                                                                                                                                                                                                                   A DNA sequence (T12068) coding for FLT4 receptor tyrosine kinase (R90528) is used as a probe that specifically binds/hybridizes to DNA encoding human FLT4. Such probes are used to detect FLT4, a novel marker for lymphatic vessels and some high endothelial e.g. in biological tissue for use in diagnosis and therapy of e.g. inflammatory, infectious and immunological diseases, metastatic lymph nodes and lymphangiomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                    Antibodies against FLT4 receptor tyrosine kinase, hybridomas and nucleic acid probes - used to diagnose and treat e.g. metastatic cancers, involving alterations to lymphatic vessels.
                                                                                                                                                                                                     Alitalo K, Kaipainen A, Karnani P, Korhonen J, Matikainen M;
Mustonen T, Pajusola K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 4195;
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                                                                                                                                                                                                                                                                                                                                                                        Claim 9; Page 27-33; 54pp; English.
                               94US-0257754
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Matches 136; Conservative
                                                                                                                                MATIKAINEN M.
                                                                                  KAIPAINEN A.
                                                                                                                                                                                                                                                      WPI; 1996-040189/04
                                                                                                                    KORHONEN J.
                                                                                                                                                                   (PAJU/) PAJUSOLA K.
                                                                                                  KARNANI P.
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                                                                 ALITALO K.
                                                                                                                                                                                                                                                                       P-PSDB; R90528
                               09-JUN-1994;
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2255 tatetgtgcagegtgtgcaaegecaagggetgegtcaaeteeteegeeagegtggeegtg 2314 2315 gaaggetecgaggataagggeageatggagategtgateettgteggtaeegge 2368 291 gggacgatctacaaggagtacggcatcaccgtggagagcatcattgcaactgcc 344 q ŏ

tacgtcggagcccaaggcaaggccattggcatcgacaagttcggcgggagtgctcctgcc 290

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q δλ Search completed: November 4, 2000, 13:45:37 Job time: 16464 sec

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November 4, 2000, 11:52:15; search time 4352.3 Seconds (Without alignments) 546.925 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	9685 9450291	16325 68/049D0	486049B0	55050 60607400	17017 707009C1	46961 WS1_56_C	90044 WHE0364_	64694 PI1_14_C	00161 707	15654 HV_CED00	65303 LG1_34	BE420889 HWM003.FU	1940 940030	BE41043/ SCHO33:CO	2000 00000	2447 WHEOU	27 TENT 00 5 TO 5 TO 5 TO 5 TO 5 TO 5 TO 5 TO	35 A085p38u	31561 s181q05	550 C99650 Ri	75545 EST3346	76336 EST3354	118 LO-594T	34032 SP	BE488527 WHEIU58_A	2000	164 sf36e03.	34 GA_Ea0	5 sf36e0	348 si41b02	00158 sc01f09	1/2 SIUSEUS	81140 SC34C0	56809 se31h02	24053 AV524053	6103 BNLGHIS	23269 AV523269	23749 AV52374	3732 AV52373	23633 AV52363	522729 AV52272
Q	1296	21632	AW2024/8	25500	14701	4696	9004	6469	0016	1565	56530	42088	4494	1843	2006	777	7 7 7	0 6	, 10	C99620	55	53	22	340	BE488527	AV391280	200	530	W2036		Ξ:			ב ע ב	0 7	17061	75037	3	3 6	33.	50
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ngth	541	226	592	204	759	526	620	581	619	540	705	811	286	747	709	185	483	004	7 Y	290	646	691	570	382	464	492	531	096	573	518	484	526	581	404	100	000	16.0	200	086	7,00	619
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ALIGNMENTS

/note="Corgan: Lassel, kernal, silk, husk, root, leaf; Vector: pGAD10; Site_1: ECORI; cDNA library from fully differentiated maize tissues from an active Mutator plant. Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned. New library number given to library 707 for additional sequencing.* ö BE129685 541 bp mRNA EST 21-JUN-2000 945029E06.X2 945 - Mixed adult tissues from Walbot lab, same as 707 (SK) Zea mays cDNA, mRNA sequence.
BE129685.1 GI:8577048 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
1 (bases 1 to 541)
Walbot, V.
Malbot, V.
Maize ESTs from various cDNA libraries sequenced at Stanford /db_xref="taxon:4577" /db_xref="taxon:4577" /clone_llb="945 - Mixed adult tissues from Walbot lab, same as 707 (SK)" /tissue_type="tassel, kernal, silk, husk, root, leaf" /dev_stage="fully-grown" /lab_host="DH10B" Gaps ö 89.2%; Score 343.6; DB 33; Length 541; 94.9%; Pred. No. 1e-82; Live 0; Mismatches 19; Indels 0; 855 California Ave, Palo Alto, CA 94304, USA rel: 650 723 2227
Fax: 650 725 8221
Email: Walbotestanford.edu
Plate: 945029 row: E column: 06.
Location/Qualifiers Unpublished (1999) Contact: Walbot V Department of Biological Sciences 1. .541 /organism="Zea mays" /cultivar="W23" Stanford University Query Match
Best Local Similarity 94.9 Matches 355; Conservative 372 tgggagttttttt 385 University Zea mays. Zea mays source BASE COUNT DEFINITION ORGANISM AUTHORS TITLE ACCESSION REFERENCE JOURNAL VERSION KEYWORDS SOURCE FEATURES Óλ q 셤 Dp рp δX g ŏ ö

181 TGAGTTTTTTTT 168

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/db_xref="texco:.4577"
/db_xref="texco:.4577"
/clone_lib="687 - Early embryo from Delaware"
/tissue_type="embryo"
/dev_stage="embryo"
/dev_stage="lu, 21, 28, and 35 days after pollination"
/dab_nost="E. col! SoLR"
/lab_nost="E. col! SoLR"
/lab_nost="E. col! SoLR"
/iste_2: Ecors: Library was prepared by Statagene using the Uni-2AP XR system (Stratagene BN937328-12). Clones were picked by a 0-bot after blue/white selection
/ampfoilin resistance - use 100 micrograms/microliter).
Developed from a pool of equal amounts of RNA from developing embryos sampled at 14, 21, 28 and 35 days after pollination of the Illinois High Oil Maize Strain Cycle 90. This closed strain has been selected for high oil concentration for 90 generations and Originates from the 1890s era open pollinated variety Burr's White"
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Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
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687049D06.x1 687 - Early embryo from Delaware Zea mays cDNA, mRNA
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Tel: 650 723 2227
Fax: 650 725 8221
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Plate: 687049 row: D column: 06.
Locatlon/Qualifiers
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Stanford University
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Matches 344; Conservative
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
1 (bases 1 to 592)
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/dev_stage="14, 21, 28, and 35 days after pollination"
/lab_host="E. coli SOLR"
/note="Organ: embryo; Vector: pBluescript_SK; Site_1: xhor
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687037D05.x1 687 - Early embryo from Delaware Zea mays CDNA, mRNA
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/clone_lib="687 - Early embryo from Delaware"
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Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot/estanford.edu
Plate: 687037 row: D column: 05.
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Magnoliophyta; Liliopsida; Poales; Poaceae; 2ea.
1 (bases 1 to 463)
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486049B09.x4 486 - leaf primordia cDNA library from Hake lab Zea
mays cDNA, mRNA sequence.
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                                                     225 cagaagtacgtcggagcccaaggcaaggccattggcatcgacaagttcggcgagtgct
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Pred. No. 8.7e-64;
0; Mismatches 6; Indels 0;
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Stanford University
855 California Ave, Palo Alto, CA 94304, USA
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/lab_host="E.coli XL1-Blue MFR'"
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/cultivar="B73"
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Fax: 650 725 8221
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/note="Organ: immature ear; Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI; Mixed ear tissue cDNA library from Schmidt lab"
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Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
1 (bases 1 to 562)
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/clone_lib="606 - Ear tissue cDNA library from Schmidt
                                                                                                                                                                                            A1855050 562 bp mRNA EST 02-FEB-2000 606074D04.x1 606 - Ear tissue cDNA library from Schmidt lab Zea mays cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 gacggtccgcgtcgtctcgttcgtctcctgggaactctttgatgagcagtcggatgagta 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     562 GACGGTCCGCGTCGTCCGTTCGTCCTGGGAACTCTTTGATGAGCAGTCGGATGAGTA 503
282 gctcctgccgggacgatctacaaggagtacggcatcaccgtggagagcatcattgcaact 341
                   283 GCTCCTGCCGGGACGATCTACAAGGAGTACGGCATCACCGTGGAGAGCATCATTGCAGCT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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Pred. No. 8.9e-64;
0; Mismatches 11; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="ear length from 0.5 cm - 2.0 cm"
/lab_host="XLOLR (Stratagene)"
                                                                     855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227
Fax: 650 725 8221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
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Location/Qualiflers
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/cultivar="Ohio43"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: walbot@stanford.edu
                                                                                                                                                                                                                                                                             GI:5499183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 71.0%;
Best Local Similarity 96.2%;
Matches 280; Conservative (
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AI855050/c
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
1 (bases 1 to 657)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:4577"
/clone_lib="707 - Mixed adult tissues from Walbot lab (SK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: tassel, kernel, silk, husk, root, leaf;
Vector: pGAD10; Site_1: EcoR1; cDNA library from fully
differentiated maize tissues from an active Mutator
plant. Tissue ratio is 4/2/1/1/1/1 (tassel, kernel, silk,
husk, root, leaf). Unitirectionally cloned.
                                                                                              AW147017 657 bp mRNA EST 03-NOV-1999 707009C12.y1 707 - Mixed adult tissues from Walbot lab (SK) Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="tassel, kernel, silk, husk, root, leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 tcacagcgaggatcagcatcgaggccgggtccactctcggctggcagaagtacgtcggag 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                               Walbot, v. Maize ESTs from various cDNA libraries sequenced at Stanford
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Similarity 96.2%; Pred. No. 9.1e-64;
80; Conservative 0; Mismatches 11; Indels 0;
cccaaggcaaggccattggcatcgacaagttcggcgcgagtgctcctgccg 291
                                                                                                                                                                                                                                                                                                                                                          Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Plate: 707009 row: C column: 12.
Location/Qualifiers
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Department of Biological Sciences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                           walbot@stanford.edu
                                                                                                                             mays cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cultivar="W23"
                                                                                                                                                          AW147017.1 GI:6194913
                                                                                                                                                                                                                                                                                                               Unpublished (1999)
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/db_xref="taxon:4558"
/db_xref="taxon:4558"
/clone_lib="Water-stressed 1 (WS1)"
/clone_lib="Water-stressed 1 (WS1)"
/note="Organ: Mix of 5-week old plants on days 7 & 8 after
/note="Organ: Mix of 5-week old plants on days 7 & 8 after
/note="Cross": The library was made from poly-A RNA;
Site_2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
                                                                                                                                                   Sorghium bicolor
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Lillopsida; Poales; Poaceae; Sorghum.
1 (bases 1 to 526)
Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                           Email: mmpratteuga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                          AW746961 526 bp mRNA EST 19-JUL-2000
WSL_56_C06.gl_A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA,
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225
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                                                                                                                                                                                                                                                                                                                           The University of Georgia
Plant Sociences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
Fax: 706 542 1805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 24; Length 526;
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An EST database from Sorghum: water-stressed plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.1%; Score 258.4; DB 24
85.0%; Pred. No. 9.9e-60;
tive 0; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Sorghum bicolor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seg primer: T7
High quality sequence start: 73
High quality sequence stop: 526
                                                                                                                                                                                                                                                                         Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                   AW746961
AW746961.1 GI:7660699
                                                                                                                                                                                                                                                                                                           Department of Botany
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                                                                                                                                        sorghum.
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/tissue_type="seedling"
/tissue_type="Five-day old seedling"
/dev_stage="Five-day old seedling"
/dev_stage="Five-day old seedling"
/dev_stage="Five-day old seedling"
/dev_stage="Five-day old seedling"
/lab_host="E. coli SOLR"
/note="vector: Lambda Uni ZAP XR, excised phagemid;
/note="vector: Lambda Uni ZAP XR, excised phagemid;
/germinated and grown aseptically in the dark at room
/ germinated and grown aseptically in the dark at room
/ germinated and grown aseptically in the dark at room
/ cefotaxime in covered crystallization dishes. Five-day
old seedlings were transferred to 5 c cold room and kept
for 48 hr. The tissue, total RNA, and poly(A) RNA were
prepared, a cDNA library was made, and the CDNA clones
were in vivo excised to give pBluescript phagemids in the
TJ Close lab (Choi, close, Fenton) at the University of
California, Riverside. Plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab (all
                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
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                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.

1 (bases 1 to 620)
Anderson,O.D., Chao,D.W., Close,T.J., Fenton,R.D., Han,P.S., Haia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.
                                                                                                                                                                                                                                                                                                                                                                            The structure and function of the expressed portion of the wheat genomes - Cold-stressed seedling CDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 cctgggaactctttgatgagcagtcggatgagtacaaggagagcgtcctccctgccgacg 180
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                                     BE490044 620 bp mRNA EST 31-JUL-2000 WHE0364_B03_C062S Wheat cold-stressed seedling cDNA library Triticum aestivum cDNA clone WHE0364_B03_C06, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: oandersn@pw.usda.gov · Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Stratgene SK primer.

Location/Qualifiers
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Pred. No. 2.4e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                       BE490044.1 GI:9609577
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Local Similarity 80.8%;
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                                                                                                                                                                                                                Triticum aestivum
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                                                                                                                                                                                            bread wheat.
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/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/db_xref="taxon:4558"
/clone_llb="Pathogen induced 1 (PI1)"
/note="Organ: Anthracnose-infected leaves from
/note="Organ: Anthracnose-infected leaves from
/note="Organ: Anthracnose-infected leaves from
/note="Organ: Anthracnose-infected leaves from
/note="Organ: Anthracnose-infected leaves pris; Site_1: XhoI;
Vector: pBluescript II from Lambda App II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623
cultivar) were infected with pathogen (isolate FRW42I of
colletotrichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptibility
to anthracnose disease. The library was made from poly-A
RNA in the cloning vector lambda ZAP II. Clones to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Sorghum.
1 (bases 1 to 581)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequenced were prepared by mass excision. WARNING: While most or all ESTs are expected to derive from the host plant, no effort was made to eliminate ESTs deriving from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                              BE364694 581 bp mRNA EST 20-JUL-2000
PI1_14_C06.g1_A002 Pathogen induced 1 (PI1) Sorghum bicolor CDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cordonnier-Pratt, M.-M., Gingle, A., Dean, R., Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                            The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    An EST database from Sorghum: pathogen-induced plants
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High quality sequence stop: 581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Cordonnier-Pratt MM
Department of Botany
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119 c
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Best Local Similarity 85.6'
Matches 274; Conservative
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Fax: 706 542 1805
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BE364694
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Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
1 (bases 1 to 619)
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/clone_lib="707 - Mixed adult tissues from Walbot lab (SK
)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: tassel, kernel, silk, husk, root, leaf;
Vector: pGAD10; Site_1: EcoRI; cDNA library from fully
differentiated maize tissues from an active Mutator
plant. Tissue ratio is 4/2/1/1/1/1 (tassel, kernel, silk,
husk, root, leaf). Unidirectionally cloned."
                                                                                                                                                                                                                                                                                                                                                                                                                                   707052H08.yl 707 - Mixed adult tissues from Walbot lab (SK) Zea aw400161.
                                                            186 gcgaggatcagcatcgaggccgggtccactctcggctggcagaagtacgtcggagcccaa 245
                                                                                                                                             306 gagtacggcatcaccgtggagagcatcattgcaactgccaagagcttttaagagctaaca 365
                                                                                                                                                                                         246 ggcaaggccattggcatcgacaagttcggcgcgagtgctcctgccgggacgatctacaag 305
                                                                                                                                                                                                        /tissue_type="tassel, kernel, silk, husk, root, leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          855 California Ave, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Biological Sciences
Stanford University
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Location/Qualifiers
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/cultivar="W23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: walbot@stanford.edu
                                                                                                                                                                                                                                                                                                                     366 acggtctgggagttttttt 385
                                                                                                                                                                                                                                                                                                                                                    301 ACAACAGTCTTGAGTTTTT 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW400161.1 GI:6918631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .619
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99
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TITLE
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KEYWORDS
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BE215654 540 bp mRNA EST 25-JUL-2000 HV_CEb0007L04f Hordeum vulgare seedling green leaf EST library HVCDNA0005 (Erysiphe infected & control) Hordeum vulgare cDNA clone HE216544 mRNA sequence.

BE215654.1 GI:8903182
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Magnollophyta; Liliopsida; Poales; Poaceae; Hordeum.
1 (bases 1 to 540)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu.Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and Wood,T.
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0
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                                                                                                                                                                                                                                           356 CGACCGGCAACAAGCCTGACCTCATTGTGATGGGCACCGGCTCCGAGCTGGAGTCGCGG 415
                                                                              61 gcaatgcggccgacgagctgaggaaggaggggaagacggtccgcgtcgtctcgtct 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: lambdazAP; Site_1: EcoR1; Site_2: Xho1" 135 c 155 g 111 t 1 others
                                                                                                      1 caaccggcaccaagcctgacatcattgggttgggcaccggctccgagctggagatcgcgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="HV_CEB0007L04f"
/clone_llb="Hordeum vulgare seedling green leaf ES
library HVCDNA0005 (Eryalphe infected & control)"
/issue_type="seedling green leaf"
/lab_host="SOLR"
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61.9%; Score 238.4; DB 34; Length 540;
Best Local Similarity 78.9%; Pred. No. 2.5e-54;
Matches 284; Conservative 0; Mismatches 76; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Hordeum vulgare"
/cultivar="CI16151 (Mla6)"
/db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: rwing@clemson.edu
Seg primer: AATTAACCCTCACTAAAGGG
High quality sequence start: 20
High quality sequence stop: 516.
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Unpublished (2000)
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KEYWORDS
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Gaps

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Ouery Match 64.0%; Score 246.4; DB 22; Length 619; Best Local Similarity 95.8%; Pred. No. 1.8e-56; Matches 253; Conservative 0; Mismatches 11; Indels 0;

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ACCESSION
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BE420889
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KEYWORDS
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//db_xref="taxon:4558"
//db_xref="taxon:4558"
//cloe_lib="Light Grown 1 (LG1)"
//note="Organ: 10. to 14-day-old light-grown (greenhouse)
//seedlings: Vector: Lambda Zap; Site_1: Xhol; Site_2: EcoRi
// yes seedlings: Yet of the poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mmpratt@uga.edu Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW565303 705 bp mRNA EST 19-JUL-2000
LG1_342_G05.g1_A002 Light Grown 1 (LG1) Sorghum bicolor cDNA, mRNA
                                                                                                                                                                                                                                                                                                                            181 tcacagogaggatcagcatcgaggccgggtccactctcggctggcagaagtacgtcggag 240
                                                                                                                                                                                                                                                          241 cccaaggcaaggccattggcatcgacaagttcggcgcgagtgctcctgccgggacgatct 300
                                                                                                                                                                                                                                                                             84 TGAAGGCTGCCGAAGAGTTGACGAAGAGGGGAAGACCGTCCGCGTTGTGTCATTTGTCT 143
                                                                                                                    121 cctgggaactctttgatgagcagtcggatgagtacaaggagagagcgtcctccctgccgacg 180
                                                                                                                                                                                                                        204 TCACCGCAAGGATCAGCATTGAAGCTGGCTCTACCCTCGGATGGCAAAAGTACGTCGGGT 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C. and Pratt, L.H.
                24 CGAGCGGAAACAAGCCTGACTACATCATAATGAGCACTGGTTCTGAAGTAGAGATTGCTG
                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Magnoliophyta; Liliopsida; Poales; Poaceae; Sorghum.
1 (bases 1 to 705)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        An EST database from Sorghum: light-grown seedlings Unpublished (2000)
Contact: Cordonnier-Pratt MM
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139 c 187 g 212 t
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High quality sequence stop: 705
POLYA-Yes.
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 61.6%;
85.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW565303
AW565303.1 GI:7219181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Botany
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primer: T7
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Hordeum vulgare
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anderson, O. A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Langridge, P., Lazo, G. K., Lin, J.J., McGuire, P., Oqihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Narburton, M. and Wenzel, G.

Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pBluescriptSK(-); 850 bp average insert
                                                                                                                                                                                                                                                   140 gcagtcggatgagtacaaggagagcgtcctccctgccgacgtcacagcgaggatcagcat 199
                                                                                                               61 ACAGTCAGATGAATACAAGGAGGTGTCCTGCCTGCAGCCGTCACCGCAAGAATCAGCAT 120
                                                                                                                                                            200 cgaggccgggtccactctcggctggcagaagtacgtcggagcccaaggcaaggccattgg 259
                                                                                                                                                                                                          121 TGAGGCCGGGTCTACTCTCGGCTGGCAGAAGTATGTCGGAGCCCAGGGCAAGGCCATTGG 180
                                                                                                                                                                                                                                                                                                                                                 320 cgtggagagcatcattgcaactgccaagagcttttaagagctaacaacggtctgggagtt 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.
1 (bases 1 to 811)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="ITEC HWM Barley Leaf Library"
/tissue_type="leaf"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: herrmann@botanik.biologie.uni-muenchen.de
International Triticeae EST Cooperative (ITEC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Herrmann RG
Botanisches Institut der LMU
Menzinger Str. 67, D-80638 Munchen GERWANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.1%; Score 235.2; DB 3:
78.3%; Pred. No. 1.9e-53;
Live 0; Mismatches 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="14 day old"
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/db_xref="taxon:4513"
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80 gaggaaggagggaagacggtccgcgtcgtctcgttcgtctcctgggaactctttgatga 139

6 ggcaccaagcctgacatcattgggttgggcaccggctccgagctggagatcgcgggcaat 65

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Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
Magnoliophyta, Liliopsida, Poales, Poaceae; Zea.
1 (bases 1 to 286)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="just after the transition from vegetative to inflorescence development"
                                                                                                                                                                                                                                                                                                                                                                                                                                                BE344940 286 bp mRNA EST 17-JUL-2000 946030B04.yl 946 - tassel primordium prepared by Schmidt lab Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:4577"
/clone_lib="946 - tassel primordium prepared by Schmidt
                                                 121 cctgggaactcttgatgagcagtcggatgagtacaaggagagggcgtcctcctgccgacg 180
                                                                                                                                                                                     181 tcacagcgaggatcagcatcgaggccgggtccactctcggctggcagaagtacgtcggag 240
241 cccaaggcaaggccattggcatcgacaagttcggcgcgagtgctcctgccgggacgatct 300
                                                                                                                                                                                                                                                                                                                       301 acaaggagtacggcatcaccgtggagagcatcattgcaactgccaagagcttttaagagc 360
                                                                                                                                                                                                       Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Fax: 650 723 2221
Fax: 650 725 8221
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Plate: 946030 row: B column: 04.
Location/Qualifiers
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Department of Biological Sciences
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/organism="Zea_mays"
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Bukaryotta, Virial plantae; Embryophyta; Tracheophyta; Spermatophyta; Majnoliophyta; Liliopsida; Poales; Poaceae; Triticum.

1 (bases 1 to 747)
Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Langridge, P., Lazo, G.R., Lin, J.M., Jid. Ji, Joudfier, P., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warburton, M. and Wenzel, G.
International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
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/dev_stage="after 24 hour challenge with LR-AVR1"
/hote="Vector: Lambda ZAP; 1.0 Kbp average insert size."
1 207 c 177 g 168 t 25 others
                                                                                                                                                                                                                                                                                                                                                                        BE418437 747 bp mRNA EST 24-JUL-2000
SCL033.C06R990602 ITEC SCL Wheat Leaf Library Triticum aestivum
BE418437
                                                                               66 gcggccgacgagctgaggaaggagggaag--acggtccgc-gtcgttcgttcgttctca 122
                                                                                                                                                              183 acagogaggatcagcatcgaggccgggtccactctcggctggcagaagtacgtcggagcc 242
                       661 CCGNCACAAGCCTGANTNCATCATAATGAGCNCTGGTTNTNAGGTAGAGATTGCCGTGAA 602
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Best Local Similarity 78.4%; Pred. No. 4e-51;
Matches 279; Conservative 0; Mismatches 76; Indels 1; Gaps
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Winnipeg MT CANADA
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/clone_lib="ITEC SCL Wheat Leaf Library"
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                                                                                                                                                                                                                                              /organism="Triticum aestivum"
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/db_xref="taxon:4565"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE418437.1 GI:9416283
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Contact: Cloutier S
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Fax: 204 983 4604
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Gaps

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59.6%; Score 229.6; DB 35; Length 286; 93.5%; Pred. No. 5.4e-52; Pred. No. 5.4e-52;); Mismatches 15; Indels

0; Mismatches

Matches 261; Conservative

Query Match Best Local Similarity

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12	54	184	483	24	42	30	36		
; tgcggccgacgactgaggaaggaaggagggaagaccgtcgctcgttcgt	GNC	ggaactetttgatgageagteggatgagtacaaggagagegteeteeetgeegaegteae		s agcgaggatcagcatcgaggccgggtccactctcggctggcagaagtacgtcggagccca 244	-8	s aggcaatggccattggcatcgacaagttcggcgcgagtgctcctgccgggacgatctacaa 304	Ö	5 ggagtacggcatcaccgtggaggcatcattgcaactgccaagagcttttaagagc 360	-0
65	601	125	541	185	482	245	422	305	362
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Search completed: November 4, 2000, 11:52:19 Job time: 18256 sec

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November 4, 2000, 13:36:23 ; Search time 4075.18 Seconds (without alignments) 293.660 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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gb_htg1:*
gb_htg2:*
gb_in1:*
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em_hum3:*
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gb_ht4:*
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em_pat:*
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                                                                                                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                       Scoring table:
                                                                                                     Sequence:
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                                                 Run on:
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44: em_hum5:*
45: qb_pl3:*
46: qb_pl3:*
47: qb_htg8:*
48: qb_htg9:*
50: qb_htg11:*
51: qb_htg12:*
52: qb_htg13:*
53: qb_htg13:*
54: qb_htg13:*
55: qb_htg13:*
55: qb_htg13:*
56: em_htg6:*
60: em_htg6:*
60: em_htg6:*
61: em_htg6:*
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77: em_htg1:*
78: em_htg1:*
79: em_htg1:*
79: em_htg2:*
79: em_h
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		ACOUSTA ALABIMODS	A93589 Secuence 1	AF154658 Nicotiana	ACOUGA 55 Arabidone	ACO11437 Arabidons	AL353862 Stroptom	ALO34355 Stroptomy	AB007563 Sequence	APON1278 Orwas cat	AFOOADO VVIDILE F	x66407 R.ruber ORF
ΩI	ATAC016972	AC006200	A93589	AF154658	ATAC009465	ATAC011437	SCE34	SCD78	AR007563	AP001278	AE004020	RRPHAS
DB		7	3	7	œ	æ	~	7	Ŋ	8	_	7
* Query Match Length DB	66653	84957	1118	1084	93234	95310	37898	36224	1288	161266	10834	3875
	29.7	29.7	24.8	22.6	19.7	19.7	17.3	17.0	16.9	16.9	16.4	16.4
Score	81.4	81.4	68	62	54	54	47.4	46.6	46.4	46.4	45	44.8
Result	-	0	m	4	ი	9	c 7	8	6	c 10	11	12

Mycobacterial Streptomy of Streptomy or Streptomy or Streptomy or Streptomy or Streptomy of Streptomy or Stre	D50642 Pseudomonas D86947 Pseudomonas A37833 Sequence 3 AR069871 Sequence	bp DNA PLN 18-JAN-2000 and chromosome I BAC F23N20 genomic sequence, 14311 and plantae; Embryophyta; Tracheophyta; Spermatophyta; dicotyledons; core eudicots; Rosidae; eurosids II; dicotyledons; core eudicots; Rosidae; eurosids II; sicaceae; Arabidopsis. Gistantae; Embryophyta; Tracheophyta; Spermatophyta; dicotyledons; core eudicots; Rosidae; eurosids II; sicaceae; Arabidopsis. Town, C.D., Benito, M., Creasy, T.H., Haas, B., Wu, D., Town, C.D., Benito, M., Creasy, T.H., Barnstead, M.E., E.O., Nierman, W.C. and Fraser, C.M. ana chromosome I BAC F23N20 genomic sequence 1953 3. 1999) The Institute for Genomic Research, 9712 3. 3. Rockville, MD 20850, USA, xlin@tigr.org 6653) 4-2000) The Institute for Genomic Research, 9712 4-2000) The Institute for Genomic Research, 9712 5. Rockville, MD 20850, USA 5. Rockville, MD 20850, USA 6653) 5. Sequence version replaced gi:6630537. 5. Sequence to:at@tigr.org 5. Sequence to:at@tigr.org 5. Trom Arabidopsis chromosome I and is near the m453.
MTCY493 AF235504 AC07789 AC07789 AC07789 AC07789 AF113605 OSHPRGP AF082100 MTU13938 AF082100 MTU13938 AC0242540 SC3F9 AC024224 AC027421 AC027421 AC027421 AC027421 AC027421 AC027421 AC027421 AC027421 AC027421 AC027421 AC027421 AC067753 AC064032 AC064032 AC064032 AC064032 AC064032 AC064032 AC064032 AC064032 AC067659 AC067659 AC067659 AC067659 AC067659 AC067659 AC067659 AC067659 AC067659 AC067659	PSEPCTA 186947 A37833 AR069871 ALIGNMENTS	ATACOL6972 66653 bp DNA Arabidopsis thaliana chromosome I BAC F23N20 complete sequence. ACOL6972. ACOL6972. GI:6714311 HTG. ATABAIGOPSIS thaliana Enkaryota; Viridiplantae; Embryophyta; Trache Magnoliophyta; endicotyledons; core endicots. In bases I to 6663. Lin,X., Kaul,S., Town,C.D., Benito,M., Creas; Ronning,C.M., Koo,H., Fujii,C.Y., Utterback; Bowman,C.L., White,O., Nierman,W.C. and Frass Mapidopsis thaliana chromosome I BAC F23N20 Upublished 2 (bases I to 6663) Lin,X. and Kaul,S. Direct Submission Submitted (09-DEC-1999) The Institute for Generic Submission Direct Submission Direct Submission Direct Submission Submitted (18-JAN-2000) The Institute for Generic Submission Address 1 to 6663) Lin,X. Bornet Submission Direct Submission Address 1 to 6663
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40790 182756 182756 1593 2847 2847 2847 2847 2848 19830 19830 19830 19830 19830 19830 1167 1167 118959 20956 20956 20956 820 820 820 820 830 841 841 841 841 841 841 841 841 841 841	21.2 9.3.4 8.8 33.6 33.6	ATACOLG972 66653 bp Arabidopsis thaliana chromplete sequence. ACOLG972.5 GI:6714311 ATG.
106.33 106.12 106.13 106.12 106.12 106.13 10	15.3 15.3 15.3 15.3	ATACOL6972 666 Arabidopsis tha complete sequen ACOL6972.5 GI: HTG. THTG. THTG. THTG. ATABIDOPSIS THA ATABIDOPSIS THA BOWMAN OLIOPHYTA BOWMAN OLIOPHYTA ATABIDOPSIS THA MAGNOLIOPHYTA BOWMAN O. L., WI BOWMAN O. L., WI ATABIDOPSIS THA ONDUBLISHED ATABIDOPSIS THA DIRECT SUBMISSI SUBMITTED (09-I MGDICCT SUBMISSI SUBMITTED (19-I MGDICCT SUBMISSI SUBMITTED (18-I MGDICCT SUBMISSI SUBM
0004044800000mmm880044444400000		ATACO16972 66653 bp Arabidopsis thaliana complete sequence. ACO16972 ACO16972. GI:6714311 HTG. Thale cress. Arabidopsis thaliana Eukaryota; Viridiplant Magnollophyta; eudicot Brassicales; Brassicaet I (bases 1 to 66653) Lin,X., Kaul,S., Town, Ronning,C.M., Koul,S., Town, Ronning,C.M., Kaul,S., Town, Bowman,C.L., White,O., Bowman,C.L., White,O., Bowman,C.L., White,O., Bowman,C.L., White,O., Bowminted (OP-DEC-1998 Chases 1 to 66653) Lin,X. and Kaul,S. Direct Submitted (OP-DEC-1998 Medical Center Dr., Rod Me
1115 1115 1116 1116 1116 1116 1116 1116		RESULT 1 LOCUS LOC
0 00 000 00 0		RESUL LOCUS DEFIN ACCES VERNO SOURC SOURC SOURC AUT TIT JOU REFER REFER AUT TIT JOU COMME

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clone.

Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/-chris/GENSCANW.html), and NetplantGene (http://www.cbs.dtu.dk/netpgene.cbsnetpgene.html), searches of the complete sequence against a peptide database and the Arabidopsis EST database at TIGR (http://www.tigr.org/tdb/at/at.html).

Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity to other proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction. programs over most of their length are annotated as 'Npothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy.

http://genome.wustl.adv/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="37813 nt before this point were not included in the submitted sequence, due to overlap with another BAC

    15580
/note="the annotation for genes within this region can be
found in the overlapping bac F15H11 sequence 92846-108425"

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/note="ATREP4|ATREP4 An AT-rich repetitive sequence - a /note="ATREP4|ATREP4 An AT-rich repetitive sequence - a consensus. from T23015 64288 to 65702 1415 nt, also present in intron 8 of Arabidopsis thaliana gene for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(4613. .4670)
/note="ATREP5|ATREP5 An AT-rich repetitive sequence - a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(4404. .4475)
/note="ATREP5|ATREP5 An AT-rich repetitive sequence - a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="ATREP5|ATREP5 An AT-rich repetitive sequence - a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(4526. .4597)
/note="ATREP5|ATREP5 An AT-rich repetitive sequence - a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="ATREP5|ATREP5 An AT-rich repetitive sequence - a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="ATREP5|ATREP5 An AT-rich repetitive sequence - a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://ftp.genome.washington.edu/RM/RepeatMasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="overlap with BAC clone F15H11 (AC008148:92846. .110514)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(4183. .4303)
/note="ATREP3|ATREP3 a consensus."
complement(4242. .4477)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="(TAAAA)n"
complement(1088..1149)
/rpt_family="POLY_A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .3842)
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complement(4015. 5903)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="(GAAAA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cultivar="Columbia"
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/chromosome="1"
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1. .66653
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VERSION
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LIEERIROSSPESEDASSSINSHECDWWSDLVVGLQAAKRLLSSATSFQARESSDGAA
RRISPOROCYTWKLERALGDLTYDRYDISDEVREQVELARGLGERAMQRYGSLNSKKF
SSGLSEPREKDASSNEWYLEKLESIPPETVHGLSDEKFESPPRKSSSYSLAFFLSKD
GDDEREKAYTENSDDSGKSDNLTTPPETCPISLELMKDPAIVSTGGTYERSFTORW
IDCGNLSCPRTQOKLENFTLTPNYLIELISGWCFRHIBDPGGYNGRTKNSDGSFR
DLSGDMAS TRAIVCKLSSGSIEDRRTAVSETRSLEKRSTDNRILLAEAGAIPULVKLL
TSGGDMASTALVCKLSSGSIEDRRTAVSETRSLEKRSTDNRILLAEAGAIPULVKLL
TSGGDFETQERAVTCILLALSTFEHNELINLAGAYTSIVURAGSMEARENAAATLE
SLSLADENKITIGASGAIMALVDLLOYGSVEKKRDATALENLIZYGGNGRARARRE
SKAAAILLCLCKRDTEKLISIGRLAVPPLMSTRAILRANAIPPLIDCLQKDOPRIR
RNAAAILLCLCKRDTEKLISIGRLAVPPLMSTRAIRANSSRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(<20139. .20559,20646. .20772,20943. .21030))
/gene="F23N20.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(20139. .20559,20646. .20772,20943. .20982))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="(GAA)n"
complement(join(15470. .16669,16760. .17146,17238. .17354,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MNKTRLRALSPPSGMQHRKRCRLRGRNYVRPEVKQRNFSKDEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(15581. .16669,16760. .17146,17238. .17354,
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LRHSSVESPLRLPTGREFDRPLVIFDRSFRKDGSIYMNATGNNPTIHPOWQPBYFGDA
IIVNGKAWPKLIVRRRKYRFRITNASNARFFRFFSNGLDFIVVGSDSAYLAKPVSTK
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complement(join(21957. .22010,22092. .22451,22492. .23616,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mepsrrantrdmlllivywawivytgdeggirgerleridgklem
FVDKLPHIPTLHGYHFVNGFLKPKSLHIGMFFKKWKFHRDLPATPVFAYGTSKRSATV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGP11EAVYGVDTYVTWRNHLPLHH1LPWDPT1SPA1PKHGG1PTVVHLHGG1HEPTS
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                                                                                                         complement(4852. .4971)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to SPORE COAT PROTEIN A GB:P07788 from [Bacillus subtilis] and BILIRUBIN OXIDASE GB:012737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to myb-related transcription factor 24 GB:S71287"
                                                                                                                                                                                                             note="ATREP5|ATREP5 An AT-rich repetitive sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="spore coat protein-like protein"
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                                                                                                         complement (4852.
                                                                                                                                                                                                                                                                                                                                                         17568. .>17861))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="F23N20.1"
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/gene="F23N20.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .17861))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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                            repeat_region
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CDS

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DTSIIPKKLIEYPPAHVSTSTRTRYIAMFEYVSSIDEPTHLYINGLEYNAPVTETPKI
GTSEFKSLALTIMKVWEVINLTEDNHPLHIHLGLFRVLEQTALVKSEEFIECMTKRUD
AVKCEISKYARGNKTAVTVHERGWKNVFKMMPGHVTKILVRFSYIHSNESYSFDATQE
PGYVYHCHILDHEDNMMRPFAMVL"
SVLLAPSEIVDVLVDFSKSTSKTAILANNAPYPYPSGDPVTEENSKVMKFIINYKSEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thallana chromosome II section 2 of 255 of the complete sequence. Sequence from clones F23H14, F10A8.
AC006200. AC0052093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lin,X., Kaul,S., Rounsley,S.D., Shea,T.P., Benito,M.-T., Town,C.D., Fujii,C.Y., Mason,T.M., Bowman,C.L., Barnstead,M.E., Feldbluum,T.V., Buell,C.R., Ketchum,K.A., Lee,J.J., Ronning,C.M., Koo, H., Woffat,K.S., Cronin,L.A., Shen,M., VanAken,S.E., Umayam,L., Tallon,L.J., Gill,J.E., Adams,M.D., Carrera,A.J., Creas,T.H., Nierman,H.M., Somerville,C.R., Copenhaver,G.P., Preuss,D., Nierman,W.C., White,O., Elsen,J.A., Salzberg,S.L., Fraser,C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Medical Center Dr., Rockille, MD 20850, USA On Dec 17, 1999 this sequence version replaced gi:4262221. The sequence and annotation of chromosome 2 were merged from those of the individual clones on this chromosome after removing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 39494 TICGAICCCTIGICACGGCCACTGAGGAICICGCCGCCGTCAACTCGGCGCCGCCACTC 39553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 39554 TCAAACCTCACGCAAGAAGAACTCCAAGAAATCGCCGCTTATAAAGCCGTCGAATTCGTC 39613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 ttcatcgccaccgagaaagccgccatggacgccgcctcctccacccctcctcccctcc 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 gtcatcctcacccaagacgatttgaagaaatcgccgcctacaaggccgtcgagtacgtg 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-APR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 66653;
                                                                                                                                                                                                                                                                                                                                       /note="similar to ATFP7 GB:AAD09511"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61; Indels
                                                                                                                                                                                                                              complement(join(<28078. .28376,28543. /gene="F23N20.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.7%; Score 81.4; DB 8; 65.9%; Pred. No. 4.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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complement(26178, 26257)
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                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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SOURCE
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For detailed information, please see the TIGR web site
                               (http://www.tigr.org/tdb/at/at.html)
      overlaps.
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prediction programs. Including wards.

(ftp://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, University of Washington), Genscan (Chris Burge, University of Washington), Genscan (Chris Burge, University of Washington), Genscan (Chris Burge, University of Washington), Genscan (Chris Burge, University, Gensity Genscale), searches of the chttp://www.cbs.dtu.dk/services/NetGene2/), searches of the complete sequence against a peptide database and plant EST annotated genes are named to indicate the level of evidence for their annotation. Genes without significant peptide after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are Genes were identified by a combination of three methods: Gene prediction programs including GRAIL numbered from the top to bottom of the chromosome. annotated as 'hypothetical' proteins. predicted by tRNAscan-SE (Sean Eddy,

We thank the CSHL/WashU/ABI consortium for sequencing BAC clones F6P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bloinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and database support.

This work was supported by the National Science Foundation, Department of Energy and the US Department of Agriculture.

FEATURES

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complement(join(463 . 924,1053 . 1163,1265 . 1417,1513 . 1572, 1662 . 1967,2287 . 2435,2515 . 2584,2718 . 2921,3271 . 3465, 3673 . 3945,4026 . 4187,4325 . 4455,4541 . 4700,4817 . 5005
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FLSRALQSPELLAVQRAIAFLKIIGALDENEDLTTLGRYLSKLPMEPKLGKMLILGAI
LGCLDPILTYVAAGLSYRDPFLTPQDKKDLAEAAKSQFSRDHSDHLALVRAYEGWKKAE
EESAVYDYCWKNFLSIQSLRAIDSLRKEFFSLLKDTGLIDGNPSICNSEGNDANLTRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEPASGVRKIVLATNIAETSITINDVAFVIDCGKAKETSYDALNNTPCLLPSWISKVS
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NICENBGPGGILIFLTGWDDISSLKEKLOIHPIFGNPDLVMLLACHGSMETFEGRLIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="putative ATP-dependent RNA helicase A"
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Address all correspondence to: at@tigr.org
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1. .84957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="At2g01130"
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                                                                         source
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CDS

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GSDFVYTGIHGGILFIHALLNSLPISVLSFIGGLAALWNLLGVLVLHILIPLVSTERA
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CLSKLKTGEEVRKLDCRHVFHKQCLEGWLQHLNFNCPLCRSPLLPHHHQGHGSDASIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="F10A8.5; identical to GP:AF019637"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative fructose-bisphosphate aldolase, plastidic form"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="RING-H2 zinc finger protein (RHA2b)"
                                                                                                                                                                                  NKKSAEKDAAAEAIQWLKGGAKESHEQVNHMSKLLKKGKKDHL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="F10A8.3; identical to GP:AF078823"
12241. .12762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative amino acid permease"
/protein_id="AAD14517.1"
/db_xref="GI:4262224"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /anticodon=(pos:13715. .13717,aa:Ala)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(<13980. .16109)
/gene="At2g01170"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAD14516.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(6441. ,>8107)
/gene="At2g01140"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="(CAAAA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="(TAAA)n"
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13681. .13754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="At2g01150"
<12241. .12943
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/gene="At2g01160"
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                                                                                                                                                                                                                                                                                                                                                                     7952. .>8107))
/gene="At2g01140"
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/gene="At2g01150"
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IISAIGISILFGWGYILGISYAVTDIPSLLSETNNSGGYAIAEIFYLAFKNRFGSGTG
GIVCLGVVAVAVFFCGMSSVTSNSRMAYAFSRDGAMMMSPLWHKVNSREVPINAVWLS
ALISFCMALTSLGSIYAFQAMVSIATIGLYIAYAIPIIIRVTLARNTFVPGPFSLGKY
GMVVGWVAVLWVVTISVLFSLPVAYPITAETLNYTFVAVAGLVAITLSYWLFSARHWF
                                                                                                                                                                                                                                                                                                                                                                                                           FYRYGKDMMTDLKYPFKDMTVPINGSVPVYAVLLPIIVFVCFYLKRTCVYDLHHSILG
LLFAVLITGVITDSIKVATGRPRPNFYWRCFPDGKELYDALGGVVCHGKAARVKEGHK
SFPSCHTSNGFAGLIFLSLYLSGKIKAFNNEGHVAKLCLVIFPLLAACLVGISRVDDY
WHHWQDVFAGALIGTLVAAFCYRQFYPNPYHEEGWGPYAYFKAAQERGVPVTSSQNGD
ITKFVFTNFNTDNGLGITSYAYIFVLGLLMSQYTITGYDASAHMTEETVDADKNGPRG
                                                                                                                                                                                                                                                                                                                                                                                       /translation="MQEIDLSVHTIKSHGGRVASKHKHDWIILVILIAIEIGLNLISP
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core-

eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.

1 (bases 1 to 1118)

Schnarrenberger, C. and Lerchl, J.

RIBOSE-5-PHOSPHATE ISOMERASE (D-RIBOSE-5-PHOSPHATE KETOL ISOMERASE,

EC 5.3.1.6)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61589 ATCCTCTTCATTACATCGGACAAATCTTTGTCCGCCTTTGATGTTGCCTCTTCACCGC 61530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61529 CTCAGCCCATGAATTTAACACAAGACGAGCTCAAACGTATGGCCGCTTACAAAGCCGTGG 61470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 acccccatttcatcgccaccgagaaagccgccatggacgccgcctcctccaccctct 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 cccctccgtcatcctcacccaagacgatttgaagaaatcgccgcctacaaggccgtcg 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 agtacgtggagtccggcatggtcctcggcctaggcaccggctccaccgccaagcatgccg 267
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                                                                                                                                                                                                                                                                                                                   /product="putative phosphatidic acid phosphatase"
/protein_id="AAD14518.1"
/db_xref="GI:4262225"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 81.4; DB 7; Length 84957;
Pred. Nb. 4.5e-06;
0; Mismatches 66; Indels 0;
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SCHNARREBREERGER CLAUS (DE); BASF AG (DE)
Location/Qualifiers
1. .1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Spinacia oleracea"
                                                                                                                              complement(<18798. .>19706)
                                                                                                                                                         /gene="At2g01180"
Complement(<18798. .>19706)
/gene="At2g01180"
                                                                                                                                                                                                                                                      complement(18798, .19706)
/gene="At2q01180"
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/db_xref="GI:6741795"
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Sequence 1 from Patent WO9737028.
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                                                                                                                                                                                                                             /note="F10A8.6"
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64.78;
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                                                                                                                TGPISNILS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 121; Conservative
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A93589
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KSLSSPSPTPVLTQDDLKKLAAEKAVDSVKSGMVLGLGTGSTAAFAVSRIGELLSAGK
LTNIYGIPTSKRTAEQAASLGIPLSVLDDHPRIDLAIDGADEVDPDLNLVKGRGGALL
REWVEAASDKFIVVYDDTKLYDGLGGSRLAMPVEVVQFCWKYNLKRLQEIFKELGCE
AKLEMBGDSSPYVTDNSNYIVDLYFPTSIKDAEAAGREISALEGVVEHGLFLGMASEV
IIAGKTGVSVKTK*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sheehan, M.J., Wang, J. and Timko, M.P. Characterization of cDNAs Differentially Expressed in Roots of Tobacco (Nicotiana tabacum cv Burley 21) During the Early Stages of Alkaloid Biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases I to 1084)
Sheehan, M.J., Wang, J. and Timko, M.P.
Direct Submitssion
Submitted (27-MAY-1999) Biology, University of Virginia, 044 Gilmer Hall, Charlottesville, Virginia 22903, USA
Location/Qualifiers
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                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248 TAACCCAAGACGAACTCAAAAACTCGCCGCCGATAAAGCCGTCGAATACGTGAAAAGCG 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="root"
/note="similar to ribose 5-phosphate isomerase"
1 245 c 250 g 302 t l others
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                                                                                                                                                                                      24.8%; Score 68; DB 5; Length 1118; 67.9%; Pred. No. 0.0032;
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                                                                                                                                                                                                                             45; Indels
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Nicotiana tabacum clone PR49 mRNA sequence.
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                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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/db_xref="taxon:4097"
                                                                                                             258 g
                                                                                                                                                                                                                                                                                                                                                                                                          255 gccaagcatgccgtcgaccg 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                283 GCCGCATTTGCTGTCTCGCG 302
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                                                                                                          264 c
                                                                                                                                                                                  Ouery Match
Best Local Similarity 67.99
Matches 95; Conservative
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Best Local Similarity 78.7
Matches 74; Conservative
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Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Simple repeats are identified by repeatmasker (Arian Smit, thetp://genome.wustl.edu/eddy/RM/RepeatMasker.html). Regions of their sequence that are not annotated as genes but have predicted
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1 (bases 1 to 93234)
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Rockville, MD 20850, USA
e-mail: xlin@tigr.org
BAC clone T9J14 is from Arabidopsis chromosome III and is near the
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/cultivar="Columbia"
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/gene="T9J14.1"
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/db_xref="GI:5932532"
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/note="exon predicted by xgrail, quality excellent"
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/note="exon predicted by xgrail, quality
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marginal_shadowexon"
4493. .4537
/note="exon predicted by xgrail, quality marginal"
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/note="exon predicted by xgrail, quality
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7364. 7412
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/protein_id="AAD56988.1"
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/note="exon predicted by xgrail, quality
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/rpt_family="(TAA)n"
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/gene="T9J14.2"
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91444 ACGATTTGAAGAAGCTCGCGGCGGAGAAGCTGTGGAGGCAATTAAACCTGGGATGGTTC 91385
                                                                                       91384 TAGGGCTCGGAACCGGATCCACCGCAGCTTTCGCTGTTGATC 91343
                                                           232 teggeetaggeaceggetecacegecaageatgeegtegace 273
                                                                                                                                                                                  ATACO11437
LOCHE
                                                                                                                                                                                                                                                       DEFINITION
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                                                           δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="identical to GB:P11829 [Arabidopsis thaliana]"
join(12067. 12114,12560. .12676,12757. .12879,12957. .13082)
/codon_start=1
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KOPFRIPTALIGIGTGVVSCTIISLGAIOFFKKLDIGTFDLGFLAFLTIFNAGOPOKK
KOPFRIPTALVSLYFGESVVNONTSVVLTARAQOFTTHINIERAFOPIGNF
VCTLOVLNODETPLIYSLYFGESVVNONTSVVLTARAQOFTTHINIERAFOPIGNF
YLFLLGTGCVANTILISAYVIKLYFGRHSTDREVALMALMAYLSYMLAELFALSGIL
DSSGTSVNANSHYTWHNVTESSRITTKHAFATLSFLARFFIFILYGMOALDIEKWRFVS
GAVSMALAYNKFTRSGHFELRGNAIMITSTITVCLESTWVFGMLTKPLIRYLMRHQKA
TTSTTSMLSDOSTPKSHIFILLNOTSTITVCLESTWVFGMLTKPLIRYLMRHQKA
TTSTTSMLSDOSTPKSHIFILLDGEQLDSFELPGSHODVPRNSLRGFLMRFTRTVHY
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IPSRRLSVSCOARQETIERVSAIVKRQLSITPDKKVVAETKFADLGADSLDTVEIVMG
LEBERNIOMABERAGATATTVGAAELIEELINEKK"
complement(13145. .13256)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /process_id="Aad56990.1"
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/db_xref="G1:5932535"
/translation="MRESTARSPEVISRLSPDSTATGGFIGGWVCKCHGFLHNTVLVLASILEVAYIANZENEKSLSKLSNRRSYIMTAYGFUWLYSLLNLAWCCLQAWECTPG
VLASILEVAYIANZENEKSKLSKLSNRRSYIMTAYGFUWLYSLLNLAWCCTGGKVCKTRVLTLFTTSGMLFLEVSLVAFLEVGGNYASGAEALTRTFLISGLVIGLDLLKR
translation="MTMFASLTSKMLSVSTSDHASVVSLNLFVALLCACIVIGHLLEE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="similar to GB:AAB61079 (contains weak similarity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the SAPB protein (TR:E236624)) (Arabidopsis thaliarity to complement(join(13483. 13560,13812. 13893,13995. 14097, /gene="radio") (14365,14560. 14751,15058. 15342))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complement(join(13275. 13560,13812. 13893,13995. 14097,
14710. 114365,14560. 14751,15058. >>15342))
/gene="rg0114.4"
complement(13275. >>15342)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IYLFGFGVPLFIDNNBHIHKFKWGLWVIHKLLLAGIYGMIFFWYNSKWRBRLPGEYID
HSYPPYARPAFYKYITVMLALNGLSLFACALTANGAHFGLWLYGITSVCYHAFYLPLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                              /product="acyl carrier protein 1 precursor (ACP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0.34;
0; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="exon predicted by xgrail, quality excellent_shadowexon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="(GA)n"
7.555. .15439
//note="exon predicted by xgrail, quality
marginal_shadowexon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YVTFLADFFQEEDLNLENVYYSEMKDAGFFDADWE"
13758. .13787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="(GA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="T9J14.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 52.7%;
Matches 117; Conservative
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Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (available by anonymous ftp from arthur epm.ornl.gov), Genefinder (Phil Green, University of Washigoton), Genscan (Chris Burge, http://gnomic.stanford.edu/-chris/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/netpgene/cbsnetpgene.html), searches of the complete sequence against a peptide database and the Arabidopsis EST database at TiGR (http://www.igr.org/tdb/at/at.html).
Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-EE (Sean Eddy, herming the seconding tRNAs are herming the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the secon
                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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e-mall: xlin@tigr.org
BAC clone F7018 is from Arabidopsis chromosome III and is near the molecular marker mil72.
The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lin,X., Kaul,S., Town,C.D., Benito,M., Creasy,T.H., Haas,B.,
Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R., Barnstead,M.E.,
Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
Arabidopsis thaliana chromosome III BAC F7018 genomic sequence
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                                                       Arabidopsis thaliana chromosome III BAC F7018 genomic sequence,
                           02-NOV-1999
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The Institute for Genomic Research
9712 Medical Center Dr.
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                                                                                                                                                                                                                       AC011437.4 GI:6175159
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Lin, X. and Kaul, S.
Direct Submission
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ATAC011437 95310 bp
                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thallana
                                                                                                              complete sequence.
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QVIEAMQKITSHIKNPSKFSKASKLAIRLIQAGSVKPETSSYFIAILEAAMSSKTPCT
DRSVRADYHALFSAAQDVAECLDKSQKNLLTIWTFKAVVANDLFTDDSFMFSKTATRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEAISDLPVSTEEDDVEEAAALEEAAVKDNGDGGTTQDVAEAAAGGNEAVESDPFGL
DAWITESGKRNGKTKIKRTNEDPDAEENKRFLRSKREALITCLEIAARRYKVPWCQTV
IDILVKHAFENVSRFTSQQRQAVEKLWASVREQHLRRKQGKSVTGKLDVTAFESLQDK
YANEKMSIRSSVGASGERRAQOWLG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="wanpwwTGQVNLSGLETTPPGSSQLKKPDLHISMNWAMDSGHNN
HHHHQEVDNNNNDDDRDNLSGDDHEPREGAVEAPTRRPRGRPAGSKNKPKPPIEVTRD
SPNALKSHVMEIASGTDVIETLATFARRRQRGICILSGNGTVANVTLRQPSTAAVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PVMLIAATESNATYERLPLEEEEAAERGGGGSGGVVPCQLGGGGSPLSSGAGGDGN
OGLPVYNMPGNLVSNGGSGGGGMSGOEAYGWAQARSGF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGGAAVLALQGRFEILSLTGSFLPGPAPPGSTGLTIYLAGGQGQVVGGSVVGPLMAAG
EADDGYYLVVAENGLKLEKGSDLKAREVKESLGMVVLVVRPPREDDDDWQTSHQNWD"
                                                                                                                                                                                                 /note="predicted by genscan, multiple est matches"
complement(join(5859. .6123,6229. .6587,6767. .6856,
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6946. .7229,7314. .7391,7514. .>7691))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <9574. .>10521
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/note="similar to putative DNA-binding proteins:
GB.ABB2621, GB:Arabidopsis thaliana, GB:CAB40946
[Arabidopsis thaliana]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.34;
0; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(8923. .8960)
/note="exon predicted by xgrail, quality
cecllent_shadowexon"
<9574. .>10521
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complement(11086)
/note="exon predicted by xgrall, quality
marginal_shadowexon"
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/db_xref="GI:6175162"
                                                                                                                                                     complement(5740. .>7691)
                                                                                                                                                                                                                                                                                                       /note="unknown protein"
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                                                                                                                           /gene="F7018.3"
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Best Local Similarity 52.7%;
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .9759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MFSLKSLISSPFTQSTTHGLFTNPITRPVNPLPRTVSFTVTASM
                                                                                                                                                                            /note="similar to calmodulin-domain protein kinase (CDPK isoform 9) GB.AB03242 [Arabidopsis thaliana], similar to hypothetical protein (F22013.13) GB.AAC14039 [Arabidopsis thaliana]; Pfam HMM hit: Eukaryotic protein kinase domain join(<1. 691,1263. .1321)
                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAF04907.1"
/db_xref="G1:6175181"
/translation="BFYACKTIDKRVLIDALDRECIETEPRIMAMLPPHPNIIRIFDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YETEDSLAIVMELVDPPMTIYDRLISAGGRLSESESASYAKQILSALAHCHRCDVVHR
VVPDNWLVDDVSGGVKLCDFGSAWMIGGETARGVOGTPYYVAREVVMGRKYDEKVDI
WSAGVVITWLAGEPPRGETARDIFESILGROLKFPPKKFGSVSSEAKDLLKRMICR
DVSRRFSAEDALHLVFTLINTQVIRLDSNVY"
                                                                                                                                                                                                                                                                                                                                                            2,
                                                                                                                                                                                                                                                                                                                                                              /product="putative calmodulin-domain protein kinase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="exon predicted by xgrail, quality good"
1658. 1742
1658. note="exon predicted by xgrail, quality excellent"
complement(1692. .1764)
/note="exon predicted by xgrail, quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="exon predicted by xgrail, quality excellent" complement(1965. .2063)
/note="exon predicted by xgrail, quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="exon predicted by xgrail, quality marginal" <4314. .5760
/gene="F7018.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="predicted by genscan, multiple est matches"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             marginal_shadowexon"
2787. 2833
/note="exon predicted by xgrail, quality good"
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3518. .3831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(3573. 3723)
/note="exon predicted by xgrail, quality marginal_shadowexon"
3957. 4004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(313. .3418)
/note="exon predicted by xgrail, quality
excellent_shadowexon"
                                                                              join(<1. .691,1263. .>1321)
/gene="F7018.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(1811...1888)
/rpt_family="(TA)n"
complement(1812...1908)
/rpt_family="(CATA)n"
1910...2023
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/db_xref="G1:6175160"
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/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(700. .730;
/rpt_family="POLY_A"
1497. .1548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         marginal_shadowexon"
          /chromosome="III"
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/gene="F7018.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <4314. .5760
/gene="F7018.2"
                                                                                                                                                          /gene="F7018.1"
                                                                                                                                                                                                                                                                                                          /gene="F7018.1"
                                                      /clone="F7018"
                                                                                                                                                                                                                                                                                                                                            /codon_start=]
                                                                                                                                .>1321
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Db 91734 regrirecterrereacerracecracecreterrererrescence 91793 Gaps ' 52 tagottcaacctttaacattaacatggccattccctacccccatttcatcgccaccgaga 111 0; complement(11936. .12012)
/note="exon predicted by xgrail, quality
marginal_shadowexon"
11965. .12019
11046="exon predicted by xgrail, quality good"
13300. .13379 complement join (13920. .14468,14558. .16713)) /gene="F7018.5" Score 54; DB 8; Length 95310; Pred. No. 0.34;

rocus

SOURCE

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codon (atg, gtg, ttg or (att)) where possible we choose an initiation ribosome binding site sequence (optimally 5-13pp before the upstream initiation codon). If this cannot be identified we choose the most IMPOSPRANT. This codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (25-APR-2000) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       are also included but some of these may be fortuitous.
The length in codons is given for each CDS.
Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database.
The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.
Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Blbbe et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adenosylhomocysteinase; integral membrane protein; L-lactate permease; mannose-6-phosphate isomerase; nucleotide phosphorylase; oxidoreductase; phosphomannomutase; rrnD; secreted protein; transcriptional regulator; transport protein; whiB. Streptomyces coelicolor A3(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 37898)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome
Mol., Microbiol. 21 (1), 77-96 (1996)
91794 CITCICCICGAACCICGTITCATICICGCGCAAGGCTCAAICCGTCGCGCTITCAGG 91853
                                                                                                                                                               91854 ACGATTIGAAGAAGCTCGCGGCGGAGAAAGCTGTGGAGGCAATTAAACCTGGGATGGTTC 91913
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                                                                                               172 acgatttgaagaaaatcgccgcctacaaggccgtcgagtacgtggagtccggcatggtcc 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMPORTANT: This sequence MAY NOT be the entire insert of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cerdeno, A.M., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                               Db 91914 TAGGGCTCGGAACCGGATCCACCGCAGCTTTCGCTGTTGATC 91955
                                                                                                                                                                                                                               232 teggeetaggeaceggetecacegecaageatgeegtegace 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCE34 37898 bp DNA Streptomyces coelicolor cosmid E34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            jun/cg1-bin/frameplot.pl. CAUTION:
correct initiation codon. Where po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saunders, D.C. and Harris, D. Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL353862.1 GI:7649483
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VERSION
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JOURNAL
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SCE34/c
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It may be shorter because we only sequence

sequenced clone.

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Complement(2470. 3477).

Gane="SCE34.01c"

Apone="SCE34.01c"

Anote="SCE34.01c, possible integral membrane protein, len:
315 aa. similar to TR:069662 (EMBL:AL022121) Mycobacterium
tuberculosis hypothetical 35.5 kD protein MTV025.042c, 330
aa. fasta scores: opt: 1119 z-score: 1285;3 E():-0;51.83
identity in 334 aa overlap. Contains possible hydrophobic
membrane spanning regions"

    16.
    1. .161
    7note="nominal overlap with Streptomyces coelicolor cosmid">/note="nominal overlap with Streptomyces coelicolor cosmid">/note="nominal overlap with Streptomyces coelicolor cosmid"//note="nominal overlap with Streptomyces coelicolor cosmid"//note="nominal overlap with Streptomyces coelicolor cosmid with Streptomyces coelicolor cosmid with Streptomyces coelicolor cosmid with Streptomyces coelicolor cosmid with Streptomyces coelicolor cosmid with Streptomyces coelicolor cosmid with Streptomyces coelicolor cosmid with Streptomyces coelicolor cosmid with Streptomyces coelicolor cosmid with Streptomyces coelicolor cosmid with Streptomyces coelicolor cosmid with Streptomyces coelicolor cosmid with Streptomyces coelicolor cosmid with Streptomyces coelicolor cosmid with Streptomyces coelicolor cosmid with Streptomyces coelicolor coeming with Streptomyces coelicolor coeming with Streptomyces coelicolor coeming with Streptomyces coelicolor coeming with Streptomyces coelicolor coeming with Streptomyces coelicolor coeming with Streptomyces coelicolor coeming with Streptomyces coelicolor coeming with Streptomyces coelicolor coeming with Streptomyces coelicolor coeming with Streptomyces coeming with Streptomyces coeming with Streptomyces coeming with Streptomyces coeming with Streptomyces coeming with Streptomyces coeming with Streptomyces coeming with Streptomyces coeming with Streptomyces coeming with Streptomyces coeming with Streptomyces coeming with Streptomyces coeming with Streptomyces coeming with Streptomyces coeming with Streptomyces coeming with Streptomyces coeming with Streptomyces coeming with Streptomyces coeming with Streptomyces coeming with Streptomyces coeming with Streptomyces coeming with Streptomyces coeming with Streptomyces coeming with Streptomyces coeming with Streptomyces coeming with Streptomyces coeming with Streptomyces coeming with Streptomyces coeming with Streptomyces coeming with Streptomyces coeming with Streptomyces coeming with Streptomyce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="SCE34.02, possible integral membrane protein, len: 318 as: similar to TR:069663 (EMBL:AL022121) Mycobacterium tuberculosis hypothetical 33.2 kD protein MTV025.043, 310 as: fasta scores: opt: 734 z-score: 602.4 E(): 4.3e-26; 42.9% identity in 319 aa overlap. Contains possible hydrophobic membrane spanning regions"
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FRFSLVRGILGVIEILMTLGVIACVASLVSARGRRLGDVFAGTLVVRERVPFSSAGFM
PPPPPWLAGRESGLDLSAVDDLWLAVQVIARMGQLDPRVGMAMAERLAADVAARTG
APVPREVPPPAYLAAVLQERQAREARRAFGGASAGGTAAMVPVADAPPARPAVPTAP
PPVPTAPPTAPPPAPPSFGGGLEVPRDVPPDRRPGTGFVPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MDLDVFVSAHRAEWDRLDALLRRRRRLTGPETDELVALYQRTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MSELVTGEAVALELRPARLPSRALAVLLDLAVAVAVYVAVTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(359. 2116)
/note="probable 16S ribosomal RNA. Coodinates taken from similarity to SW.SARRND (EMBL: M27245) Streptomyces ambifaciens rrnD gene cluster encoding 165, 23S and 5S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Coodinates taken from similarity to SW:SARRND (EMBL:M27245) Streptomyces ambifaciens rrnD gene cluster encoding 165, 23S and 5S ribosomal RNAs"
                                                   small overlap between neighbouring submissions.
Cosmid E34 Overlaps cosmid E33 on the Asel-E genomic restriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"probable 23s rRNA (fragment), coordinates taken from similarity to SW:SARRND (EMBL:M27245) Streptomyces ambifaciens rrnD gene cluster encoding 16s, 23s and 5s
overlapping sections once, or longer, because we arrange for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative integral membrane protein"
/protein_id="CAB68904.1"
/db_xref="GI:7649484"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="putative integral membrane protein"
                                                                                                                                                                                                                                                                                                                             /organism="Streptomyces coelicolor A3(2)"
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/db_xref="G1:7649485"
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/gene="SCE34.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:100226"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(<1, .105)
                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'clone-"cosmid E34"
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3604. .4560
/gene="SCE34.02"
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                       /strain="A3(2)"
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δ g δ g LOCUS

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APPLACATION - MATVONROPEKVADLSLAAFGRKEITLAEHEMPGLMAIRKEYAE
AQPLAGARVTGSLHWTVQTAVLIETLVALGAEVRWAGNITESTOBHAAAALANGYONGT
PUDPGGVPVARWGETLEETWWCTEGALTWWTPTGGPWILLDDGGDATLLVHKGVEY
EKDGKVEVDTARESPHRVILEELLFRYGESPOKWTQLASEIRGVTEETTGVHRLYE
MHRDGTLLFPAINVNDAVTKSKFDNKYGCRHSLIDGINRATDVLIGGKTAVVCGYGDV
GKGCABELRGGGARVIITEIDPICAAAAAGSWYTLUEVYRADIETTGVHTGNKDII
MAKDMAKMKHQAIVGIGHFDNEIDMAGLAQTPGIVKDEWFROYNTALDFYTTGORNDII
SEGRLLALGANTGHFDNEIDMAGLAQTPGIVKDEWFROYHTWTYPDGKVLIVL
HLDSLGVKLTTLRPEGAAD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="SCE34.04c, sahH, adenosylhomocysteinase, len: 485 as; highly similar to SW:SAHH TRIVA (EMBL:U40872)
Trichomonnas vaginalis adenosylhomocysteinase (EC 3.3.1.1)
SahH, 486 as; fasta scores: opt: 2114 z-score: 2420.8 E(): 0; 65.2% identity in 477 as overlap. Contains Pfam match to entry PP00670 Addergase, S-adenosyl-L-homocysteine hydrolase and matches to Prosite entries PS00738
S-adenosyl-L-homocysteine hydrolase signature 1 and
                                                                                                                                                                                                                                                                                                                                      OGSVDLAIDELGRPIRLELHAADWOYRGAAIDGYTWYRTDPTGIHATEGNARHAFTG
TSPAFLVAVARLIRITPSESATRVRLVALTDPVLAPRTVDGSWALLNREAHATDNDPL
TVDEYQVTALDTGEGYAVHIAGDVVLAAPGIELEDLETPPSVFP"
                                                                                                                                                                                                                                                                                                                      /translation="MPRGRYSLHDPHDHTPLAEEHFQCAPGPSGWRYVSRLTTPTGDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00739 S-adenosyl-L-homocysteine hydrolase signature 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="PS00739 S-adenosyl-L-homocysteine hydrolase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Pfam match to entry PF00670 AdoHcyase,
                                                                                                                                                                                                                       /product="hypothetical protein SCE34.03c"
/protein_id="CAB88906.1"
/db_xref="G1:7649486"
complement(4581. .5195)
/gene="SCE34.03c"
complement(4581. .5195)
/gene="SCE34.03c"
/note="SCE34.03c"
/note="SCE34.03c, unknown, len: 204 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="adenosylhomocysteinase"
/protein_id="CAB88907.1"
/db_xref="G1:7649487"
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/note="comp.
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/gene="sahH"
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complement(7037. .8017)
/gene="SCE34.05c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(5480..6733)
/gene="sahH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(5306, .6763)
/gene="sahH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(5306. .6763)
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Gaps

; 0

56; Indels

Pred. No. 6.4; 0; Mismatches

17.3%; 59.1%;

81; Conservative

Query Match Best Local Similarity Matches 81; Conserv

Score 47.4; DB 2; Length 37898;

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strand).

The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot-program of Bibb et al., Gene 30:15-66(1984) as implemented at http://www.nih.go.jp/
jun/cgi.bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, qtg, ttg or (atl)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (25-NOV-1998) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA E-mail: barzellésanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces coelicolor A3(2)
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Streptomycescales; Streptomyciaes.
1 (bases 1 to 36224)
Redenbach,M., Rieser,H.M., Denapaite,D., Eichner,A., Cullum,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          available on the World Wide Web. (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces coelicolor sequencing at The Sanger Centre is funded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kinashi, H. and Hopwood, D. A.
A set of ordered cosmids and a detailed genetic and physical map
for the 8 Mb Streptomyces coelicolor A3(2) chromosome
Mol. Microbiol. 21 (1), 77-96 (1996)
97000351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                histidinol-phophate aminotransferase; integrase/recombinase; integrated element; oxidoreductase; partial thiamin biosynthesis protein thic; phea, plasmid replication initiator protein; prephenate dehydratase; secreted peptidase; serine /threonine phosphatase; sers!-tRNA synthase; thic'; two component
                                          ccacccctcctccctccgtcatcctcacccaagacgatttgaagaaaatcgccgccta 196
                                                                                                                                       caaggeegtegagtacgtggagteeggeatggteeteggeetaggeaceggetecacege 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 (bases 1 to 36224)
Bentley,S.D., Parkhill,J., Barrell,B.G. and Rajandream,M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABC transporter; ftsK/spoIIIE family protein; hisC2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Colney, Norwich, Norfolk NR4 7UH, UK
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Streptomyces coelicolor cosmid D78.
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Saunders, D.C. and Harris, D.
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                                                                                                                                                                                                                                                                                                                                                  6239 CGAGCACCGCGTCATCC 6223
                                                                                                                                                                                                                                                                                  257 caagcatgccgtcgacc 273
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VERSION
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TLDNATGEILRHYDTRNEPGERJHRAGGTCRPRRDGGACHGRPLCGGTVHAPDAPA
TLDNATGEILRHYDTRNEPGERJHRAGGTCRPRRDGGACHGRPLCGGTVHAPDAPA
VGQPLCPDCYDYTAHVLWHAHASKLWDRFVIDVRRRLASSAGIVQSRFAHHARLSFAR
NVPASVRTRRAVHVHTVRLAGGPGPDDDAVAAVYKVSKGTDETGAGTDHKVTTCDDID
SARVSRHVRTLMHTCWRLGGLPEYAPLARVRYVKYSKGTDETGAGTDHKVTTCDDID
SARVSRHVRTLMHTCWRLGGLPEYAPLRRWTHTLGYRGHILTRSRAYSTTYAALRA
ORAHHGHTDTPDAITDAHWRYVGSGHTPGAALIAAGVAEDIAQNRAAVRDALSAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(2805. .4292)
/gene="SCD78.04c"
complement(2805. .4292)
/gene="SCD78.04c"
complement(2805. .4292)
/gene="SCD78.04c, possible integrase/ recombinase within putative integrated plasmid, len: 495 as; similar to TR:037839 (EMBL:D38173) ORR469 protein (possible site-specific recombinase) from Actinophage R4 (469 aa), fasta scores; opt: 261 z-score: 320.1 E(): 1.4e-10, 29.1% identity in 306 as overlap integrase from M.
TCY336.18 (Rv1586c) possible integrase from M.
tuberculosis integrated phage phiRv1 (469 aa), fasta scores; opt: 371 z-score: 270.8 E(): 7.8e-08, (26.6% identity in 489 aa overlap). Probable coiled-coil from 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative integrase /recombinase"
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PWRYIMSTTSODGRAYHDSNGLQDFYAGFEBIEKGLVGVAMASLSETRKGRRSKNSHR
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/focte="SCD78.05"
/focte="SCD78.05; thic', probable thiamin biosynthesis protein thic, partial CD5, len: 43 as, sinlar to the extreme C-terminus of e.g. THIC_ECOLI thiamin biosynthesis protein thic (631 aa), fasta scores; opt: 97 z-score: 137.7 E(): 246.28 identity in 39 as overlap and THIC_MYCTU (547 aa), fasta scores; opt: 143 z-score: 272.4 E(): 6.4e-08, 53.18 identity in 49 as overlap. Note that this gene appears to have been interrupted by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRAIRGQSVSAWRPFGWEDDKVTLRPDEAEAIRTAVHDVIAGASISEITRRWEEAGFI
ISRGNPFQYQTVKQVLVNARLCGYREIKGEIVRDGDDQPIVGEWEAIVTPKQWFAVTA
KIRERGHGTGTPRGGLVHKYLLINILRCGNVLEDGTVCNNKMIGIKANDWLKYQHAYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CKKTVDGGCNKTYKRGDKTDKIIEELVIAKLERDAATKAQDVPDWDKAEALERALGSR
RELERRWHDDEDTDIDDEAFFRNLPVLERRIKELRVDQKAHEALKAEREEBEAEDIRKS
WGAKTLTQKREAMKKVLGAVIALPGGKGNKTFDPDLLKPVWKTSE"
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/protein_id="CAA22210.1"
/db_xref="GG1:392874"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 36224;
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52.9%; Pred. No. 9;
:ive 0; Mismatches
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/gene="SCD78.05"
/note="thic'"
4444. .4575
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/gene="SCD78.06"
4655. .6103
/gene="SCD78.06"
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="SCD78.01, ftsK /spoilie family protein, partial CDS within putative integrated plasmid, len: 271 aa; similar to many members of the ftsK /spoilie family e.g.SPI_STRAZ (EMBL:S58719) sporulation-regulatory protein from Streptomyces azureus plansid pSA1.1 (303 aa), fasta scores; opt: 736 z-score: 1014.5 E(): 0, 49.0% identity in 247 aa overlap and TRSA_STRAM (EMBL:31959) transfer protein trasA from Streptomyces ambofaciens plasmid pSAM2 (306 aa), fasta scores; opt: 222 z-score: 676.5 E(): 26-30, 47.8% identity in 203 aa overlap. Also similar to SC6A9.34, a protein within another putative integrated plasmid (on Streptomyces coelicolor cosmid StGA9)(E(): 5.46-24, 45.7% identity in 247 aa overlap). Contains PS00017 ATP /GTP-binding site motif A (P-loop)"
   If this cannot be identified we choose the most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVALVGIDOKGGMEGGLFADRISALATSRREAVAVLTALVVDIQERMSACRTAGVRSV
WELPDKLRPVPVVVLVDEIAELYLSDGTRQSKSEAEQCSTLLLRLAQLGAALGLHLVV
AGORVGSDLGPGVTALRAQLGGRICHRVNDPGTAEMTLGDLNKDAVAQAITAQERG
                                                            IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid D78 lies to the right of Q11 on the Asel-D genomic restriction fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="IGALETGGAWVMNLRLVPHWLIAGATRSGKSTLLARVITQLAPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein from Streptomyees ambofaciens plasmid pSAM2 (459 aa), fasta scores; opt: 712 z-score: 983.7 E(): 0, (43.7% identity in 467 aa overlap). Note that there is no possible initiation codon upstream of the start of homology (or close downstream). The CDS given here has an arbitrary start."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein within putative integrated plasmid, len: 452 aa, similar to REPS_STRAM (EMBL:219594) replication initiator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="SCD78.03, possible plasmid replication initiator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VAVCTGPDGGWARARSHLTPTDEAVATARKHSGMTPELPALDRALVALEGDGK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="PS00017 ATP /GTP-binding site motif A (P-loop)"
                                                                                                                                                                                                                                                                                                      /organism="Streptomyces coelicolor A3(2)"
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/protein_id="CAA22207.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="ftsk /spoIIIE family protein"
/protein_id="CAA22206.1"
/db_xref="G1:3928710"
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                                                                                                                                                                                                                                                                                                                                                                                                             'clone="cosmid D78"
initiation codon). If this upstream initiation codon.
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/transl_table=11
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/gene="SCD78.03"
1308. .2666
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                                                                                                                                                                                                                                                                                                                                   /strain="A3(2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dellaporta, S.L.
Nucleic acid molecules that encode tassel seed 2(TS2), a protein
involved in the control of flower development in plants
patent: US 5750873-A 9 12-MAY-1998:
                                                                                                                                                                                              28816 GCCGACGAGGCCCTCGCGACCGTGGAGATGGCCTACGCCCAGGACCGGAAGATCGCCACG 28875
                                       28756 CTCACCGGCCGCGAGTTCGTCCTCGCCAACGCCGAACTGCACGGGCTGGGGGCCAGGGCG 28815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 tcatcgccaccgagaaagccgccatggacgccggcctcctccacccctcctccccctccg 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 tcatcctcacccaagacgatttgaagaaaatcgccgcctacaaggccgtcgagtacgtgg 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 aacatggccattccctacccccatttcatcgccaccgagaaagccgccatggacgccggc 131
                                                                                     132 etectecacecetectececetecgteatecteacecaagaegatttgaagaaaategee 191
                                                                                                                                                            192 gectacaaggeegtegagtaegtggagteeggeatggteeteggeetaggeaceggetee 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-FEB-2000
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Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0434D08
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Oryza sativa genomic DNA, chromosome 1, clone:P0434D08.
AP001278
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                                                                                                                                                                                                                                                                                                                                                        PAT
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                                                                                                                                                                                                                                                                                                                                                                         Sequence 9 from patent US 5750873.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="unknown"
368 c 349 g
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Best Local Similarity 48.3%;
                                                                                                                                                                                                                                                                                                                                                        1288 bp
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/translation="MSKKTVIRADLIGRSCKKDILHAVSTLQGIKSMDIDEEKCTLTV
LGPVDPVKIVHRLKKKCFAAAVVSVEDDKPKEPDPPAPEKKKEDDDDPCQCQCKEAEC
ACVKVCAASCHHSPCSLPDCYFYKSYSYSYKPSPSFGFGYHLESGGHCIIQ"
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APUGVVVVNDRAHGLARLSPALPNQSSTOPSCYPTIPOPSRADAABTGSOSSRSSTRAV
TROGVVVVNDRAHGLARLSPALPNGSSTOPSCYPTIPOPSRADAABTGSOSSRSSTRAV
TROGVTKLYHRLRICLIGKRTHLREHRIHGSLUVSGRRGGAPSSRABEBEFRRAALPPP
RPSRLAAMLSGGGEBYRVSPPSRPCESDAVVPIEARKKLETKRSKQQEHSEFOLOLLIT
                                                                                                                                                                                                                                                                                                                                                                                    Genes were predicted from the integrated results of the Genes were predicted from the integrated results of the Genes were predicted from the integrated results of the following:GENSCANI.0, BLASTX2.0, BLASTX2.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against the non-redundant database NRP (PIR, SWISSPROT, GENPEPT, PDB) from MAFF DNA bank and the cDNAssequence database at RGP. Protein similarities of the cording regions were searched against NRP with BLASTP2.0. ESTS represent the identified cDNA sequences using BLASTN 2.0 with the corresponding DDBJ accession
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/db_xref="G1:7106506"
/translation="MSDMKDTNAAGPETVGNPDPMDQTEDNSMPSAQEQCSVGNLMIQ
SSSLFVDRTRSYDVPOXIDMKRNVFFKDRC"
complement(join(0430. .8746,8794. .8839)).
/note="hypothetical protein"
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/db_xref="G1:7106507"
/translation="MASDDTSSATPPIGYRLNHLVCSEPEGNYFGPALELSRSPKPVH
VDFHVNKWALQLANSRSSHCRGLTDTTGDGNDKEWCSRCCRTAALCSVAHQATVKTGC
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TLSKLASFPISNPTHGTTKFSRQHHCSYCSSAAAELQQPSLPNRPIIVVQVAKTTEIL
SVTQQLRPHCDATPTPKRANRNDTHEEHQPKLPKNHFLHEASINNPIRKMQCVIYAKL
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This sequence of this clone has an overlap with P0503G09 clone,
This sequence of this clone and at the 3' end. This clone ends at the position 31,961
of P0503G09. Detailed information on overlap and assembly quality
together with annotation of this entry at
http://www.dna.affrc.go.jp.B2/genomicdata/GenomeFinished.html.
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13368 ...13652,13685 ...13950,17214 ...17269,18661 ...18851)
/note="hypothetical protein"
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                                                                                                                                                                Submitted (24-FEB-2000) to the DDBJ/EMBL/GenBank databases. Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
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/note="ESTs AU029333(E30170),C74020(E30170) correspond a region of the predicted gene.; hypothetical protein"
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                                                                                                                                                                                                                                                         (E-mail:tsasakieabr.affrc.go.jp,
URL:http://www.dna.affrc.go.jp;82/, Tel:81-298-38-7441,
Fax:81-298-38-7468)
Published Only in DataBase (2000) In press 2 (bases 1 to 161266)
                                                                                    Sasaki, T., Matsumoto, T. and Yamamoto, K.
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/db_xref="G1:7106508"
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/protein_id="BAA92194.1"
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join(28965. .29024,29098. .30608,31416. .32066,32089. .32627,
32682. .33058)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MPCGYGVPIISTLDFTARRGTTFASHQYDTGPFYDEIRRRLSFD
FTKSQLVEKLRRLKKKYRLCAARMASSPHAAAAGFAFRTPHEGAIYDLARHIMPPALK
RDGTASDDDDINPAAAAATAAVMTFVAMEDGFGGSAPTPTFPFRGRGGRRVRRRMAQE
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TSSPPACLRRRLVPPPTRLAYYASVVGRLHLHRRPASVAADWCLRLHGWPIMPPLLG
TYFTAGLLPPSPPTGAGLCYRRCWASATPSPPACLRRRWVPPPTRLAYYAAV
GCLHPHRWLFPVAVDWIQIQICIKGTHGFKLISYALGMDGSKHHRPPRPPTGAYYAAV
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PAWLAFWPPTDRLAFAADWCFRLHGRLIMLPLLGVYVFTDRLAYAADW
                                                                                                                                                                         /translation="mskrtVikabligrackseilaivatikgiksmbidaekctltv
VgiVDPVRIVRKLRKKGFSACIVSVEDDKPKEEEKKDPCKEAKEKLEKAWKEYCEKCN
                                                                                                                                                                                                                                               VKLKPGCPCSCSTPCSFPPIGCHDRGICPPPCPPPCPLPCPPCPLPCPPRGYG
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RSVLSRLIKEFITSFAVVGGTGPGMCINMGFGGAGINADIAGLGFGIAGINPGVPGAD
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VELPIEKCDGIDYRRNGEINLDGSNLQSGAAPTDALRPPRHHGHMGAAAYSLLGEISC
MHELIQQINIQLAYQAAVVGRLRLHRPACLRRRRLVSLPTRLAYYAAAVGRLRIHRRP
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LHGWPVITPTDAIFFTAGYIAVTTNRHQYLQHKLPTFAMAADWFLHFHGCMILDYLTG
LTIFIAATTTDGHHRLPSPTDYAAADWCFYLHNCASSLPVCFCCRRLVFTSLRQYNFV
IMVERLHLYYLRHWQTLLLLRRFCYFTNHDVFVNLDISACDAVLFYYNKWLSNIQDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASVAAEWCLRLHGWPIMPPLLGVYDFTTGLPPSPPSGASAYTAGLLLCRRCWASTTSP
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TTGLPPSPPIGASAYTAGLLCRRCWVSTTSPPACLRCRRVVPPPARLAYYATVVGRLH
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CLYAAVVGRLRLHRPACLRRYRLVLPLARLAFYAAVVGRLRLHRPAASSAADWCFRLH
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ESYDKSROHDNKNHKREIEILCSNTICDTLNNTRCDTSKLYTPESFFYSARTPHTTRQ
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VSDRTDQLGAWQRGIIAWFSSVGSLTALCAITTPHVIDGISYSSGGAASPD
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GGERRRREMAEGEGEGWREFVVVVAGEVGVMVSWWKKGRDDDHPVVQPLPAVGRKANA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(47013. .47907,47926. .48720,48802. .49137,49409. .50012,50104. .51310))
/note="similar to Arabidopsis thaliana chromosome II BAC T13921 genomic sequence, putative helicase. (AC006067)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"EST C98429(E0138) corresponds to a region of the predicted gene.; hypothetical protein"
join(25864. .25872,26022. .26097,26354. .26802)
/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                        complement(join(27737. .27749,27842. .28764))
                                                                                                                                                                                                                                                                                                                                                      /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="hypothetical protein"
                                                                                                          /protein_id="BAA92195.1"
/db_xref="G1:7106510"
                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="BAA92196.1"
/db_xref="G1:7106511"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BAA92197.1"
/db_xref="G1:7106512"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(33441. .33596)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="BAA92199.1"
/db_xref="G1:7106514"
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/db_xref="GI:7106515"
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                                                                                                                                                                                                                                                                                   YGCYYEERYPGGECVIQ"
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/translation="MLANLLRFDGDRRSRRFLRQIRSYNSLFAFTSLGADVDKSINNG
TAPCVFKINGIVHHRIGSLLPQQGAPPKFAQLYIYDTENEVSNRMRVFDKESSTDEPD
PFIVTELGAMLDEHNDLVKSFRFARKRLKDHGDEKIALRLLGCNSKDEVQYNLPTSGE
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NFPAHKLALKKGVTVMLLRNLNQSMGLCNGTRLLALSLGQRLLECQILTGTNIGDRVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPRIALTTISPKWPFTLQRRQFPVRVCYAMTINKSQGGTLKRVGVYLKKAVFTHGQLY
VAVSRSTSRDGLRILTEGDDEACSSKTRNVVYHEVLQTVDLMVHHVLPDLIAVTHEYL
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DAAGLSAPTVAAPVVSTGAPSPSSILLPSLFALPRCPPCREEEKETGAARFTRHGPPA
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WEICLAPVKVGKYTIQTRAIQEVECTNAALNNADVNDTIAWAGGILDLPLSRRINTNA
ATROLLSSSSTPFSERRPTTIAAPHRPSPPSRLRSCMEPIPLGQAQRRQGQRYGLIEK
IGSLGWPRAHAHTGGGRDPVAAVARTSAASRGRRQRVSGKHDPFVSHFSKVDSPFAPK
                                                                                                                                         IAGIIVGDYSNDKYTYDVVVQSCDSRLRRVSALHPSYMALQYPLLFPYGERGFHLGIK
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ATAKRGKTGAKHTSEPNQQQPRAELTNRMHVHQDFCGINQRIISQLLSMVLGERAPSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNTHIGKHLCDGGPWCTTLVGEPRIDVSHTERQCIVLSKSGRCTKRKACQAGKKLPST
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Xylella fastidiosa
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
Xylella.
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/db_xref="G1:7106516"
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Simpson.A.J.G., Reinach, F.C., Araya, J.E., Bala, G.S., Baptista, C.S., Barros, M.H., Alvas, L.M.C., Araya, J.E., Bala, G.S., Baptista, C.S., Barros, M.H., Bonaccorsi, E.D., Bordin, S., Bove, J.M., Briones, M.R.S., Baeros, M.H., Bonaccorsi, E.D., Bordin, S., Bove, J.M., Briones, M.R.S., Camargo, A.A., Camargo, L.B., Carraro, D.M., Carrer, H., Colauto, N.B., Colombo, C., Costa, F.F., Costa, M.C.R., Costa-Neto, C.M., Coutinho, L.L., Cristofani, M., Dias-Neto, E., Costa-Neto, C.M., Ferror, J.S., Faraca, S.C., Franco, M.C., Ferreira, V.C.A., Ferror, J.S., Franca, S.C., Franco, M.C., Ferreira, V.C.A., Forro, J.S., Franca, J.S., Franca, S.C., Franco, M.C., Fronme, M., Fradania, J.S., Franca, S.C., Franco, M.C., Krieger, J.S., Franca, S.C., Franco, M.C., Krieger, J.S., Kuramae, E.E., Ladigret, F., Lambais, M.R., Leitel, L.C.C., Lemos, B.G.M., Lemos, M.V.F., Lopes, S.A., Machado, J.A., Mardues, M.V., Martins, E.M.F., Martuka, D.C., Mardues, M.W., Martins, E.M.F., Martuka, M.M., Martura, H.M.F., Martuka, M.M., Martura, M.A., Martuka, M.C., Goliveira, M.A., Martins, E.M.F., Oliveira, M.Y., Monto, D.H., Nagai, M.A., Nancas, L.R., Oliveira, M.A., Peixoto, B.R., Pereira, G. Sankasaki, H.E., da Silva, A.P., Pereira, Jr., C.K., da Silva, F.R., da Silva, M.J., de Souza, A.J., de Souza, A.P., Terrallia, M.C., Siqueira, W.J., Ge Souza, A.A., de Souza, A.P., Terrallia, M.L., Silveiri, M.L., Silveiri, M.H., Vallada, H., Van Sluys, M.A., Verlore, A.L., Zago, M.A., Zatz, M., Meddanis, J. and Setubal, J.C., Directiva, M. Submitted (O2-IMN-2000) Organization for Numberial and Setubal, J.C., Submitted (O2-IMN-2000) Organization for Numberial and Setubal, J.C., Submitted (O2-IMN-2000) Organization for Numberial and Setubal, J.C., Submitted (O2-IMN-2000) Organization for Numberial and Setubal, J.C., Submitted (O2-IMN-2000) Organization for Numberial and Setubal, J.C.
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                                                                                                                                                                        The genome sequence of the plant pathogen Xylella fastidiosa. The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing and Analysis, Sao Paulo, Brazil
Nature 406 (6792), 151-157 (2000)
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122. .775
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13083-970, Brazil
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2986. .3207
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                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                      AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /traislation="METATYTRVNSTOPANACAPSHIPIIINNPMSEAKTRAAEKAIE
YVENDMIIGVGTGSTVAYFIDALGRTPKRIKGAVSSSEQSTAHLKOHGIEVLEINHTG
TLPIXVDGADECDPYKRLIKGGGASLTREKIIAEASKQFICIIDPNKQVATLGKLPLP
IEVIPMARSLVARQIMARTDGQPVWREGVIIDNGNVILDVHHLRITDPVKLEQELNQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="hypothetical protein; identified by sequence
similarity; putative; ORF located using Glimmer/RBSfinder"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to SP|P27252 (percent identity: 57 %/query alignment coverage: 84.5 %/subject alignment coverage: 94.5 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder/Start codon shift: -147"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5163 CGCCGCCGAAAAGGCCATCGAATACGTCGAGAACGATATGATTATCGGCGTCGGCACCGG 5222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 egecgectacaaggecgtegagtaegtggagteeggeatggteeteggeetaggeaeegg 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus. I (bases 1 to 3875) Steinbuechel, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.4%; Score 45; DB 1; Length 10834; 70.6%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="ribose-5-phosphate isomerase A"
/protein_id="AAF84817.1"
/db_xref="GI:9107130"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25; Indels
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/protein_id="AAF84818.1"
/db_xref="G1:9107131"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGVVCVGLFARRCADLVIIGSEPPHIL"
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R.Tuber ORF1, phbCRr, ORF3 and ORF4.
X66407.1 G1:46398
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                                                                                                                                                                              /transl_table=11
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                   5053. .5790
/gene="XF2015"
5053. .5790
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/gene="XF2015"
                                     4637. .5080
/gene="XF2014"
1637. .5080
'gene="XF2014"
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/gene="XF2016"
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/gene="XF2016"
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E 2 (bases 1 to 3875)
Spiept, U. and Steinbuechel, A.
Pieper, U. and Steinbuechel, A.
Identification cloning and sequence analysis of the
poly(3-hydroxyalkanoic acid) synthase gene of the gram-positive
bacterium Rhodococcus ruber
L FEMS Microbiol. Lett. 96, 73-80 (1992)
S pleper, U. and Steinbuchel, A.
S pleper, U. and Steinbuchel, A.
Identification, cloning and sequence analysis of the
poly(3-hydroxyalkanoic acid) synthase gene of the gram-positive
bacterium Rhodococcus ruber
L FEMS Microbiol. Lett. 75 (1), 73-79 (1992)
E 92406022
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/translation="MRCPLSRTGVRSIIRDGGDHPRRQSPNAPSARSGARGSRTYADP
MEDDASRPPTLGELIRRQRELAELPURQLAAWGISNPYLSGIERNIRAPSERVLQAI
AEQIHLSAAALTAEVGRPDPGESAVVRAIHEDPDLTNAQRRSLVEWYEAFREVTVGKR
RRGARPDDGFE"
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TAAANQATAEFTKALDDSAARLSEFNDKVVDAAKQSONLTVDTYERAVSSLLDLQEKL
ASASPVAWVEDLTKAQVSFARELTATVTTTARDLLK"
2969. 3009
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GRLAKIPAAATRVFNANDPDAPMPVDPRDRRFSDTAWGENPAYFSLLQSYLATRAYVE
ELTEAGSGDPLQDGKARQFANLMFDALAPSNFLWNPGVLTRAFETGGASLLRGARYAA
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PPWINKYYILDLAFGRSLAEWAVQHGRTVFMISYRNPDESWRHITMDDYYDGIATAL
DVVEEITGSPKIEVLSICLGGAMAAMAARARAFAVGDKRVSAFTMLNTLLDYSQVGELG
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LAMNEDSTSMPAEMHSHYLRSLYGRNELAEGLYVLDGQPLNLHDIACDTYVVGAINDH
IVPWTSSYQAVNLLGGDVRYVLTNGGHVAGAVNPPGKRVWFKAVGAPDAESGTPLPAD
Submitted (25-MAY-1992) A. Steinbuechel, Inst. fur Mikrobiologie der Georg-August-Universitaet, Grisebachstr. 8, W-3400 Goettingen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PQVWDEAATRYEHSWWEDWTAWSNKRAGELVAPPAMGSTAHP¤LEDAPGTYVFS"
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tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBLO 1SA Unite de Genetique Moleculaire Bacterienne, Institut Pasteur. 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk on Jun 24, 1998 this sequence version replaced gi:2131042.
                  CIVDLSSDRSOVQALRGGGITRLYCLDWAPAGPATDSASLDDHLAVLABAVDLIGGRV
NLIGGSQGGWLAAMHTALHPQTVHSLTVAGAPIDFHADRPAAVAFDHLPRAVSTSVLN
LWYDTGRLFGVLPTDPVSEIERSLELLGLLDDPETLAQAIEERRWFLWRQEIPAAFRT
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(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markow Wodel of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is
I A DWWRALT DREPPHWAHPWPVAHSWPLARLRDCSDPDAPEPEAVPTLLLPPQSGSHS
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Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C.E.,
Tekala, F., Badcock, K., Basham, D., Erown, D., Chillingworth, T.,
Connor, R., Davies, R., Devlin, K., Feltwell, T., Gentles, S.,
Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J.,
Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S.,
Squares, S., Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MTCY493 40790 bp DNA BCT 19-JUN-1998
Mycobacterium tuberculosis H37Rv complete genome; segment 63/162.
295844 AL123456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  2546 CATGACCACGCCAAGACCCCGGTCGACGCCGCCGTCGCCAAGACCACCGCGGACGCGC 2605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2606 CAAGGCCAACGAGGCCGCTGCCAAGGCCACCGCGGCGCCGCCGCCGCCGCTCAGAAGAT 2665
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Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                          98 categecacegagaaageegecatggaegeeggeeteeteeaeeeeteeteeeteegt 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            catecteacecaagaegatttgaagaaaategeegeetacaaggeegtegagtaegtgga 217
                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                         Length 3875;
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Mycobacterium; Mycobacterium tuberculosis complex.
1 (bases 1 to 40790)
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                                                                                                                                                                                                                                                                                         Score 44.8; I
Pred. No. 32;
0; Mismatches
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Nature 393 (6685), 537-544 (1998)
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                                                                                                                                                                                                                                                                                                                     Local Similarity
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/note="Rv1424c, (MTCY21B4.42c,MTCX493.30), len: 253.
Possible membrane protein, contains PS00402
Binding-protein-dependent transport systems inner membrane
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RELVPPWIAGILTLISACQTASASSOYNEMROWSDRAINLKPSEMDLGMCLNRFTVDS
KLABSRPQVVACDSREARIRNDGFHANAPSOMIDYELITQNHRAYYCLKYVVVGY
YPAVTTPGKPPSVLLYAPSACDESLPSPRVATALVPGTRSANREFSRFVVTEIKSLGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPPOQETVGFYGFOTFGLERRAIGALINVGIMTPFRIVRLLEQTVRQOIAALGVAGKP
ARYEEAPKTRFNAPVSPHRRVTGTRVELARAKAVKDAFGVKLNDVVLALVAGAARQYL
OKRDELPAKPLIAQIPVSTRSEETKADVGNQVSSMTASLATHIEDPAKRLAAIHESTL
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LIIERLPEIPQLRWRVTGAPLGLDRPWFVEDEELDIDFHIRRIGVPAPGGRRELEELV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAKEMAKAPSAHQIMGLTETTPPGLLQLAARAYTASGLSHNLADINLVVSNVVGPPFP
LYMAGARLDSLVPLGPPVMDVALNITCFSYQDYLDFGLVTTPEVANDIDEMADAIEPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="PS00402 Binding-protein-dependent transport systems
inner membrane comp signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRLMSYKLDRSRPLWELWVIEGVEGGRIATLTKMHHAIVDGVSGAGLGEILLDITPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similar to many M. tuberculosis hypothetical proteins e.g. MTCY28.26, fasta scores; E(): 0, 36.3% identity in 460 aa
an increase in the observed/expected third position G + C. CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="Rv1425, (MTCY21B4.43, MTCY493.29c), len: 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="lipo"
/note="Rv1426c, (MTCX493.28), len: 420. Unknown,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
/product_hypothetical protein Rv1424c"
/protein_id="CAB09346.1"
/db_xref="GI:2131072"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
/product="hypothetical protein Rv1425"
/protein_id="CAB09245.1"
/db_xref="G1:2131071"
/db_xref="SpTREMBL:P71694"
                                                                                                                                                                                                                                                                          /organism="Mycobacterium tuberculosis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mycobacterium tuberculosis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="SPTREMBL:P71693"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(2176. .3438)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(2176. .3438)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(10. .771)
/gene="Rv1424c"
complement(10. .771)
/gene="Rv1424c"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:1773"
/clone="Y493"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(520. .606)
/gene="Rv1424c"
                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:1773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:1773"
                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comp signature."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="H37Rv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="Rv1425"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 775. .2154
/gene="Rv1425"
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                                                                                                                                                                                                                                                                                                  /strain="H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="Y21B4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=
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                                                                                                                                                                                                                                                                                                                                                                  .40722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .1638
                                                                                                                                                                                                                                                 .40790
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                                                                                                                                                                                       initiation codon.
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MTCY21B4.16chighly similar esp. in C-terminus to M. tuberculosis hypothetical protein 050681 (431 aa) (50.1% identity in 411 aa overlap), and also similar in central region to AAAD-HUMAN P22760 arylacetamide deacetylase (398 aa), fasta scores; opt:210 z-score: 248.8 E(): 7.6e-07, 29.3% identity in 191 aaoverlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Rv1427c, (MTCV493.27), len: 535. fadD12, Possible long chain long-chain-fatty-acid-CoA ligase similar to eg. PCO_YEAST P38137 peroxisomal-coenzyme a synthetase (543 aa), fastascores; opt: 507 z-score: 579, 4 E(): 2.9e-25, 30.4% identity in 365 aa overlap Contains PSO0455 putative tuberculosisproteinseg. MTCX06A4.14 (44.8% identity in 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTSEVPGVYLGASVICANTANTAN TANAN VALIMANGUEN TO VARIANGEN VARIANDEN VALEAGLYEGASVICANTAN VALIMANGUEN VALEAGLYEGASVICANTAN VALIMAN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="SPTREMBL:006831"
/translation="MRIRQAFGLIATMRRAGLIAPLRPDRYLRIVAAMRREGMGFTAG
FAGAARRCPDRPGLIDELGTLTWRQLDERGNALAAALQALPAGPRYVGIMCRNHRGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MRFRRMARPRPLTRAAVELLNAANGLRPLSGSGYSTVLAFWLGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLKAILDRTPWRAEEVTVIVAPWFHANGFSQLVLASSLACTIVTRRRFDPEATLDLID
RHHATGLVVVPVWFDRIMDLPAEIRNRYDGRSLRFAAASGSRNRPDVVIAFMDOFGDV
IYNNYNATEAGMIATATPADLRTAPDTAGRPAEGTEIRILDQQFTEVPTGEVGTIYVR
NDSQFDGYTSGAAKDFHAGFNSSGDVGYLDENGRLFVVGRDDEMIVSGGENIYPIEVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KTLATHPDVAEAAVIGVDDQQYGQRLAAFVVLKPGVSATPETLKQHVRDNLANYKVPR
DIAVLDELPRGITGKILRTELQSRVGS"
complement(4422. .4457)
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TRIVAWTDEDHDLTVEKLVAAHAGRRPEHTGSHGKVILLTSGTTGTPKGARHSGGGIG
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VHGLDSFPPGGALVVANHSGGMFPMDVPVFSVDFYDKFGYDRPVYTLSHDILFMGLTG
DLFRRTGYIRATRENAAKALRSGGVVVVFPGGDYDAYRPTFAENVIDFNGRKGYVSTA
VEAGVPIVPAVSIGGQESQLYLSRGTWLARRLGLKRLLRSDILPISFGFPFGFSAAIP
possibleesterase, similar to MTCY493.28, MTCY08D5.15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="PS00455 Putative AMP-binding domain signature" complement(5048. .5050)
/note="possible RBS upstream of Rv1427c"
complement(5049. .5876)
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/protein_id="CAB09256.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="lip0"
/protein_id="CAB09244.1"
/db_xref="G1:2131070"
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/db_xref="GI:2131069"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(3438. .5045)
/gene="fadD12"
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complement(5049. .5876)
/gene="Rv1428c"
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PNLPLPAKIVMQVLDPINLTKQFGEDPDVDAVDEHVRSVMQQALNDLAAKRRFPILG"
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HCARLSQLRVPAAARQQADCLDELTTAGTAATGHTDPADWAGLTPKNLATPTGVPGIQ
IDGYFPDTSTTNTNHGWNHDAQFVIRLPDRRNGGLVVAGTPGNREQYANDRAIADWVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Streptomyces hygroscopicus var. ascomyceticus"
/db_xref="taxon:133248"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces hygroscopicus var. ascomyceticus FK520 biosynthetic gene cluster, partial sequence.
                                                                                                                                                                                                                                                                                                                                                33768 GGAACGGCGACGCCATGCCGCCTTTGCCGCCCGCCCTTACCAAC 33827
                                                                                                                                           5995. .7263
/gene="Rv1429"
/note="Rv1429, (MTCX493.25c), len: 422. Unknown, some
                                                                                                                                                                                                                                                                                                           78 gecattecetacececattteategecacegagaaageegecatggaegeegeeteete 137
                                                                                                                                                                                                                                                                                                                                                                                            138 caccctcctcccctccgtcatcctcacccaagacgatttgaagaaaatcgccgcctac 197
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reeves, C.D., Wu,K., Chung, L., Revill, P. and Katz, L. Direct Submission
Submitted (16-FEB-2000) Kosan Biosciences Inc, 3832 Bay Center Place, Hayward, CA 94545, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wu, K., Chung, L., Revill, W.P., Katz, L. and Reeves, C.D.
The FK520 gene cluster of streptomyees hygroscopicus var.
ascomyceticus (ATCC 14891) contains genes for biosynthesis of
unusual polyketide extender units
20323220 (1), 81-90 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198 aaggeegtegagtacgtggagteeggeatggteeteggeetaggeaeeggeteeaeegee
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                                                                                                                                                                                                                                 DB 2; Length 40790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces hygroscopicus var. ascomyceticus
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                            Indels
                   complement(5882. .5885)
/note="possible RBS upstream of Rv1428c"
                                                                                /note="possible RBS upstream of Rv1429"
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                                                                                                                                                                                                                                                                        94;
                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                      Pred. No. 20;
                                                                                                                                                                                                                                 Score 44.6;
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/db_xref="GI:9280382"
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                                                                                                                 /gene="Rv1429"
5995. .7263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="Fkbw"
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51.8%;
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Wu, K., Chung 1
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Best Local Similarity
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/translation="MPERDALLTDLVGDRAAEMDTSGELPRDLLVRLGADGLLCAEVA
AEHGGLGLGSRENGEFTAHVGSLCSSLRSVWTSQGMAAWTVQRLGDAGQRATFLKELT
SGKLAAVGFSERQAGSDLSAMRTRVRLDGDTAVVDGHKVWTTAAAYADHLVVFGLQED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOPAERAEVAFHLPEVRCYTAEOAATILSLPEFSPPVSTVDSRRRLMYQAGFARDQA
REAYSGPDEDFLRSLDLSMTTAPAGEEELSRVEELTLRTSQMNATGVHYSDADLRACF
TDPAHEVLVVTMGDRFGPHGAVGIILLEKRPSTWHLKLLATSCRVVSFGAGATILNWL
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AASLAYGRKSVAWGCVGILRACRTAAVAHARTREQFGRPLGDHQLVAGHIADLWTAEQ
IAARVCEYASDHWDEGSPEMVPATILAKHVAAERAAAGAATAAQVLASÄGAREGHVVE
RAYRDAKLMEIIEGSSEMCRVMLAQHALALPA"
                                                                                                                                                                                                                                                                                                                                                                     HSALEKNHLIVYSGGLLEAGTFAFNLAVAAVSWLVLGRRRLEPHDLDEDTDPTEGDPAS
RPGAEHVWTLTAAMALVLGTTVLSLDTGFLALTLAALLALLELEPRTSGOOATKELAWPVV
LLCGIVTYVALLQELGIVDSLGKMIAAIGTPLLAALVJCYVGGVVSAFASTTGILGA
LMPLSEPFIKSGAIGTTGWWALLAAAATVVDASPFSTNGALVVANAPERRPGVYQGL
LWWGAGVCALAPAAWAAFVVA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="WIIVKCLVWDLDNTLWRGTVLEDDEVVLTDEIREVITTLDDRGI
LQAVASKNDHDLAWERLERLGVAEYFVLARIGWGPKSQSVREIATELNFAPTITAFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QAEEGQFLEFLVRLTGARQVLEIGTYTGYSTLCLARGLAPGGRVVTCDVMPKWPEVGE
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LYRRGGLIVYDNTLFFGRVADEAYQDPDTVAVRELNAALRDDDKVDLAMLTTADGYTL
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                                                                                                                                                                                                                                                    /db_xref="G1:9280387" /translation="MPNELTGVVALDATFLLGVVALDRT PDEVLAGFPASMFLVLVAVTFLFGIARVNGTVDWLVRVAVRAVGARVGAVVAVFLFGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MANQITLSDTLLAYVRKVSLRDDEVLSRLRAQTAELPGGGVLPV
                                                                                                                                                                                                                                                                                                                                               ALLCATGAASPAAVAIVAPISVAFAVRHRIDPLYAGLMAVNGAAAGSFAPSGILGGIV
                                                                               /note="similar to Rhizobium trifolii MatC; dicarboxylate
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/codon_start=1
/transl_table=11
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/db_xref="G1:9280390"
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/gene="fkb1"
complement(9895. .10995)
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/gene="fkbH"
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/gene="fkbJ"
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/transl_table=11
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/gene="fkbG"
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'gene="fkbF"
                                                /gene="fkbF
                                                                                                                carrier"
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VPLFDRHQNRLRLNKYGEVFRAHALRAISEVSGAEGRITALIDPDFGTVALGFLHSYG
VPLFDRHQNRLLACYTRELAEGTAEBANVDDVRNSRLDLGLTSPRPAGDVVEMTPL
RDEALCLLVPPGHRLARRRKYRTAELADEAVALEVYGLRQITDELCAAGFYDRV
LESTELSTLRALVAAGGGVANAPLTGSPSGPODHAVAVPLDDPQARRTVGVYTLAGGP
RAPVVARFYDYVRSRAHAPHV"
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VIKTERPGSGDLARGYDRTVRGMSSHFVWLNRGKESVQLDVRSPEGNRHLHALVDRAD
VLVQNLAPGAAGRLASATRSSRGATEADHLRTYPATAVPAATADRKAYDLLVQCEAGL
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GYAEYTRYGGTAPARAGSTATIAPYGPFTTROGGIINLGLOBREWASFGCYVLQR
PGLCDDPRFSGNADRYAHRTELAIVSEVGTLTGEELVARLEEASIAYARGETS
SEHPOLIRDRGRWAPPOSPVGALEGLIPPVTFHGEHPRRLGRVPELGEHTESVLAMLAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATDOSSAYLCMNORTOLTADORACHES VENALES VENALES POPERADE POPERADE CATDOSSAYLCMNORTOLTADORACHES VALLES VENASCEWIPERA INHCOKOTTOLTADORACHES VENASCEWIPERA INHCOKOTTOVANOR SOVEREN LAND CONTRIBER VENADOCOSTCANAY FLDS ICSSYWITOPFGLSGSASDPGSLPAPSGLAATGATDTIST TWRPUDGATDYAVHRDGAQITTSATTSYTDTGLRAGTSHTAVAARDADGKAGPLSGA VTAOTTGAATGATACWITAGNYAHVQAGRATTSATGYTAKGSGQNMGLYNFFVTTILKESPF GYFTVANDTCP
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LHFDRHYSAGTTWGKPLVDSTFTLALVTGQSVTDISQHVMANLGWDRVRLPNPVFEGD
TIYSQSEVLNTRESASRPDVGIISVRTIGYNQDGVIVITFERTLMYYRGHGPRFAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                           LGAALLGPAPTAHAAAGLAKPGLTKADLTEVADFGTNPGRLNMYVYRPASLPAEPAVV
FALHGCTQDAQGYADNSGLLSFADRYGFLLVFAETTSSNNANRCFNWFQSSDNRRGQG
EAASTRQMAAHTVSAYGADPQRTYTTGLSAGGAMTSVMLATYPDVFQAGAVVAGLPFG
                              GPAAGQAREALLRAGFPADS EFLWPYHHEVYWDLTQRVYREEFDPGFDGEKEAGTPYC
APGTVPGCDADYDYATRSSGYHAAVERIALTGRIGKPLITIQALSTCCCLPPGLRRVR
AYVRQRPGGRYRYYRIEDGTHTDALVDTFPDRLRPLLPCHRSAFTALESWLTTGHRPP
                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAF86381.1"
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/translation="MOPPPFRGILTPLFPLSSSPPVGSLSRPGRRGVLTRLVAVVALV
      LVTGMSNGGYLVRWQLENHPELYDGGVDWEGTLWRAEGPNLFTFLPAALRDYPTYAAG
                                                                                                                                                                                                                                                                                                                                /product="polyhydroxybutyrate depolymerase"
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                                                                                                                ANHTVVRPAGADQASLLAECRLDG"
complement(2020. .3579)
/gene="fkbu"
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/gene="fkbR2"
complement(3969. 4496)
/gene="fkbR2"
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5601. .6818
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/gene="fkbE"
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ELVVYLEKTFDVTIAGPDLQANFRTVESMVALVHRLRAVDA"
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Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.
1 (bases 1 to 182756)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC007789 182756 bp DNA PLN 03-DEC-1999
Oryza sativa BAC OSJNBa0049B20 genomic sequence, complete sequence.
AC007789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Buell, R., Benito, M.-I., Lin, X., Mason, T.M., Umayam, L., Shea, T.P., Vili, C.Y., Shen, M. and Fraser, C.M.
Oryza sativa BAC OSJNBa0049B20 genomic sequence
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                           46349 TACCICGCCGCCGCCGCCGCCGCCGTCGCCGCTCACCCGGACGCCGCCGAC 46290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46289 GCCGAACTCGCCCACTTCCTGACGGACTCCGGCGGGCGTGCTGGTCACCGACGAAACC 46230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (11-JUN-1999) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA (bases 1 to 182756)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (15-JUN-1999) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (18-JUN-1999) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA 5 (bases 1 to 182756)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 46229 CACCTCGACCAGCGGCCGCACCGACCGACCGTCGTCGTCGTCGGGGCGCG 46171
                                                                                                                                                                                                                                                                                                                                                                                                                 96 ttcatcgccaccgagaaagccgccatggacgccggcctcctccaccctcctcccctcc 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 glcatcctcacccaagacgatttgaagaaaatcgccgcctacaaggccgtcgagtacgtg 215
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 gagtccggcatggtcctcggcctaggcaccggctccaccgccaagcatgccgtcgaccg 274
                                                                                                                                                                                                                                                                                                                                        DB 1; Length 77534;
                                                                                                                                                                                                                                                                                                                                                                                  84; Indels
                                                                                                                                                                                    /note="acyl CoA dehydrogenase"
                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                 16.3%; Score 44.6; 53.1%; Pred. No. 17;
                                                                                                 complement(11245. .12093)
                                                                                                                                             complement(11245. .12093)
/gene="fkbK"
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Robin Buell or Maria-Ines Benito
The Institute for Genomic Research
                                                                                                                                                                                                                            /transl_table=11
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'product="FkbJ"
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Benito, M.-I.
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                                                                                                                                                                                                                                                                                                                           Query Match
16.3%;
Best Local Similarity 53.1%;
Matches 95; Conservative
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Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (available by anonymous ftp from arthur.epu.orl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://ww.cbs.dtu.dk/netpgene/Dsnetpgene.html), searches of the complete sequence against a peptide database and the Arabidopsis and Rice EST databases at TIGR, and the maize EST database at thtp://www.tigr.org/tdb/dst/ar.html). Annotated genes Genbank.(http://www.tigr.org/tdb/dst/ar.html). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database htts. Genes without significant peptide similarity but with EST similarity, that are predicted by more than two gene with similarity are named as 'unknown' proteins. Genes without proteins over most of their length are annotated as thypothetical' proteins. Genes encoding tRNAs are predicted by thomber between that two gene challed the protein sequence that are needing tRNAs are predicted by simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RW/RepeatMasker.html). Regions of exons by GRAIL are annotated as misc features.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .204,660. .775,896. .1020,1264. .1303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="predicted by genscan and genefinder"
complement(join(179, 204,660, 775,896, 1020,1264, 1303,
1587, 2987,3531, 3610,3722, 3766))
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WTLQQSDAGEESVWSLRHRVRVDEIMDHVTYRKTMMPRRVPULALHPKELGYVFFFFO
ITSRNSWMFAVDLVTRIVLECKKYKMPQLPTWYHSSRHVRAWELPHSICRGEDDETDG
TSYNVYMLYFDHVSNLTDELDLNFSRDKADELLSTTGRLFINPRFQELRNATAFPKYL
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RMAAPPREATWVILACVPSVSSSDGDFEAGDHLAFDWRDPPGVSLLTIRQSDSVFVSP
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CHATLRMAYLYPPCSDEYRLLYAGNVGMIRRTAADGDHPIRLLAELQIESGNGIHRAT
LLRYSQELGLGGWASTKVNYPPGRRSWCGDGVIVHAGMLWWVDLSFGLLTCDAFAAKP
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                          e-mail:rbuell@tigr.org or mbenito@tigr.org
BAC clone OSJNBa0049B20 is from Oryza sativa.
The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFVIVKATDAYEASCLMRDFVSHVSMDGSNIVPRVSEPYEYDDD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Oryza sativa"
/cultivar="Nipponbare"
/sub_species="japonica"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="OSJNBa0049B20.2"
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/rpt_family="(CGG)n"
Rockville, MD 20850, USA
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mRNA

gene

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complement(10672..10787)
/note="exon predicted by xgrail, quality good_shadowexon"
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ISSSAMLOGTWPTNSRTLSPSLSSASPTITTQQLCGWNSGAGLFSSSSSGRGRTAMM
ACLDVEMPFLRGIDVNWPAPAGETTTVRGRGGRGAAAARRTRSPARPPPTLRHTLQPA
TTTRTPAVAADLVYRSRGRDGSSSSSSRREKRREKRERRKEMKIRYAADWWAPRALF
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10664. .10857
/note="exon predicted by xgrail, quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IIVCGPTRRSSMAKATAGRRRSRTYVVDTVVLRVKFEFKDCTFAPFD"
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LAGGS 1. 6665

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complement(7469. 7548)
/rpt_family="(CGA)n"
9207. 9483
/note="MITE element Ditto-like"
complement(9758. 9826)
/note="won predicted by xgrail, quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="hypothetical protein"
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5311. .5360
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                                                                                                                  .5308
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gene

CDS

mRNA

mRNA

gene

CDS

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CTTANDESORVETEELLSYGGEDONTCNCGMERLIFEPPPRECALCFKIINSTG
SYYEVENGRDKSSICGRCHHLSSAGARYORRESYSTETDARAWWOODDCRCAMADHO
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PYKSRAILLFQKNEGYDVCLFAMYYOEXGSACPSPRORPHVIATIOSYDFKFKEOYPGEF
SGRALFFFYRJAILGYLDFCKREGEVSCSIWTCPSTKRDDYLYCHPTIGKNESS
IGRARFYROLLYKKAVKEGYVVERWILYDPFLQPTNECKTNISAAMLPYCDNDFWPGEBE
LLEKKDDDTSQKKETQLGRILLRVAKRDDRKGNILDILLVHKLGERLRTMKEDFLMCL
                                          IGHTKBHFSAEVTWHIRKHYGQILPGDAYQNDSSQPSTSGSSSSLSAVWDQTTCSSAMR
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                                                                                                                                                                                161 cctcacccaagacgatttgaagaaaatcgccgcctacaaggccgtcgagtacgtggagtc 220
                                              0; Gaps
Query Match 16.3%; Score 44.6; DB 7; Length 18
Best Local Similarity 53.8%; Pred. No. 14;
Matches 92; Conservative 0; Mismatches 79; Indels
                                                                                                  δλ
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DB 7; Length 182756;

Db 157114 caccagaagacraaccaccarcraccacaacaacaacaararcaaga 157164 221 eggcatggtcctcggcctaggcaccggctccaccgccaagcatgccgtcga 271

Search completed: November 4, 2000, 13:37:55 Job time: 17324 sec

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November 4, 2000, 13:45:16; Search time 320.8 Seconds (without alignments) 320.859 Million cell updates/sec
                                                                                                                                                                                                                         1 cttacattcctttctccacc......gccaagcatgccgtcgaccg 274
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                       480022 seqs, 187831343 residues
                                                                     OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                             IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                              US-09-300-482-311
274
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	DNA encoding ribos Nucleotide sequenc GAL4 DNA binding d Human METH1 relate DNA encoding synth Nelsseria meningit snaB gene encoding M. tuberculosis im Mycobacterium tube M. tuberculosis an M. tuberculosis an M. tuberculosis re Sequence comprisin
SUMMARIES	1 1
£	T87859 A14850 T94500 Z32020 Z87214 Z12317 Q64203 V44403 Z19313 Z19101 Q64201
DB	18 18 20 20 20 19 19 19
% Query Match Length DB	1118 77536 701 38734 1371 771 833 882 882 882 882 882
% Query Match	24.8 16.73 15.77 15.3 15.3 15.3 15.3 15.3 15.3
Score	68 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
Result No.	C C 2 3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

Mycobacterium tube	M. tuberculosis im	Mycobacterium tube			Sordbin biologic		The cinetinopinting ga	THEODIES CHIEFT	M. Cuberculosis im	Mycobacterium tube	M. tuberculosis an		Marze 182 CDNA nuc	. venezuelae d	COULTY UUZ IFOM CO	. Venezuelae	S. venezuelae deso	Streptococcus pneu	Neisseria meningit	Neisseria gonorrho	Rice inositol 1,3,	Sequence encoding	Nucleotide seguenc	Streptomyces frad:	ANGO PENCHAMINA	Musloctide comme		wastedine sequenc	Nucleoride seduenc	Nucleotide sequenc	Nucleotide sequenc	Miedt beta-caroten Entire amylase den	
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ALIGNMENTS

RESULT T87859	JLT 1 859	
£	87859	Standard; cDNA: 1118 BP
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X X	T87859;	
ä	21-APR-1998	first ontre:
×		(A TIP CONCT)
DE	DNA encoding	DNA encoding ribose-5-phosphate isomerase
×	•	
X X	Ribose-5-phos	Ribose-5-phosphate isomerase; screen; inhibitor; herbicidal agent;
×	. 22	
sox	Spinacia oleracea.	icea.
E	Kev	[Ocation /One] if ion
FT	CDS	25894
FT		/*tag= a
FT		+
XX		
ΡN	WO9737028-A2.	
××		
Z X	09-OCT-1997.	
ΡF	26-MAR-1997;	97WO-EP01539.
XX	30-MAD-1006	
X	1066T WWH 67	30DE-4017/7.
PA XX	(BADI) BASF AG.	G.
I M	Kellermann J, William M;	Lerchl J, Schmidt R, Schnarrenberger C;
DR.	WPI; 1997-503113/46.	13/46.
DR	P-PSDB; W27505	

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                                                                       The present sequence represents DNA encoding a novel spinach ribose-5-phosphate isomerase. The invention relates to a protein with ribose-5-phosphate isomerase activity, comprising at least 100 residues of a 289 residue spinach manno sequence, preferably residues 50-239. Novel phosphate isomerase inhibitors can be identified by incubating potential inhibitors with the enzyme and determining the ribose-5-phosphate isomerase activity. These inhibitors can be used as herbicidal agents.
                                                                                                                                                                                                                                                                                                                195 tacaaggeegtegagtaegtggagteeggeatggteeteggeetaggeaeeggeteeaee 254
                                                                                                                                                                                                                                                                                                                             223 gaaaaagccgtcgactccgtcaaatccggcatggttctcggtctcggtaaccggaagtact 282
                                                                                                                                                                                                                                                               135 etceaececteeteececteegteateeteaeceaagaegatttgaagaaaategeegee 194
                                                                                                                                                                                                                                                                                       163 ctctctctcccccaacaccagtcttaactcaagacgatctcaagaaactcgccgcc 222
                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FK-520; polyketide synthase; PKS; gene cluster; immunosuppressant; Streptomyces hygroscopicus var. ascomyceticus; immunophilin; FK-506 binding protein; polyketide compound; transplant rejection; graft-versus-host disease; uveitis; alopecia universalis; autoimmune chronic active hepatitis; inflammatory bowel disease; multiple sclerosis; primary biliary cirrhosis; scleroderma; neurite outgrowth; nerve regrowth; parkinson's disease; Alzheimer's disease; stroke; traumatic spinal cord; brain injury; peripheral neuropathy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleotide sequence of the FK-520 biosynthetic gene cluster.
                                                                                                                                                                                                             24.8%; Score 68; DB 18; Length 1118; 67.9%; Pred. No. 1.7e-08; tive 0; Mismatches 45; Indels
           Spinach ribose-5-phosphate isomerase - useful to screen for inhibitors, i.e. herbicidal agents
                                                                                                                                                                          Sequence 1118 BP; 261 A; 264 C; 258 G; 335 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "fkbR2 gene"
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/note= "fkbv gene"
3969..4496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "fkbW gene"
                                                    Claim 5; Figure 2; 22pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A14651 standard; DNA; 77536 BP
                                                                                                                                                                                                                                                                                                                                                                     255 gccaagcatgccgtcgaccg 274
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/*.4496
/*tag= ~
'no+
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                                                                                                                                                                                                                                Best Local Similarity 67.99
Matches 95; Conservative
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/*tag= ad
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complement (13452..13662)
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complement (11244..12092)
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/*tag= f
/note= "fkbF gene"
8156..8824
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'note= "ACP6"
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/note= "ER6"
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/note= "KS6"
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/note= "KR5"
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complement (43777..44629)
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16754..47788
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complement (31018..32185)
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/note= "DH2 (inactive)"
complement (35749, 37144)
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complement (41842..43093)
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complement (29092..29740)
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complement (40609..41842)
                                                                                                                                                                                                                             complement (28750..28960)
                                                                                                                                                                                                                                                                                           complement (37145..38296)
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/note= "fkbo gene"
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52275..71465
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52362..53576
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note= "KR2"
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/note= "AT2"
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/note= "KS7"
53577..54716
/*tag= bb
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54717..55871
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/note= "DH7"
56019..56819
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/note=
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          misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                              156 gicatoctcacccaagacgattigaagaaaatcgccgcctacaaggccgicgagtacgig 215
                                                                                                                                                                                                                                                          16.3%; Score 44.6; DB 21; Length 77536;
53.1%; Pred. No. 0.029;
tive 0; Mismatches 84; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAL4; GAL4 DNA-binding domain; gene expression; plant;
HSV VP16 transcriptional activation domain; plant enhancer sequence;
glucuronidase; green fluorescent protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAL4 DNA binding domain fused to transcription activating VP16 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= c
/note= "HSV VP16 transcriptional activation domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= b
/note= "GAL4 DNA-binding domain"
459..701
/*tag= bc
/*tag= bc
/*tag= bd
/*tag= bd
/*note= "RK7"
57710.57920
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Chimeric - Human herpes simplex virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T94500 standard; DNA; 701 BP.
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                                                                                                                                                                                                                                                                                       95; Conservative
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1..458
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                                                                                                                                                                                                                                                                           Sest Local Similarity
                            misc_feature
                                                                     misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-AUG-1997.
                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T94500;
                                                                                                                                                                                                                                                                                     Matches
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Ruben SM;

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Human METH1 related EST AL021529.
                                    Example 1; Fig 1; 40pp; English.
                                                                                                                                                                                                   232020 standard; DNA; 38734 BP
                                                                                                                                                                                                                    10-JAN-2000 (first entry)
                                                                                                                         Best Local Similarity 59.33
Matches 73; Conservative
   WPI; 1997-425039/39.
        P-PSDB; W14300.
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                                                                                                                                                                                                                                                                                  New isolated metalloprotease thrombospondin polypeptides, useful for treating hyperproliferative disorders, cancers or autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 caccgagaaagccgccatggacgccggcctcctccaccctcctccccctccgtcatct 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232000 and 232001 encode, and Y49501 and Y49502 represent, human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 53.2%; Pred. No. 0.063;
Matches 91; Conservative 0; Mismatches 80; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 38734 BP; 6142 A; 13140 C; 13585 G; 5867 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 296-321; 457pp; English.
                                                                                                                                                              Hastings GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10..1362
                            (IRUE/) IRUELA-ARISPE L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium botulinum. Synthetic.
                                                               (HAST/) HASTINGS G A. (RUBE/) RUBEN S M.
                                                                                                                                                                                                                                    WPI; 1999-590684/50.
                                                                                                                                                                     Iruela-Arispe L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a chimeric gene, encoding the 5' portion of the GAL4 DNA-binding domain and encoding in the 3' portion the transcriptional activation domain from HSV WP16. The A/T content of the GAL4 nuclectide sequence in this gene is less than 40% (contrasting with 59% in yeast). Reducing the A/T content optimises expression in plants. Constructs containing the A/T content optimises expression in plants. Constructs containing this nucleic acid can be used to express genes in a known pattern (temporal or spatial) in a plant, and to co-ordinate expression of several genes and, as traps, to isolate plant enhancer sequences. Particular applications are in studies of metabolic pathways and to modulate synthesis of e.g. dyes or lipids. Constructs containing sequences encoding the altered GAL4 DNA binding domain may include a reporter gene linked to a GAL4 responsive upstream activating sequence, particularly one encoding glucuronidase or green fluorescent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; METH1; METH2; anti-anglogenic; metalloprotease thrombospondin; cancer; diagnosis; hyperproliferative disorder; autoimmune disease; anglogenesis inhibitor; abnormal wound healing; inflammation; rheumatoid arthritis; psoriasis; endometrial bleeding disorder; diabetic retinopathy; macula degeneration; haemangioma; detection; arterial-venous malformation; immune deficiency; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 atggacgccggcctcctccaccctcctcccctccgtcatcctcacccaagacgattg 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 aagaaaatcgccgcctacaaggccgtcgagtacgtggagtccggcatggtcctcggccta 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 atggactccctccaggacatcaaagccctgctcaccggcctcttcgtccaggacaacgtg 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                     DNA encoding GAL4 DNA binding domain optimised for plant expression - used for expressing genes in known pattern, for co-ordinating expression of several genes and for trapping plant enhancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43; DB 18; Length 701; Pred. No. 0.028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50; Indels
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59.3%;
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Gaps

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6542 ccccatcgtcgaactggaccgcccggtctcggtcatgcgcgtcggggagaaggacggcgg 6601
164 cacccaagacgatttgaagaaaatcgccgcctacaaggccgtcgagtacgtggagtccgg 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Botulinum neurotoxin; heavy chain; BONT; serotype C;
C-terminal fragment; Venezuelan equine encephalitis virus replicon;
VEE; botulism; vaccine; diagnosis; drug screening; ds.
                                                                                                                                                                                                                                                        6602 cytecaccycytecacygecgecetteytecycygayegegegacy 6652
                                                                                                                                                                                           224 catggtcctcggcctaggcaccggctccaccgccaagcatgccgtcgaccg 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding synthetic BoNT serotype C (BoNTC) Hc fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                            Z87214 standard; DNA; 1371 BP
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Homo sapiens WO9937660-A1 22-JAN-1999; 23-JAN-1998; 28-AUG-1998;

29-JUL-1999.

212317/c ID 212317 standard; DNA; 771 BP.

Z12317;

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/product= "Synthetic botulinum neurotoxin serotype C (BoNTC) heavy chain C-terminal fragment (Hc)"
                                                                                                                                                  Novel Botulinum neurotoxin vaccine comprising a fragment from botulinum toxin serotypes A-G, is used for inducing an immune response against
                                                                                                              Pushko P, Smith JF, Parker M, Dertzbaugh MT,
                                                                                              (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
                                                                                                                                                                                Disclosure; Page 41-42; 54pp; English.
                                                            99WO-US15570.
                                                                                   99US-0133870.
                                                                         98US-0092416
                                                                                                                             WPI; 2000-160827/14
                                                                                                                                     P-PSDB; Y77136.
                              WO200002524-A2
                                                           09-JUL-1999;
                                                                          10-JUL-1998;
                                                                                 12-MAY-1999;
                                            20-JAN-2000
                                                                                                                                                                  botulinum -
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The invention relates to novel vaccines that induce a protective immune response against botulinum neurocoxin (BONY) serotypes A, B, C, D, E, F and G (BONYA-BONYG). The vaccine of the invention is novel recombinant from G (BONYA-BONYG). The vaccine of the invention is novel recombinant fragment comprising a vector, and at least one nucleic acid fragment comprising a vector, and at least one nucleic acid fragment comprising a C-terminal heavy chain fragment (Ho) from BONY venctor selectives A-G. In preferred embodiments of the invention, the vector is a vector results in the production of large amounts of a protein encoded by vector results in the production of large amounts of a protein encoded by vaccines against botulism. The constructs are used to produce tools for the diagnosis of botulism. The transformed host cells can be used a manifest the effectiveness of drugs and agents which inhibit toxin effects. The vaccine currently used against botulism is dangerous of and expensive to produce, and contains formalin, which is very painful the recipient. Also, the vaccine is incomplete, in that only 5 of the the recipient. Also, the vaccine is incomplete, in that only 5 of the recipients. Botulism is easily purified, and available in large quantities. It is also expressed in the lymph nodes for a better immune response. Sequences 287212-287217 represent synthetic DNA very expensive to recombinate of the present invention. These very sequences encoding BONT He fragments used in the present invention. These
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1371 BP; 397 A; 416 C; 265 G; 293 T; 0 other;
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ö 61 cetttaacattaacatggccattccctacccccatttcatcgccacgagaaagccgcca 120 121 tggacgccggcctcctccaccctcctccctccgtcatcctcacccaagacgatttga 180 734 aggacatcaacatcctgttcaactccttgcagtacaccaacgtcgtcaaggactactggg 793 181 agaaaatcgccgcctacaaggccgtcgagtacgtggagtccggcatggtcctcggcctag 240 794 gtaacgacctgagatacaacaaggagtactacatggtcaacatcgactacttgaacagat 853 Gaps ó 15.5%; Score 42.6; DB 21; Length 1371; 50.2%; Pred. No. 0.04; Pred. No. 0.04; 0; Mismatches 104; Indels 241 gcaccggctccaccgccaagcatgccgtc 269 854 acatgtacgccaactccagacagatcgtc 882 Best Local Similarity 50.29 Matches 105; Conservative Query Match δ ŏ g õ g δ

RESULT

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                                                                            Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
treatment; Neisseria infection; meningitis; septicaemia; gonorrhea; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequences 211972-212358 represent open reading frames (OREs) of Neisseria meningitidis and N. gonorrhoeae which encode antigenic proteins (see Y38499-Y38944). The antigenic proteins, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 acccaagacgatttgaagaaaatcgccgcctacaaggccgtcgagtacgtggagtccggc 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                Proteins from Neisseria meningitidis and N. gonorrhoeae useful for diagnosis, treatment and prevention of infection
                                                                                                                                                                                                                                                                                                                                                              Grandi G, Masignani V, Pizza M, Rappuoli R, Scarlato V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.3%; Score 42; DB 20; Length 771; 61.7%; Pred. No. 0.05; tive 0; Mismatches 41; Indels
                                                  Neisseria meningitidis strain A complete ORF122 sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as hybridisation probes and antisense reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 9; Page 440; 524pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q64203 standard; cDNA; 833 BP
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97GB-0026147.
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                                                                                                                                                                                                                                                                                                             98GB-0000759
                        08-OCT-1999 (first entry)
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                                                                                                                     Neisseria meningitidis.
                                                                                                                                                                                                                                            97GB
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                                                                                                                                                                                                                                                                                                                                     (CHIR-) CHIRON SPA.
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                                                                                                                                             W09924578-A2.
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14-JAN-1998;
                                                                                                                                                                         20-MAY-1999,
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                                                                                                                                                                                                                                                       14-NOV-1997;
18-NOV-1997;
                                                                                                                                                                                                                                                                                  27-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 ctcacccaagacgatttgaagaaaatcgccgcctacaaggccgtcgagtacgtggagtcc 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 cagggccggttcgagacgacgacgctgaccgccgcgctggccgccgtcaccgagcacatc 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The snaB gene product is involved in the biosynthesis of streptogramins, antiblotics active against Gram-positive bacteria. The identification of the sequences encoding the enzymes involved in the biosynthetic pathway means that they can be isolated and manipulated. Mutant microorganisms in which a step in the streptogramin biosynthetic pathway is blocked can be cultured to produce streptogramin intermediates, which may later be converted to streptogramin derivatives. Recombinant cells may also be used for the bioconversion of streptogramins from one form to another or for the production of hybrid antibiotics.
                                 Antibiotic; streptogramin; snaA; snaB; snaC; biosynthesis; enzyme;
biosynthetic pathway; Streptomyces pristinaespiralis; ds.
snaB gene encoding enzyme in streptogramin biosynthetic pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 ggcatggtcctcggcctaggcaccggctccaccgccaagcatgccgtcgaccg 274
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15.3%; Score 41.8; DB 15; Length 833;
Best Local Similarity 52.6%; Pred. No. 0.057;
Matches 91; Conservative 0; Mismatches 82; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA involved in streptogramin antibiotic biosynthesis - for prodn. or bio-conversion of streptogramin(s) or prodn. of streptogramin intermediates, derivs. or hybrid antibiotics
                                                                                                                                                                                                                                                                                                                                                                                        Crouzet J, Jacques N, Lacroix P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 833 BP; 106 A; 395 C; 250 G; 82 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M. tuberculosis immunogenic polypeptide TbH-29 DNA.
                                                                                                                              Location/Qualifiers
1..834
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                       (RHON ) RHONE POULENC RORER SA.
                                                                                         Streptomyces pristinaespiralis
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                                                                                                                                                                                                                                                                                                                                                                                              Blanche F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-128286/16.
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                                                                                                                                                                                                          FR2696189-A
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                                                                                                                                                                                                                                                                                                                                                                                              Blanc V,
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This sequence encodes an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               508 egecgecaacgaegecgecgaecaegecggtgaecaegecaacgaecgtegececga 567
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     Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB; vaccine; pharmaceutical; infection; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                             Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - use to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    448 egcegecegaccaegecegtegaccaegecegeceaecgacegecegaceaegecegetegacea
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Best Local Similarity 51.9%; Pred. No. 0.058;
Matches 94; Conservative 0; Mismatches 87; Indels 0
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                                                                                                                                                                                                                                                                      Lodes MJ;
                                                                                                                                                                                                                                                                      DC, Houghton R, Lodes M.
Twardzik DR, Vedvick TS;
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                                                                                                                                                        97WO-US18293.
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96US-0730510.
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                                                           Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                      Dillon DC,
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Reed SG, Skeiky YAW,
                                                                                                                                                                                                                                                                                                                      WPI; 1998-261042/23.
                                                                                                                                                                                                                                        (CORI-) CORIXA CORP.
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                                                                                                                                                          07-OCT-1997;
                                                                                             W09816646-A2
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152 ctccgtcatcctcacccaagacgatttgaagaaaatcgccgcctacaaggccgtcgagta 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This DNA sequence codes for an antigenic portion (see W64359) of Mycobacterium tuberculosis antigen TbH-29. It was isolated from a M. tuberculosis strain H37kv genomic library. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see W64291-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or the contact of the diagnosis of the contact of the diagnosis of the contact of the diagnosis of the contact of the diagnosis of the contact of the diagnosis of the contact of the diagnosis of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 882 BP; 141 A; 355 C; 277 G; 109 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DC, Houghton R, Lodes MJ;
Twardzik DR, Vedvick TS;
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                                   Location/Qualifiers
                                                                                                                                                                                                                                                         97WO-US18214.
                                                                                                                                                                                                                                                                                                                 97US-0818111.
96US-0729622.
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                                                                                           /*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Campos-Neto A,
                                                                                                                                       WO9816645-A2
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                                                                                                                                                                                               23-APR-1998
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The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's. DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T. B or natural killer cells and/or macrophages in tuberculosis immune subjects. 219249 to 219460 and v39083 to v39225 are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 coatttoatcgccaccgagaaagccgccatggacgccggcctcctccaccctcctccc 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antigens from Mycobacterium tuberculosis useful in diagnostic
skin tests and protective or therapeutic vaccines or compositions
                                                  Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection; immune response; skin test; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.3%; Score 41.8; DB 20; Length 882; Illarity 51.9%; Pred. No. 0.058; Conservative 0; Mismatches 87; Indels 0.
                                                                                                                                                                                                                                                                                                                                                     Campos-Neto A, Dillon DC, Hendrickson RC, Houghton R;
Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 882 BP; 141 A; 355 C; 277 G; 109 T; 0 other;
                M. tuberculosis antigen TbH-29 DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 141; 299pp; English.
                                                                                                                                                                                                                                  99WO-US03268
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                                                                                                                                                                                                                                                                   98US-0072967
                                                                                                                        Mycobacterium tuberculosis,
                                                                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-527409/44.
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les 94; Conserv
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                                                                                                                                                          WO9942076-A2.
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                                                                                                                                                                                             26-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
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biosynthetic pathway; Streptomyces pristinaespiralis; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention describes novel recombinant antigens and their encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152 ctccgtcatcctcacccaagacgatttgaagaaaatcgccgcctacaaggccgtcgagta 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cgtggagtccggcatggtcctcggcctaggcaccggctccaccgccaagcatgccgtcga 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 ccatttcatcgccaccgagaaagccgccatggacgccggcctcctccaccctcctcctcct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       388 ccatccccaccgcaccgccgacgacgccggtgaccacgtcggcgacgacgccgccgacca 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibiotic; streptogramin; snaA; snaB; snaC; biosynthesis; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      448 egeegeegaecaegeeggtgaecaegeegeeaaegaegeegeegaeeaegeeggtgaeea
                                                                        Antigen; diagnosis; detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
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Best Local Similarity 51.9%; Pred. No. 0.058;
Matches 94; Conservative 0; Mismatches 87; Indels 0
                                                                                                                                                                                                                                                                                                                                 co A, Dillon DC, Hendrickson RC, Houghton R;
Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence comprising the snaA, snaB and snaC gene cluster.
                                          M. tuberculosis recombinant antigen DNA encoding TbH-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 882 BP; 141 A; 355 C; 277 G; 109 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 186; 323pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q64201 standard; cDNA; 5392 BP
                                                                                                                                                                                                                                                       98US-0072596
                                                                                                                                                                                                                        99WO-US03265
                                                                                                                                                                                                                                                                      98US-0024753
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                                                                                                                             Mycobacterium tuberculosis.
               (first entry)
                                                                                             vaccine; immunity; ss.
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-527416/44.
P-PSDB; Y39013.
                                                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                        Campos-Neto A,
                                                                                                                                                             WO9942118-A2.
                                                                                                                                                                                                                                                        05-MAY-1998;
                                                                                                                                                                                                                                                                         18-FEB-1998;
                                                                                                                                                                                                                          17-FEB-1999;
               05-NOV-1999
                                                                                                                                                                                          26-AUG-1999
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2833 cagggccggttcgagacgacgacgctgaccgccgccgctggccgccgtcaccgagcacatc 2892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 ctcacccaagacgatttgaagaaaatcgccgcctacaaggccgtcgagtacgtggagtcc 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 gecaecgagaaageegecatggaegeegeeteeteeaeeeeteeteeteegteate 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence comprises the snah, snaB and snac genes which are involved in the biosynthesis of streptogramins, antibiotics active against Gram-positive bacteria. The identification of the sequences encoding the enzymes involved in the biosynthetic pathway means that they can be isolated and manipulated. Mutant microorganisms in which a step in the streptogramin biosynthetic pathway is blocked can be cultured to produce streptogramin intermediates, which may later be converted to streptogramin derivatives. Recombinant cells may also be used for the bioconversion of streptogramins from one form to another or for the production of hybrid antibiotics.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2893 ggcctgatcaccgccccgctcccggccgaccaggcccctaccacgtgtcccg 2945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 5392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA involved in streptogramin antibiotic biosynthesis - for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prodn. or bio-conversion of streptogramin(s) or prodn. of streptogramin intermediates, derivs. or hybrid antiblotics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5392 BP; 811 A; 2161 C; 1671 G; 749 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                   Crouzet J, Jacques N, Lacroix P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.3%; Score 41.8; DB 15;
52.6%; Pred. No. 0.083;
tive 0; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 44-47; 83pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             skin testing; M.tuberculosis; ss.
Streptomyces pristinaespiralis.
                                                                                                                                                                                                                                                                                                           (RHON ) RHONE POULENC RORER SA
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T91500/c
ID T91500 standard; DNA; 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                          Thibaut D, Zagorec M;
                                                                                                                                                                                                                                                                                                                                                                             Blanche F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1994-128286/16.
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                                                                                                                                                                                      25-SEP-1992;
                                                                                                                                                                                                                                                    25-SEP-1992;
                                                                 FR2696189-A
                                                                                                                           01-APR-1994
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                                                                                                                                                                                                                                                                                                                                                          immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence encodes a specifically claimed M.tuberculosis antigen, TDM-7. The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins plus ESAT-6, are useful in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         occocatticategecacegagaaageegecatggaegeegeeteeteeaceeteete 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228 GGCCTGGCCACCTTACCGCGTTGCCACCGAAGCCGCCGTCCGGGGGCGTTGCCTCCGC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 ccctccgtcatcctcacccaagacgatttgaagaaaatcgccgcctacaaggccgtcga 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 cacceccececceccaagaccecerreccecceregagecececcarreccecer 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209 gtacgtggagtccggcatggtcctcggcctaggcaccggctccaccgccaagcatgccgt 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                         New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 GCCCACCGAGGCCGCCCTGGCCGGCACCGGCAAAAAACACGCCGTCGCCGCCCCGGCCCC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
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                                                                                                                                                                                                                                                                                                                                               new immunogenic polypeptide has been developed comprising an
                                                                                                                                                                                      Skeiky YAW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              n 15.2%; Score 41.6; DB 18; Length 290; Similarity 51.6%; Pred. No. 0.052; 95; Conservative 0; Mismatches 89; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis antigen TbM-7 encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 290 BP; 30 A; 83 C; 142 G; 33 T; 2 other;
                                                                                                                                                                                      Reed SG,
                                                                                                                                                                                  Dillon DC, Houghton R,
                                                                                                                                                                                                                                                                                                               Claim 4; Page 78; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     skin testing; M.tuberculosis; ss.
                                                         96US-0680574.
95US-0523436.
95US-0533634.
96US-0620874.
                               96WO-US14674.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95; Conservative
                                                                                                                                                                                              Twardzik DR, Vedvick TH;
                                                                                                                                                  (CORI-) CORIXA CORP.
                                                                                                                                                                                                                           WPI; 1997-192903/17
                                                                                                                                                                                Campos-neto A,
                                                                                                                                                                                                                                                                                         or diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 cgac 272
                            30-AUG-1996;
                                                         12-JUL-1996;
                                                                                                                     05-JUN-1996;
                                                                         01-SEP-1995;
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13-MAR-1997
                                                                                                       22-MAR-1996
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                                                                                         22-SEP-1995
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Best Local S
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W09709429-A2

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A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence encodes a specifically claimed M.tuberculosis antigen, TBM-7. The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89 occocatticatogocacogagaaagoogocatggacgooggootootocacootooto 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209 gtacgtggagtccggcatggtcctcggcctaggcaccggctccaccgccaagcatgccgt 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 ccctccgtcatcctcacccaagacgatttgaagaaaatcgccgcctacaaggccgtcga 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 cacceccedececeaagacceceargececegegegegececeargagececeargecec 109
                                                                                                                                                                                                                                                                                                  New immunogenic polypeptide(s) from soluble M. tuberculosis antigens - useful for diagnosis of M. tuberculosis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 deceacedadecedeceradecedecedecaradadecerearedecedecede 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB; vaccine; pharmaceutical; infection; diagnosis; ss.
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                                                                                                                                                                                                                      Houghton R, Reed SG, Skeiky YAW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.2%; Score 41.6; DB 18; Length 290; 51.6%; Pred. No. 0.052; tive 0; Mismatches 89; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 290 BP; 30 A; 83 C; 142 G; 33 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M. tuberculosis immunogenic polypeptide TbM-7 DNA
                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 82-83; 190pp; English.
                                                                               96US-0680573.
95US-0523435.
95US-0532136.
96US-0620280.
                                                 96WO-US14675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V64483 standard; DNA; 290 BP.
                                                                                                                                                   96US-0658800
                                                                                                                                                                                                                   Dillon DC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 15.2%
Best Local Similarity 51.6%
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JAN-1999 (first entry)
                                                                                                                                                                                                                                    Twardzik DR, Vedvick TH;
                                                                                                                                                                                 (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                  WPI; 1997-192904/17.
                                                                                                                                                                                                                 Campos-neto A,
                                                                            12-JUL-1996;
01-SEP-1995;
22-SEP-1995;
22-MAR-1996;
05-JUN-1996;
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                                               30-AUG-1996;
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              13-MAR-1997
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WO9816646-A2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 gtacgtggagtccggcatggtcctcggcctaggcaccggctccaccgccaagcatgccgt 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenic\ Mycobacterium\ tuberculosis\ polypeptide(s)\ and\ DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 15.2%; Score 41.6; DB 19; Length 290; Best Local Similarity 51.6%; Pred. No. 0.052; Matches 95; Conservative 0; Mismatches 89; Indels 0;
                                                                                                                                                                          DC, Houghton R, Lodes MJ;
Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 290 BP; 30 A; 83 C; 142 G; 33 T; 2 other;
                                                                                                                                                                                                                                                                                                                             Claim 4; Page 84-85; 230pp; English.
                                                              97WO-US18293.
                                                                                           97US-0818112.
96US-0730510.
                                                                                                                                                                            Campos-Neto A, Dillon DC,
                                                                                                                                                                                             Reed SG, Skeiky YAW,
                                                                                                                                               (CORI-) CORIXA CORP.
                                                                                                                                                                                                                            WPI; 1998-261042/23.
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Search completed: November 4, 2000, 13:45:31 Job time: 16458 sec

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November 4, 2000, 13:33:58 ; Search time 189.35 Seconds (without alignments) 218.855 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                               262060 seqs, 75620727 residues
                                                                    OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                         IDENTITY_NUC Gaport 1.0
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                  Sequence:
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Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 9, Appli Sequence 2, Appli Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Appli Appli Appli Appl Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Sequence 1, A Sequence 1, A Sequence 1, A Sequence 1, Sequence 1, Sequence 21, Sequence 21, Sequence 14, Sequence 17, Sequence 7, Description Sequence 1, Patent No. Sequence 7, Sequence 3 Sequence 6 Sequence 6 Sequence 6 Sequence Sequence Sequence Sequence US-08-440-856A-2 US-08-440-856A-2 US-08-510-646B-3 US-08-403-852D-1 US-08-510-646B-1 US-08-510-646B-1 US-08-310-878-21 US-08-32-468-1 US-08-32-463-14 US-08-08-232-463-14 US-08-08-232-463-14 US-08-08-232-463-14 US-08-08-232-463-14 US-08-08-232-463-14 US-08-08-232-463-14 US-08-08-232-463-14 US-08-08-232-463-14 US-08-08-232-463-14 US-08-272-882D-1 5244792-1 US-08-804-227C-7 US-08-304-198-1 US-08-387-942C-1 US-09-013-067A-6 US-09-013-067A-7 US-09-013-067A-7 US-08-532-547-6 US-08-532-547-6 US-08-363-255-1 US-08-363-255-1 US-08-440-856A-9 SUMMARIES Query Match Length DB 5392 5392 1236 5970 2064 7218 2943 1910 2261 3472 44377 12588 756 1897 1897 Score 41.8 40.4 40.4 Ş. Result

Sequence 6, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli	seduence 14, Appl
3 US-08-403-852D-6 5 US-08-510-646B-6 2 US-07-642-7340-3 5 US-08-439-009A-3 5 US-08-025-691-2 3 US-08-025-691-2 1 US-09-190-982-2 1 US-08-125-468-1 3 US-08-248-33-1 2 US-08-248-33-1 2 US-08-174-745A-1 3 US-08-174-745A-1 3 US-08-195-947-1 3 US-08-433-885-1 4 US-08-433-885-1 5 US-08-433-885-1 5 US-08-433-885-1 5 US-08-433-885-1 5 US-08-433-885-1 5 US-08-433-885-1 5 US-08-433-885-1 5 US-08-433-885-1 5 US-08-433-885-1 7 US-08-433-885-1 5 US-08-433-885-1 5 US-08-433-885-1 7 US-08-433-885-1 7 US-08-433-885-1	1
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ALIGNMENTS

RESULT 1
FALCHT NO. 5/50873; GENERAL INFORMATION:
ORI
TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
STREET: 2000 DENNSVIVANTA AVER 3
CITY: WASHINGTON
; STATE: D.C.
RY
; ZIP: 20037
READABLE FORM
MEDIUM TYPE: Floppy disk
COMPOSITION COMPOSITION OF COMPOSITION COM
CURRENT APPLICATION NAME.
APPLICATION NUMBER: 115 YOR / AAA
-MAY
CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLMAN, ROBERT A.
KEFERENCE/DOCKET NUMBER: 05463-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1517
TELEFAX: (202) 887-0763
THE CHAPTION FOR SEQ 1D NO: 9:
LENGTH: 1988 back vaive
TYPE: nucleic acid
STRANDEDNESS: Doth
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Match 16.9%; Score 46.
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US-08-403-852D-3
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                              US-08-403-852D-3
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                                                                                                                                                                                             APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 cattaacatggccattccctacccccatttcatcgccaccgagaaagccgccatggacgc 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                  666 TCTCCGTCGCCAGCGTCGCSGSCGTGCTSGGCGGCCTCGGCCCGCACGCCTACACCGCCT 725
                                                                                                          217 agtocggcatggtcctcggcctaggcaccggctccaccgccaagcatgccgtcgaccg 274
                                                                                                                             786 TCGSGTCAACTGCRTCTCSCCTTGGCGTCGCCACSCCSATGCTCATCAACGCCTG 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.2%; Pred. No. 0.018;
Matches 104; Conservative 0; Mismatches 103; Indels 0
                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: DELLAPORTA, STEPHEN L.
TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05463-20001.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/440,856A FILING DATE: 15-MAY-1995 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVE. N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248 ctccaccgccaagcatgccgtcgaccg 274
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                                                                                                                                                                                                                                        Sequence 2, Application US/08440856A Patent No. 5750873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: MILLMAN, ROBERT A. 217
REGISTRATION NUMBER: 36,217
REPERENCE/DOCKET NUMBER: 054
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 887-0763
TELEX: 706141
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1187 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFHONE: (202) 887-1517
TELEFAX: (202) 887-0763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Blosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 gecacegagaaageegecatggaegeeggeeteetecaceeteeteeteegteate 161
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                                                                                                                                                                                                                                                                                                                                                                   E: Finnegan, Henderson, Farabow, Garrett & Dunner
1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Meyers, Kenneth J. REGISTRATION NUMBER: 25,146 REFERENCE/DOCKET NUMBER: 03806.0054-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCI/FR 93/00923
FILING DATE: 25-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/403,852D FILING DATE: 10-MAY-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM KAREN FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: S.pristinaespiralis
Sequence 3, Application US/08403852D Patent No. 5891695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                       Debussche, Laurent
                                                                                                                                    Nathalie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202) 408-4000
TELEPAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                           Patricia
                                                                                                                                                                                                     Zagorec, Monique
                                                                       Blanc, Veronique
                                                                                          Blanche, Francis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 52.6
Matches 91; Conservative
                                                                                                                                                                                Thibaut, Denis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        833 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 25-SEP-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                               APPLICANT: Crouzet, APPLICANT: Jacques,
                                                                                                                                                             Lacroix,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1..833
                                                                                                                                                                                                                                                                                                                                                                                                                          Washington
                                              GENERAL INFORMATION:
APPLICANT: Blanc,
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APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
222 ggcatggtcctcggcctaggcaccggctccaccgccaagcatgccgtcgaccg 274
                                                                                                   202 GGCTGATCACGCCCCGCTCCCGGCCGACCAGGCCCCTACCACGTGTCCCG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/510,646B
FILING DATE: 03-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-01000
TELECOMMUNICATION INFORMATION:
TELEFRAN: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION 1473.

APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                            Sequence 3, Application US/08510646B
; Patent No. 6077699
; GENERAL INFORMATION;
APPLICANT: Blanc, Veronique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: S.pristinaespiralis
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
                                                                                                                                                                                                                                                                              Blanc, Veronique
Blanche, Francis
Crouzet, Joel
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Thibaut, Denis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Meyers, Kenneth J. REGISTRATION NUMBER: 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 833 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
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MOLECULE TYPE: CDNA
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                                                                                                                                                                     RESULT 4
US-08-510-646B-3
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APPLICANT: Thibaut, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-lagard, Valerie
APPLICANT: De Crecy-lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Blosynthesis of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides and Their Use
                                                                                       162 ctcacccaagacgatttgaagaaaatcgccgcctacaaggccgtcgagtacgtggagtcc 221
                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                         222 ggcatggtcctcggcctaggcaccggctccaccgccaagcatgccgtcgaccg 274
                                                                                                                                                                                                                                                                                            202 Geceráardacedececerecedecedadeseceraceadereced 254
        15.3%; Score 41.8; DB 5; Length 833; 52.6%; Pred. No. 0.02; tive 0; Mismatches 82; Indels
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STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852D
FILING DATE: 10-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03806.0054-00000
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APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
FILOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08403852D
Patent No. 5891695
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 036
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jacques, Nathalie
Lacroix, Patricia
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Blanche, Francis
Crouzet, Joel
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Query Match
Best Local Similarity 52.6%
Matches 91; Conservative
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 5392 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Meyers, Kenneth J. REGISTRATION NUMBER: 25,
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ADDRESSEE: Finnegan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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US-08-403-852D-1
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APPLICANT: Thibaut, Denis
APPLICANT: Thibaut, Denis
APPLICANT: Zagorc, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 45
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                                                                                                                                                                                                                           2833 CAGGGCCGGTTCGAGACGACGCTGACCGCCGCGCTGGCCGCCGTCACCGACACATC 2892
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                                                                                                                               Query Match 15.3%; Score 41.8; DB 3; Length 5392; Best Local Similarity 52.6%; Pred. No. 0.031; Matches 91; Conservative 0; Mismatches 82; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Finnegan, Henderson, Farabow, Garrett & Dunner 1300 I Street, N.W., Suite 700
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,6468
FILING DATE: 03.AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION: 435
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REGISTRATION NUMBER: 25,146
REGISTRATION NUMBER: 25,146
REFRENCE/DOCKET NUMBER: 03806.0054-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
TELEFAX: (202) 408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUBBER: US 08/403,852
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUBBER: PCT/FR 93/00923
FILING DATE: 25-5EP-1993
PRIOR APPLICATION NUBBER: FR 92/11441
FILING DATE: 25-5EP-1993
APPLICATION NUBBER: 25-5EP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08510646B Patent No. 6077699
       ; ORIGINAL SOURCE:
GRGANISM: S.pristinaespiralis
US-08-403-852D-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Blanche, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Veronique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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ANTI-SENSE:
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                                                                                                                                            Query Match
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2833 caggecegerresagaceaceaceacereacecececececececercaceaacaare 2892
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                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 52.6%; Pred. No. 0.031;
Matches 91; Conservative 0; Mismatches 82; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: DELLAPORTA, STEPHEN L.
TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTAM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2: MORRISON & FOERSTER
2000 PENNSYLVANIA AVE. N.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08440856A Patent No. 5750873 GENERAL INFORMATION:
APPLICANT: DELLAPORTA, STEPHEN L.
                                                                                                                                                                                                                                ORGANISM: S.pristinaespiralis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MILMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 059
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 706141
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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(202) 887-0763
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TYPE: nucleic acid
STRANDEDNESS: single
                                            LENGTH: 5392 base pairs
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                      MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 2000 PEN
CITY: WASHINGTON
STATE: D.C.
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                                                                                                                                                                                    ANTI-SENSE: NO ORIGINAL SOURCE:
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US-08-440-856A-1
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US-08-440-856A-1
                                                                                                                     TOPOLOGY:
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                                                                             157 tcatcctcacccaagacgatttgaagaaaatcgccgcctacaaggccgtcgagtacgtgg 216
                                                  0; Gaps
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                                                                                                                                                                                                                                                                         775 TCCGGGTCAACTGCGTCTCGCCTTCGCCTCGCCCACGCCCATGCTCATCAACGCCTG 832
  14.7%; Score 40.4; DB 2; Length 1236; 51.7%; Pred. No. 0.051; tive 0; Mismatches 86; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MCDANIEL, Robert
APPLICANT: TANG, L1
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V Match 14.7%; Score 40.4; DB 5; Length 5970; Local Similarity 53.1%; Pred. No. 0.072; nes 86; Conservative 0; Mismatches 76; Indels 0.
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CURRENT APPLICATION: INCLOMBLINANI NARBONCLIDE FULING
CURRENT APPLICATION NUMBER: US/09/320,878A
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: CIP OF 09/141,908
EARLIER FILING DATE: 1998-06-26
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1999-02-06
EARLIER PRILICATION NUMBER: CIP OF 09/073,538
EARLIER PRILICATION NUMBER: CIP OF 08/846,247
EARLIER PRILICATION NUMBER: 60/119,139
EARLIER PRILICATION NUMBER: 60/119,139
EARLIER APPLICATION NUMBER: 60/100,880
EARLIER APPLICATION NUMBER: 60/100,880
EARLIER APPLICATION NUMBER: 60/100,880
EARLIER APPLICATION NUMBER: 60/087,080
EARLIER APPLICATION NUMBER: 60/087,080
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21, Application US/09320878A
Patent No. 6117659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-320-878-21
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; Patent No. 5665586
                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: ASHLEY, GATY
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
                                       92; Conservative
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                      Best Local Similarity
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LENGTH: 5970
Query Match
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137 ccaccctcctccctccgtcatcctcacccaagacgatttgaagaaaatcgccgccta 196
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                                                                                                                                                                                                                                                                                                                       Diskette, 3.50 inch, 720kb storage
                                                                                                                                                                               .E: James F. Haley, Jr., Fish & Neave
1251 Avenue of the Americas
              APPLICANT: Nakamura, Etsuo
APPLICANT: Tsuzuki, Hiroshige
APPLICANT: Kitadokoro, Kengo
APPLICANT: Kitadokoro, Kengo
APPLICANT: Shin, Nasaru
APPLICANT: Teraoka, Hiroshi
ITLE OF INVENTION: NO. 5665586el Protease
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: MS DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,428
FILING DATE: 18-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION: 435
APPLICATION: WUMBER: POT/J93/00592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by experiment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 30-APR-1993
APPLICATION NUMBER: JARAN 4-126511
FILING DATE: 19-MAY-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Haley, Jr., James F.
REGISTRATION NUMBER: 27794
REFERENCE/DOCKET NUMBER: SHGN-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Streptomyces fradiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 435..1505
IDENTIFICATION METHOD:
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LOCATION: 435..944
                                                                                                                                                                                                                                                                                 ZIP: 10020-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: -35 signal LOCATION: 359..364
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GENERAL INFORMATION:
                                                                                                                                                                                                                     CITY: New York
STATE: New York
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LOCATION:
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257 caagcatgccgtcga 271

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; Sequence 7, Application US/08042747A
; Patent No. 5487969
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 210-554-5500
TELEFAX: 210-226-8395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haymond, W. Bradley
REGISTRATION NUMBER: 35186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 210-226-8395
TELEX: 767609
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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1282 GCGAGGCCGTGGACCG 1297
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EDNESS: single
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                                                                              GENERAL INFORMATION:
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; LOCATION: 87..
US-08-042-747A-7
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           RESULT 11
US-08-042-747A-7
                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                          APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
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14.2%; Score 39; DB 1

Best Local Similarity 3.2%; Pred. No. 0.17;

Matches 6; Conservative 118; Mismatches
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STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                  Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30.
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: single
677 GGCCGCCGCCGAA 691
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139 accetectececetecgteatecteaeceaagaegatttgaagaaaategeegeetaea 198
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Best Local Similarity 49.5%; Pred. No. 0.31;
Matches 97; Conservative 0; Mismatches 99; Indels 0
APPLICANT: Bearle, Richard
APPLICANT: Back, Darla
APPLICANT: Scinicariello, Franco
APPLICANT: Hilliard, Julia K.
TITLE OF INVENTION: Cloning and Amplification of Monkey B
TITLE OF INVENTION: Virus Genes
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/042,747A
                                                                                                                                                                                  SEE: Cox & Smith Incorporated : 112 East Pecan Street, Suite 2000 San Antonio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S-0072.179
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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OTHER INFORMATION: bp 12 to 1910 comprises
OTHER INFORMATION: S. lividans DNA sequence, including Protease X.
OTHER INFORMATION: bp 1 to 11 represents cloning vector DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 cogccatggacgccggcctcctccaccctccccccccgtcatcctcacccaagacg 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lichenstein, Henri
TITLE OF INVENTION: Isolation and Characterization of No. 5516685el
TITLE OF INVENTION: Protease from Streptomyces Lividans
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 13.6%; Score 37.4; DB 6; Length 1910; Best Local Similarity 52.2%; Pred. No. 0.32; Matches 83; Conservative 0; Mismatches 76; Indels 0
                                        Sequence 1, Application PC/TUS9205532
GENERAL INFORMATION:
APPLICANT: Lichenstein, Henri
TITLE OF INVENTION: Isolation and
TITLE OF INVENTION: Characterization of a Novel Protease
TITLE OF INVENTION: from Streptomyces Lividans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76; Indels
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                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.5 inch, DS, 1.4 MB
                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: Macintosh OS 6.0.4 SOFTWARE: Microsoft Word Version 4.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: DNA sequence encoding
                                                                                                                                                                                                                                   STREET: Amgen Center
STREET: 1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08272882D Patent No. 5516685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: NUCLEIC ACID
STRANDEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                               Apple Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19920629
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1910 base pairs
                                                                                                                                                                                                                   Amgen Inc.
                                                                                                                                                                      NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                              Thousand Oaks
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Thousand Oaks
STATE: Calif.
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                                                                                                                                                                                                                                                                                                                             USA
                    -US92-05532-1/c
                                                                                                                                                                                                                 ADDRESSEE:
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RESULT
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115 ecgccatggacgccggcctcctccaccctcctccctccgtcatcctcacccaagacg 174
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APPLICANT: BURKE, RAE L.; PACHL, CAROL; VALENZUELA, PABLO D.T.
TITLE OF INVENTION: EXRESSION OF RECOMBINANT GLYOPROTEIN
B FROM HERPES SIMPLEX VIRUS
NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/587,179
FILING DATE: 20-SEP-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/272,882D
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                                                                                                  E: Floppy disk
IBM PC compatible
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; MOLECULE TYPE: DNA (genomic)
US-08-272-882D-1
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FILING DATE: 20-OCT-1986
APPLICATION NUMBER: 597,784
FILING DATE: 06-APR-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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                                    COMPUTER READABLE FORM:
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91320-1789
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Db 26899 GAGCTGGTCGCCGAACTCGGTGGGGGGGGGGCGTGCACCCCGCCCCATCCCCGGCGTCGAC 26958
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Query Match
Best Local Similarity 53.1%; Pred. No. 1;
Matches 78; Conservative 0; Mismatches 69; Indels 0;
                                                                                                                                                GENERAL INFORMATION:
APPLICANT: DeHoff, Bradley S.
APPLICANT: Rubstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
CORRESPONDERS: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPOLIDLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATE:
APPLICATION DATE:
APPLICATION INMES: US/08/804,227C
FILING DATE: February 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISCHARTON NUMBER: 35,784
REGISCHARTON NUMBER: 35,784
REGISCHARTON INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 4437 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                  Sequence 7, Application US/08804227C Patent No. 5876991
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36155..41830
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LOCATION: 14046..20036
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20110..31284
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31329..36071
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LOCATION: 350..14002
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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NAME/KEY:
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LOCATION:
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US-08-804-227C-7
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Db 26959 ACCGCCGGCCATCGCCGCAGGTCGAC 26985
243 accggctccaccgccaagcatgccgtc 269
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Search completed: November 4, 2000, 13:34:08 Job time: 16684 sec

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November 4, 2000, 11:52:13 ; Search time 4352.3 Seconds (without alignments) 389.240 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                             7189864 seqs, 3091403243 residues
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Maximum Match 100%
Listing first 45 summaries
                           OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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em_gss8:*
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117: gb_gss18:*
118: gb_gss19:*
110: gb_gss13:*
120: gb_gss20:*
121: gb_gss21:*
123: gb_gss22:*
124: gb_gss23:*
124: gb_gss24:*
125: em_gss14:*
126: em_gss14:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

AV411127 AV411127 AV422350 AV422350 AW720035 LineST15d BE191206 sn94c03. Y AV428885 AV428885 A1460598 sa80f07.y AW734685 sk98b05.y AW313275 seneff08.y AW31050 sg43f01.y AW508055 s149e02.y AW509048 s139e02.y AV428988 AV428988 AV423868 AV428988 AV423866 AV428988 AL389216 MEBC53E05 AW266520 LO-1376T3 AV418782 AV418782 AW329181 N200393e AV413309 AV413309 BE321103 NF025A04I AV422025 AV422025 AV425897 AV425897 AV406595 AV426595 AV4018494 AV418494 AV411127 AV411127 AW683698 NF017G11L BE472193 EST417046 AW559864 EST314912 AW559587 EST314635 AI900328 sc04b07.y AV424584 AV424584 AA660339 00210 MtR AV416699 AV416699 AV414597 AV424000 AV424000 AV413372 AV413372 AV412358 AV412358 AV421081 Description AV420477 AW329181 AV413309 AW720651 AL389216 AW266520 AV418782 AW133275 AW311650 AV415702 AV424000 AL372866 AW683698 BE321103 BE472193 AW720035 AW734685 AV418494 AV416699 AV425897 223 1188 1188 1188 1188 1188 1188 1189 1189 1189 1189 1189 1189 B 385 389 389 389 422 425 426 428 428 429 573 Match Length Score 141.6 133.6 133.6 126.4 112

ALIGNMENTS

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[ hases 1 to 563) Endough L., Samac,D.A., Vance,C.P., Gantt,G.S., Peng Fedorova,M., Plerson,B.L., Rowman,C.L., Craven,M.B., Hansen,T.S., H.) Holt,I.E. and Fraser,C.M.
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Medicago.
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                                                                                                                                             Lotus japonicus.
Lotus japonicus
Eukaryote, Viridiplantae, Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Lotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Lotus japonicus"
/db_xref='taxon:34305"
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/dev_stage="young plants (two-week old)"
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/note="vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
/note="wilyakojima MG-20"
* 157 c 63 g 111 t
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                                                                                                                                                                                                                                                       Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S. Generation of 7137 non-redundant expressed sequence tags from legume, Lotus japonicus
DNA Res. 7 (2), 127-130 (2000)
20277479
Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
AV412358 Lotus japonicus young plants (two-week old) Lotus japonicus cDNA clone MWM218g11_r 5', mRNA sequence.
AV412358
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51.7%; Score 141.6; DB 18; Length
Best Local Similarity 81.7%; Pred. No. 9.6e-28;
Matches 178; Conservative 0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295 CTCGGCACCGGCTCCACCGCCAAACACGCCGTCGCCCG 332
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AW559864
AW559864.1 GI:7205290
                                                                                                   AV412358.1 GI:7741522
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                                   DEFINITION
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COMMENT
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KEYWORDS
SOURCE
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                                                                                  ACCESSION
                                                                                                     VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                              REFERENCE
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With Phytophthora medicaginis.

/dev_stage="roots harvested at 10 days post inoculation with Phytophthora medicaginis."

/lab_host="E. coli strain Solis."

/note="Vector: pluescript SK +/-: Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA from roots harvested at 10 days post inoculation with Phytophthora medicaginis. The cDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using digapack III Gold packaging extracts.

Plasmids containing CDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in SOLR cells. Note: EST may be of fungal
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                                                        Contact: Carroll P. Vance
Department of Agronomy and Plant Genetics
University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
Tel: 612-625-7219
Fax: 651-649-5058
                                                                                                                                                                                               Email: vance004@maroon.tc.umn.edu
Minesota EST name:M21150e; TIGR sequence name:MTBAP91TK; More
information, including clone ordering, is available at. .
'http://chrysie.tamu.edu/medicago'
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
1. .563
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EST114635 DSIR Medicago truncatula cDNA clone pDSIR-24115, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="roots infected with Phytophthora medicaginis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.8%; Score 133.6; DB 23; Length 563; 80.8%; Pred. No. 1.3e-25;
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                                                                                                                                                                                                                                                                                                                                                           /organism="Medicago truncatula"
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                                                                                                                                                                                                                                                                                                                                                                                 /cultivar="genotype A17"
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                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="pDSIR-24P14"
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                     Phytophthora medicaginis
Unpublished (1999)
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193 c
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Matches 173; Conservative
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A1900328 428 bp mRNA EST 06-DEC-1999 sc04b07.yl Gm-c1012 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1012-1166 5' similar to SW:RPIA_ECOLI P27252 RIBOSE 5-PHOSPHATE ISOMERASE A ;, mRNA sequence.
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/note="Vector: pBluescript SK +/-; Site_1: EcoRI; Site_2:
xhoi; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10 days post inoculation with
Phytophthora medicaginis. The cDNA was directionally
ligated into the Uni-ZAP XR vector from Stratagene and
packaged using Gigapack III Gold packaging extracts.
Plasmids containing cDNA inserts were excised from the
recombinant lambda-ZAP phage using Ex-Assist helper phage
                                                                                                                                                                                                                                                                                       Fax: 651-649-5058
Email: vance004@maroon.tc.umn.edu
Minnesota EST name:M250873e ; TIGR sequence name:MTBAM56TK ; More
information, including clone ordering, is available at.
                                                                                                                                                                                                   Department of Agronomy and Plant Genetics
University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
Tel: 612-625-7219
                   1 (bases 1 to 668)

Fedorova, M., Pierson, B.L., Samac, D.A., Vance, C.P., Gantt, G.S., Pe, H. Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and Fraser, C.M.

ESTs from roots of Medicago truncatula after inoculation with
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/organism="Medicago truncatula"
/organism="genotype A17"
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/clone="pDSIR-24115"
/clone="lib="DSIR"
/clone_lib="DSIR"
/clone_lib="rocts infected with Phytophthora medicaginis"
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Fabaceae; Papilionoideae; Medicago.
                                                                                                                                                                                                                                                                                                                                                                                 'http://chrysie.tamu.edu/medicago'
Seg primer: SKmod (CTA gAA CTA gtg gAT CC)
Location/Qualifiers
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Pred. No. 1.4e-25;
0; Mismatches 29
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Unpublished (1999)
Contact: Carroll P. Vance
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80.8%;
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Fabales;
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                   REFERENCE
                                          AUTHORS
                                                                                                                                                      JOURNAL
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
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Kazusa DNA Research Institute
Yana 153-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamuekazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Lotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Lotus japonicus young plants (two-week old)"
/dev_stage="young plants (two-week old)"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
xhoI; isolate=Miyakojima_MG-20"
                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 275)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
Generation of 7137 non-redundant expressed sequence tags from a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 ttgaagaaaatcgccgcctacaaggccgtcgagtacgtggagtccggcatggtcctcggc 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 TIGAAGAAAATCGCCGCCTACAAAGCCGTCGAGTATGTCGAATCCGGCATGGTCCTCGGC 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 TCTCTCTGCGATTTCATTATGGCTATTCCCTATCCCCATTTCATCTCTCCTGGAGAAGCA 159
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                                                                                                                           AV424584 275 bp mRNA EST 23-MAY-2000 AV424584 Lotus japonicus young plants (two-week old) Lotus japonicus cDNA clone MWM042b08_r 5', mRNA sequence.
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Pred. No. 6.6e-20;
0; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Lotus japonicus"
/db_xref="taxon:34305"
/clone="MWMM042b08_r"
121 ACCGGCTCCACTGCCAAGCACGCCGTCGACCG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Res. 7 (2), 127-130 (2000) 20277479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   legume, Lotus japonicus
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80.2%;
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Matches 146; Conservative
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Lotus japonicus
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AV424584
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XhoI; This cDNA library was constructed from mRNA isolated
from the apical shoots of 9 to 10 day old etiolated
seedlings. The shoot tips including any emerged leaves
were harvested for mRNA isolation. The cDNA library was
prepared using the Stratagene pBluescribt II XR cDNA
library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a poly
(dT) sequence with a XhoI restriction site. EcoRI adapters
were ligated to the blunt-ended cDNA fragments followed by
XhoI digestion. The cDNA fragments were directionally
cloned into the EcoRI.XhoI restriction site of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                               Shoemaker, R. Kelm, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Waylie, T., Underwood, K., Steptce, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

Unpublic Soybean EST Project
Unpublished (1999)
                                                                                                  Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
Magnoliophyta; eudicotyledons; core_eudicots, Rosidae; eurosids I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3222 Fax: (888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or info@genomesystems.com web site: www.genomesystems.com Seq primer: 408P from Gibco High quality sequence stop: 411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pBluescript vector. The ligated cDNA fragments were transformed into XL10-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Apical shoot tips, 9-10 day old etiolated seedlings"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="GENOME SYSTEMS CLONE ID: Gm-c1012-1166"
/clone_lib="Gm-c1012"
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                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
                                                                                                                                                         Fabales; Fabaceae; Papilionoideae; Glycine.
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/organism="Glycine max"
/db_xref="taxon:3847"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.18;
89.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
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Best Local Similarity
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                                                                                     Glycine max
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Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ij
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Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Lotus.
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Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Lotus japonicus"
/db_xref="taxon:34305"
/db_ar="MWALJ4002_r"
/clone_lib="Lotus japonicus young plants (two-week old)"
/dev_stage="young plants (two-week old)"
                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Lotus japonicus young plants (two-week old)"
/dev_stage="young plants (two-week old)"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; isolate=Miyakojima MG-20"
               1 (bases 1 to 265)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
Generation of 1137 non-redundant expressed sequence tags from a legume, Lotus japonicus
DNA Res. 7 (2), 127-130 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 tcaacctttaacattaacatggccattccctaccccatttcatcgccaccgagaaagcc 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 TCTCTCTGCGATTTCATTATGCTATTCCCTATTCCTTTCATTCTCCTCGAGAAAGCA 162
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Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
Generation of 7137 non-redundant expressed sequence tags from
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9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 265;
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Pred. No. 1.9e-16;
                                                                                                                                              Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
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Kazusa DNA Research Institute
Fabales; Fabaceae; Papilionoideae; Lotus.
                                                                                                                                                                                                                                                                                            /organism="Lotus japonicus"
/db_xref="taxon:34305"
/clone="WMW216f10_r"
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DNA Res. 7 (2), 127-130 (2000)
20277479
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78.7%;
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Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids I,
Fabales, Fabaceae, Papilionoideae, Lotus.
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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                                                                                                                                 1 (bases I to 309)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
Generation of 7137 non-redundant expressed sequence tags from legume, Lotus japonicus
DNA Res. 7 (2), 127-130 (2000)
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                                                                               Score 99; DB 18; Length 266;
Pred. No. 1.9e-16;
0; Mismatches 30; Indels
                                                                                                                                                                                                                                           32.1%; Score 88; DB 18; Length 309; 80.5%; Pred. No. 1.6e-13;
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               XhoI; isolate=Miyakojima MG-20"
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/db_xref="taxon:34305"
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78.78;
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Generation of 7137 non-redundant expressed sequence tags from
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AV421081.1 GI:7774338
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Matches 103; Conservative
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1 (bases 1 to 374)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Lotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Lotus japonicus"
/db_xref="taxon:34305"
/clone="mwM182b12_r"
/clone="lib="Lotus japonicus young plants (two-week old)"
/dev_stage="young plants (two-week old)"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; isolate=Myakojima MG-20"
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Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
Generation of 7137 non-redundant expressed sequence tags from a
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                                                                                                               AV420477 366 bp mRNA EST 23-MAY-2000 AV420477 Lotus japonicus young plants (two-week old) Lotus japonicus cDNA clone MWM182b12_r 5', mRNA sequence.
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Pred. No. 1.6e-13;
0; Mismatches 25; Indels
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DNA Res. 7 (2), 127-130 (2000)
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                   298 TCGTCGCC 305
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Lotus japonicus

Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Budaryota; Hodons; Core eudicots; Rosidae; eurosids I;

Rabales; Fabaceae; Papilionoideae; Lotus.

1 (Dases I to 379)

Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.

Generation of 7137 non-redundant expressed sequence tags from a legume, Lotus japonicus

DNA Res. 7 (2), 127-130 (2000)
                                                                                                                               The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakame@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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/organism="Lotus japonicus"
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/dev_stage="young plants (two-week old)"
/note="yector: planescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; isolate=Miyakojima MG-20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 88; DB 18; Length 374;
Pred. No. 1.6e-13;
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                                             DNA Res. 7 (2), 127-130 (2000) 20277479
Contact: Yasukazu Nakamura
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RESULT 13
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Pabaceae; Papilionoideae; Lotus.
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Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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/dev_stage="young plants (two-week old)"
/fnote="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; isolate=Miyakojima MG-20"
154 c 56 g 87 t
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AV415702 Lotus japonicus young plants (two-week old) Lotus
japonicus cDNA clone MWM115h03_r 5', mRNA sequence.
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0
                                           Score 88; DB 18; Length 379;
Pred. No. 1.6e-13;
0; Mismatches 25; Indels
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Pred. No. 1.6e-13;
0; Mismatches 25; Indels
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
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/db_xref="taxon:34305"
/clone="MWM115h03_r"
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                                           32.1%;
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80.5%;
                                                                   Matches 103; Conservative
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Lotus japonicus
Bukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papliionoldeae; Lotus.
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Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabacee; Papilionoideae; Lotus.
1 (bases 1 to 389)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
Generation of 7137 non-redundant expressed sequence tags from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Lotus japonicus young plants (two-week old)"
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XhoI; isolate=Miyakojima MG-20"
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Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
Generation of 7137 non-redundant expressed sequence tags from a legume, Lotus japonicus
DNA Res. 7 (2), 127-130 (2000)
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                AV424000 385 bp mRNA EST 23-MAY-20 AV424000 Lotus japonicus young plants (two-week old) Lotus japonicus cDNA clone MWM034a08_r 5', mRNA sequence.
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32.1%; Score 88; DB 18; Length 38
Best Local Similarity 80.5%; Pred. No. 1.6e-13;
Matches 103; Conservative 0; Mismatches 25; Indels
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Lotus japonicus"
/db_xref="taxon:34305"
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DNA Res. 7 (2), 127-130 (2000)
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Bukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Lotus.
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                  Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu. Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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/db_xref="taxon:34305"
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/note="Yoetor: pBluescriptII SK; Site_1: EcoRI; Site_2:
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162 c 67 g 84 t
                                                                                                                                                                          /organism="Lotus japonicus"
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/note="vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
Xhoi; isolate=Miyakojima MG-20"
a 163 c 67 g 81 t
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Asamizure, Watou, Sato, Sato, S. and Tabata, S.
Generation of 7137 non-redundant expressed sequence tags from a legume, Lotus japonicus
DNA Res. 7 (2), 127-130 (2000)
20277479
Contact: Yasukazu Nakamura
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SUMMARIES

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/product="D-ribulose-5-phosphate 3-epimerase"
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/protein_id="C1:600783"
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FVPNLTIGAPVIQSLRKHTKAYLDCHLMVTNPSDYVEPLAKAGASGFTFHIEVSRDNW
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Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.

I (bases 1 to 930)

Ropriva, S., Koprivova, A. and Suss, K.H.

Identification, cloning, and properties of cytosolic

D-ribulose-5-phosphate 3-epimerase from higher plants

20092904
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AF270217 Staphyloc
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Continuation (2 of
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/db_xref="taxon:4530"
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Organization (1927)

Morison, H.G., McArthur, A.G., Nixon, J., Eakin, N.O., Kim, U.,

Crocker, M.C., Hinkle, G., Holder, M.E. and Sogin, M.L.

Direct Submission

Submisted (18-APR-2000) Josephine Bay Paul Center for Comparative

Molecular Biology and Evolution, Marine Biological Laboratory, 7

MBL Street, Woods Hole, MA 02543-1015, USA

* NOTE: This record contains 1 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely.
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Giardia intestinalis clone MJ2761 strain WB-CG, LOW-PASS SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       326 tatccaaagaatcaagtcacatggcatgattcctggtgtcagcattaaagcctgggacccc 385
                                                                                                                                                                                                                              Gaps
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Glardia intestinalis.
Glardia intestinalis.
Eukaryota: Diplomonadida; Hexamitidae; Glardiinae; Glardia.
1 (bases 1 to 927)
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                                                                                                                                            Query Match 61.8%; Score 239.8; DB 7; Length 930; Best Local Similarity 78.8%; Pred. No. 6e-55; Matches 286; Conservative 0; Mismatches 77; Indels 0
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Submitted (20-MAY-1998) Program in Infectious Diseases, University
of California, 235 Warren Hall, Berkeley, CA 94720-7360, USA
Location/Qualifiers
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Stephens, R.S., Kalman, S., Lammel, C.J., Fan, J., Marathe, R.,
Aravind, L., Mitchell, W.P., Olinger, L., Tatusov, R.L., Zhao, Q.,
Koonin, E.V. and Davis, R.W.
Genome Sequence of an Obligate Intracellular Pathogen of Humans:
                                                                                                                                                                                                                                                                                   101 AGGICCICAACIGIGGAGCAGACIGGITACAIGGAIGGAIGGAAACIIIGICC 160
                                                                                                                                                                                                                                                                                                                                                                                              151 ccaatttaactattggcgctccagttat---tgaaagtttgagaaagcacaaaggcat 207
                                                                                                                                                                                                                                                                                                                                                                                                                             161 CCAATCTGACCATTGGCCCGCCCGTCATCAGTGCCCTACATGCTGCCGTCCCCAACGCAT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 attiggatigicaccitatggitacaaatccictigatiatgitigaacccitggcaaaag 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221 Titradaciercactitatidaccaargaccaaggerritggaritcarcaccactaagg 280
                                                                                                                                                                                                                                      3; Gaps
                                                                                                                                                                                                                                                              31 cgaaaatagctccttcgatgctcttccgacttcgccaatttggcttccgaggctcagc 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydia trachomatis section 13 of 87 of the complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science (1998) In press 2 (bases 1 to 14229) Stephens,R.S., Kalman,S., Lammel,C.J., Fan,J., Marathe,R., Aravind,L., Mitchell,W.P., Olinger,L., Tatusov,R.L., Zhao,Q., Koonin,E.V. and Davis,R.W.
                                                                                                                                                                                                      Length 927;
                                                                                                                                                                                                                                      Indels
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               1 927: contig of 927 bp in length. Location/Qualifiers
                                                                                                                                                                                               Score 85.2; DB 53;
Pred. No. 8.5e-13;
                                                                                                                                                                                                                                 0; Mismatches 108;
                                                           /organism="Giardia intestinalis"
/strain="WB-C6"
/db_xref="taxon:5741"
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/product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268 ctggtgcttctggttttacatttcacgtagagac 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281 CAGGTGCTTCCACCTTTACCTTTCATATTGAGGC 314
                                                                                                                               233 g
                                                                                                               /clone="MJ2761
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                                                                                                                                                                                         Query Match
Best Local Similarity 59.54
Matches 163; Conservative
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KEYWORDS
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/db_xref="G1:3328517"
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//translstan=
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GTIGFLALLGHLVGFLIAPQITIVLLALFIISLAGNALYLQKTANLHLYQDLQREVGS
GTIGFLALLGHLVGFETAHLSKEPATTSKDLSAVSQDFYSCLQGFRDNYKGFESLLDEYK
NSTEEMRKLFSQEIIADLKSVASLREEIRFLTPLAEVRRLAHNQQSLTVYIEELKT
IRDSLANDEIGQLSQLSKTLTSQIALQRKESSDLCSQIRETLSSPRKSASPSTKSS"
COMPLEMENT(1643. .1885)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MAIIFGELRVSLYPPFLFTYISRQAHPKAILHCADKNFLESLHS
NOCFRIANATCSTLSYMQKLIVNPVNNINANALENM"
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ENIKEIISYIQKGGVQAGVAFSPETSIEFVTSFIPLCDVILLMSVHPGFCGQKFIPDT
IERIQFVKQAIQVLGREGSCLIEVDGGIDKESARACREAGADILVAASYFFEKDSINM
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MFLKAGVTVFALVHEGTVFSMELPHFLELMVAKTDFPGDSLSLSGGAKKALLETGVEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="C. psittaci hypothetical protein"
/protein_id="AAC67711.1"
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/product="Ribulose-P_Epimerase"
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                              /note="CT119"
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1969. .2670
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3227, 3721
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/note="CT122"
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/gene="araD"
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us-09-300-482-298.rge

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                                                                                                                                                                                                                                                                                                                                                                GGGGRGIRIVREKDEFVRAFTAARAEAEAGFNNPDVYIEKFIENPRHLEVQVIGDKHG
NYVLLGEROCTVQRRRQKLIEETPSPILTPEWRAKVGKVADLARSAGYFSVGTVBFL
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KNREEAIAIMKRALKEFHIGGVHSTIPFHQFMLDNPKFLLSDYDINYVDQLLASGSTF
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STGQINHVMMKISEHEFIHAAEKIGKVEKVILGNRAFFKGNLFCSLGEPPIEAVFGVP
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KPAYVIEHAVKGMLPKTKLGRRQMKSLRVLKGSSYAQYEAIKPIVLDA"
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SLSPASIALLNSNSRSNYAKAFCSTKEIRFLNSSFSPRDLVSFAEQLIDTPYVWGGRC
                                                                                                                                                                                                                                                                                                                       DEAVCIGEAQAAKSYLKIANILAACEITGVDAVHPGYGFLSENANFASICESCGLTFI
GPSAESIATMGDKVAAKQLAKKIKCPVIPGSEGVVKDEVEGIRIAEKIGFPIVIKAVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="predicted polysaccharide hydrolase-invasin
repeat family"
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/transl_table=11
/product="L13 Ribosomal Protein"
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                                                                                                                                                                                                                        /product="Biotin Carboxylase"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 122925)
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Home sapiens chromosome 10 clone RP11-332019, *** SEQUENCING IN
PROGRESS ***, 30 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2006 TACCICCATCIATIATGGGGAGCTGACTTAGCTTGCATAGGAAGAGGGGGGAAATATAG 2065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2126 TTACTTTTGGTCCCGGAGTTGTTGCTGCGATTAATCGGTCAACAGAGCTATTTCTGGAAG 2185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2186 Ticarccrargarrraraccccrrrrgaarrrgragagccrrrrrgrraggccgggggg 2245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2246 ATCGTATCATTGTGCATTTTGAGGCAGCGGAAAATA---TTAAAGAAATTATTAGCTATA 2302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 gtcaccttatggttacaaatcctcttgattatgttgaacccttggcaaaagctggtgctt 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 ctggttttacatttcacgtagagacatcaaaagataactggaaagaacttatccaaagaa 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 taactattggcgctccagttattgaaagtttgagaaagcacacaaaggcatatttggatt 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.0%; Score 85.2; DB 1; Length 14229; 54.9%; Pred. No. 1e-12; ive 0; Mismatches 153; Indels 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       337 tcaagtcacatggcatgattcctggtgtagcattaaagcctgggac 382
                                                                                                                              QSILDSLSASLVYQERDCCNCDCDDED"
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/gene="glnP"
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KEYWORDS
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misc_feature
                                                                                                                                                                                                                       FEATURES
                                                                                 Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Bi4 Dye; 100% of reads
Consensus quality: 107697 bases at least 040
Consensus quality: 110797 bases at least 040
Consensus quality: 115383 bases at least 020
Consensus quality: 115383 bases at least 020
Insert size: 120025; sum-of-contigs
Insert size: 170770; 12.7% error; agarcse-fp
Quality coverage: 0.00x in 020 bases; sum-of-contigs Quality
coverage: 0.00x in 020 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown is soon as it is available and the accession number will be breserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27409: contig of 2777 bp in length 100 bp 27509: gap of 100 bp 31499: contig of 3990 bp in length 3159: gap of 100 bp 36750: contin effect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3340 3439: gap of 100 bp 3440 6321: contig of 2882 bp in length 6322 6421: gap of 100 bp 6422 10506: contig of 4085 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3339: contig of 3339 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39845 39944: gap of 100 bp 39945 42665: contig of 2721 bp in length 42666 42765; gap of 100 bp 42766 45870: contig of 3105 bp in length 48871 45970: gap of 100 bp 48371 48390: contig of 2420 bp in length 45971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19684: gap of 100 bp 22008: contig of 2324 bp in length 22108: gap of 100 bp 24532: contig of 2424 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11500 31599; gap of 100 bp 100 bp 36750; contig of 5151 bp in length 16751 36850; gap of 100 bp 100 bp 139844; contig of 2994 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  p of 100 bp contig of 2850 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54823; gap of 100 bp 55829; contig of 2006 bp in length 56929; gap of 100 bp in length 60492; contig of 3563 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51440: gap of 100 bp
54723: contig of 3283 bp in length
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83214: contig of 2351 bp in length
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                            Project Information
                                                                     --- Summary Statistics
Contact: humquery@sanger.ac.uk
                                           Center project name: bA332019
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19584: conf
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51340: cont
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70877: cont
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73415: con
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87723: cont
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103589 103688: gap of 100 bp 10 length 103689 103688: gap of 100 bp 109234: contig of 5446 bp in length 109235 112265: contig of 3031 bp in length 112366 122925: contig of 1050 bp 112366 122925: contig of 10560 bp in length. Location/Qualifiers
93512 97223: contig of 3712 bp in length 97224 97323: gap of 100 bp 97324 103588: contig of 6265 bp in length
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/note="assembly_fragment:00514.0"
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/note="assembly_fragment:00646.0"
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//note="assembly_fragment:01357.0"
103689. .109134
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109235. .112265
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/note="assembly_fragment:01079.0"
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/note="assembly_fragment:01273.0"
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/note="assembly_fragment:01345.0"
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/db_xref="taxon:9606"
/chromosome="10"
/clone="RR11-332019"
/clone_11b="RRC1-11.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN PROGRES. ***, 1 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29274 GCAGAAGCCAATCAGTACACCTTTCATCTCGAG---GCTACTGAGAACCCAGGGACTTTG 29330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19034 AAGATIGGCCCGTCCATCCTCAACAGCGACCTGGCCAATTAGGGGCCAAGTGCCTCCAG 29093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29154 AACATCACCTTTGGTCACCCTGTGGTAGAAAGCCTTCGAAAGCAGCTAGGCCAGGACCCT 29213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 aatttaactattggcgctccagttattgaaagtttgagaaagca----cacaaaggca 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 tatttggattgtcaccttatggttacaaatcctcttgattatgttgaacccttggcaaaa 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        327 atccaaagaatcaagtcacatggcatgattcctggtgtagcattaaagcctgggacccc 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267 gotggtgcttctggttttacatttcacgtagagacatcaaaagataactggaaagaactt 326
                                                                                                                                                                                                                                                                                                                                                                                                                                              93 atgeteceaetteggegeegattggetecaeatggaeateatggatgggeattttgteeee 152
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                               33 aaaatageteettegatgetetetteegaettegeeaatttggetteegaggeteagege 92
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1 (bases 1 to 153804)
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* NOTE: This is a 'working draft' sequence. It currently consists of I contigs. Gaps between the contigs.

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have
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This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

1 153804: contig of 153804 bp in length.
                                                                                                                                                                                              Query Match 20.8%; Score 80.8; DB 85; Length 122925; Best Local Similarity 55.5%; Pred. No. 1.8e-11; Matches 201; Conservative 0; Mismatches 152; Indels 9:
                                                                                               2961 others
/note="assembly_fragment:01395.0"
112366. .122925
/note="assembly_fragment:01400.0"
34448 a 26006 c 25505 g 34005 t 296.
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malaria parasite P. falciparum.
Plasmodium falciparum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC004709.3 GI:4558585
HTG: HTGS_PHASE1.
HTG: HTGS_PHASE1.
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
I (Dases I to 196149)
Hyman, R.W., Fung, E.L., Qin, F., Tamaki, T., Kurdi, O.B., Conway, A.B. and Davis, R.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         71794 GTATITITITIGAIGIACACITAAIGGIIGAATAICCAGAAAAIAIGIACCAIIGIAA 71853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum chromosome 12, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 ttgtccccaatttaactattggcgctccagttattgaaagtttgagaaagcacacaaagg 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205 catatttggattgtcaccttatggttacaaatcctcttgattatgttgaacccttggcaa 264
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                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1999
                                                                                                                                                                                                                                                                                    3; Gaps
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Hyman,R.W., Qin,F., Fung,E.L., Conway,A.B. and Davis,R.W.
Direct Submission
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NOTE: This is a 'working draft' sequence. It currently a consists of 3 contigs. The true order of the pieces 1s not known and their order in this sequence record is
                                                                                                                                                                                                                                       DB 27; Length 153804;
                                                                                                                                                                                                                                         20.4%; Score 79.2; DB 27; Length 35.4%; Pred. No. 5e-11; tive 0; Mismatches 138; Indels
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                Plasmodium falciparum 3D7 chromosome 12
Unpublished
                                                                                                                                                    61558 a 16268 c 14690 g 61288 t
Location/Qualifiers
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                                                                                                         /clone="PFYAC724"
/clone="3D7"
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                                                                                                                                                                                                                                                                Best_Local Similarity 55.49
Matches 175; Conservative
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Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13686 GTATTTTTTTGATGTACACTTAATGGTTGAATATCCAGAAAATATGTACCATTGTTAA 13745
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gene EP11 encoding ribulose-5-phosphate 3-epimerase
Yeast 11, 500-500 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                           145 ttgtccccaatttaactattggcgctccagttattgaaagtttgagaaagcacacaaagg 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265 aagotggtgcttctggttttacatttcacgtagagacatcaaaagataactggaaagaac 324
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                                                                                                                                                                                                         20.4%; Score 79.2; DB 27; Length 196149; 55.4%; Pred. No. 5.1e-11;
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179129: contig of 131298 bp in length 179329: gap of unknown length 196149: contig of 16820 bp in length.
                                                                                                                                          401 others
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0; Mismatches 138; Indels
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    196149
/organism="Plasmodium falciparum"
/db_xref="taxon:5833"

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rep gene; Ribulose-5-phosphate-epimerase.
                                                                                                                 /chromosome="12"
19753 c 18800 g 77138 t
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Curr. Genet. 30 (5), 404-409 (1996)
97074231
                                                    Location/Qualifiers
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S.cerevisiae RPE gene.
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Juhnke, H.
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                                                                                                                                                                                                                                  Matches 175; Conservative
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47832
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/translation="MVKPITAPSILASDPANIGCECHKVINAGADWLHIDVMDGHFVP
NITLGQPIVTSILRSYPRPGDASNTEKKPTAFFDCHMMVENPEKWVDDFAKCGADQFT
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KFMEDWMPKVETLIRKFPHLNIQVDGGLGKETIPKAAKAGANVIVAGTSVFTAADPHD
VISFMKEEVSKELRSRDLLD"
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Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                 20.4%; Score 79; DB 45; Length 911;
54.6%; Pred. No. 4.2e-11;
Live 0; Mismatches 150; Indels 42; Gaps
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                                                                                                                                                                           /product="Ribulose-5-Phosphate-Epimerase"
                              /organism="Saccharomyces cerevisiae"
                                                                         /clone_lib="plasmid library"
120. .836
                                                                                                                                                                                                                          /db_xref="SWISS-PROT:P46969"
                                                                                                                                                                                                                                                                                                                        254 t
                                                                                                                                                                                        /protein_id="CAA58554.1"
/db_xref="GI:609674"
                                             /isolate="clone 6" /db_xref="taxon:4932"
 Location/Qualifiers
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Saccharomyces cerevisiae
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                                                                                                         /gene="RPE"
120. .836
                                                                                                                                             /gene="RPE"
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RVCFIFLFTGGFFLFWLSYNRDHERSSSLRIKKVPIHIQKSDYFPSSTWIAVLVFSWR
           Direct Submission
Submitted (25-SEP-1995) Data collected by MIPS on behalf of the Submitted (25-SEP-1995) Data collected by MIPS on behalf of the Buropean yeast chromosome X sequencing project. MIPS at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152 Martinsried, FRG; E-mail: Mewes@mips.embnet.org
2 (bases 1 to 1328)
Cziepluch,C., Kordes,E., Pujol,A. and Jauniaux,J.C.
Sequencing analysis of a 40.2 kb fragment of yeast chromosome X sequencing analysis of a 12.2 kb fragment of yeast chromosome X spr10, GCD14, RPE1, PHO86, NCA3, ASF1, CCT7, GZF3, two tRNA genes, three remnant delta elements and a Ty4 transposon
Feast 12 (14), 1471-1474 (1996)
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KFMEDMMPKVETLRAKFPHLNIQVDGGLGKETIPKAAKAGANVIVAGTSVFTAADPHD
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NITLGQPIVTSLRRSVPRPGDASNTEKKPTAFFDCHMMVENPEKWVDDFAKCGADQFT
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Genetic and functional analysis of the Saccharomyces cerevisiae
gene EPI1 encoding ribulose-5-phosphate 3-epimerase
Yeast 11, 500-500 (1995)
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/db_xref="taxon:4932"
/chromosome="X"
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/gene="POS18"
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RCU23145 5960 bp DNA BCT 28-OCT-1997 Abdodbacter capsulatus Calvin cycle carbon dioxide fixation operon: fructose-1,6-/sedoneptulose-1,7-bisphosphate aldolase (cbbA) gene, partial cds, Form II ribulose-1,5-bisphosphate carboxylase/oxygenase (cbbM) gene, complete cds, and Calvin cycle operon: pentose-5-phosphate-3-epimerase (cbbE), phosphoglycolate phosphatase (cbbZ), and cbbY genes, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (21-MAR-1995) Frank W. Larimer, Biology Division, Oak
Ridge National Laboratory, P.O. Box 2009, Oak Ridge, TN 37831-8080,
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Larimer,F.W., Lu,T.Y.S. and Buley,D.M.
Sequence and expression of the Form II ribulose-bisphosphate
carboxyganase (Rubisco) gene from Rhodobacter capsulatus
FASEB J. 9, A1275 (1997)
2 (bases 1786 to 5960)
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/product="fructose-1,6-/sedoheptulose-1,7-bisphosphate
aldolase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Rhodobacter capsulatus"
/strain="C.B. van Niel ATH 2.3.1; ATCC catalog #11166"
/db_xref="taxon:1061"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence and expression of the pentose-5-phosphate 3-epimerase (cbbE) Calvin cycle operon of Rhodobacter capsulatus Unpublished
                                                                                                                                                                                                                                                                                                                                  326 tatccaaagaatcaagtcacatggcatgattcctggtgtatagcattaaagcctgggacccc 385
                                                                                                                                                                                                                                                                                                                                                               503 TA---AGTTGATTAAGTCTAAGGCATCAAAGCTGCATGCGCCATCAAACCTGGTACTTC 447
---aaagcacacaaaggc 205
                                                                                                                                                 623 GTTCTTCGATTGTCACATGATGGTTGAAAATCCTGAAAAATGGGTCGACGATTTTGCTAA 564
                                                                                                                                                                                                                    266 agctggtgcttctggttttacatttcacgtagagacatcaaaagataactggaaagaact 325
                                                                                                                                                                                                                                                                           563 ATGIGGIGCIGACCAAITIACGIICCACTACGAGGCCACACAAGACCCTIIGCAITIAGI 504
                                                                                                              206 atatttggattgtcaccttatggttacaaatcctcttgattatgttgaacccttggcaaa 265
                                                    On Oct 27, 1997 this sequence version replaced gi:727416.
Location/Qualifiers
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/note="aldolase; fbaB; cfxB"
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/db_xref="G1:727417"
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Larimer, F.W.
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        185 tttgag
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GYLIKRKYLGLRPKFRADACYEFWLGGDFIKNDEPQGNQTFAPLKETIRLVADAMKRA
ODETGEAKLFSANITADDHYEWVARGEYILEFFGRNADHYAFLVDGYVTGPAITTAR
RSFPROFLHYTRAGAAVTSPOSMRGYTAFVLSKWSRLQGASGIHTGTWGYSKMEGDA
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GGGAFGHLLDGATAGARSLRQSCDAWKAGVDLVTYAKSHRELARAFESFPNDADKLYPG
/translation="LQDIINEFGGAMPQTFGVPVEEIVRGIKMGVRKVNIDTDCRWRM
TGQFRRIAEQNKAEFDPRKFLKPAMDAMRDLCKARLEAFGTAGHASKIKVIPMDDMAK
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/translation="MDQSNRYARLDLKEADLIAGGRHVLCAYIMKPKAGYGYLETAAH
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KIRAMIGDRPWHIEIDGGMDPVTAPLMAAAGADVFVAGGSGVFKGGSVSTPEVYGKNIA
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Anote-"hypothetical protein: similar to A. brasilense flcA gene, encoded by GenBank Accession Number 712363,
Synechocystis sp. ORE_ID:sil1289, encoded by GenBank Accession Number D90904, M. tuberculosis MTCY04C12.12 orf, encoded by GenBank Accession Number 281360, and M. leprae hypothetical protein MLCB2052.40, encoded by GenBank Accession Number 298604"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAAESSTGTNVEVSTTDDFTRGVDALVYEIDPEKEIMKIAYPVELFDRNIIDGGAMLC
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NHCPYVOAILDRLGRDAEALMDLGIGVAAISSNDVASYPEDSPANMARLAAEEGFRFP
YLFDETQAVAKAYDAICTPDFFGFNAECQLQYRGRLDASGRTPGPADARRELYEAMLS
                                                                                                                                                                                                                                                                                                                    /function="carbon dioxide fixation"
/product="Form II ribulose-1,5-bisphosphate
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/protein_id="AAB82051.1"
/db_xref="G1:2564975"
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/db_xref="G1:2564974"
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/rpt_type=inverted
1786. .2483
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                                                RYASGSLAPKTN"
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1786. .1790
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1797, 2482
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                                                                           351. .1740
/gene="cbbM"
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/gene="cbbM"
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RBS CDS

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VGQGAPHLVRCLLTTAGEDPEGPLFDAIYADLVSRYETDVEGNTLYPGVITALQRLRE
                                                MGCPMAITTUKPYKPALAAIAHVGLIDYFOLVIGGDSLPTRKPNPEWNNEARRŸLRRP
HALYIGDSEIDAQTAQNAGLPFVIYTEGYRKTPLDALPHAAKFHDFSALPGIVEGWTW
/translation="MAPALIFDLDGTLIDSAPAIHKVSNDVLRARGYAPLGLDQIRSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLLRTTGGKERMAKHRDNLGSGPSDAKIADLHKAKTORYVETIASGOYGLLPGVAELI
DRAKASGLRLAIATTTRANVDALIAATFSKPAGDIFEVIAAGDEVAOKKPAPDVYLR
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NLGSLDDTLILSNHDPAYLNSFLGAGLFSEAPMVKWAIDSVGACSWRMVAERWAAGEL
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LEGERKVIELNRRFQYSIGFPDTSARAGAGLGLAQPGLTQADYDAINDEHGRD
LRVLNSIMHLKISALFSTTRRPLTARQREVLEWVGDGKTSADIAQILGLTTATVEKH
LRLAREALEVETTAQALLKASWQQLFITSAP"

1908 c 1857 g 1072 t
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/note="hypothetical protein"
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/note="hypothetical protein"
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26-MAY-2000

BCT

DNA

gene

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TOBSITEMENT STATEMENT SEGWVDKY ENONKRSGAY SSGCYDSKPY I LLNYTGTL YDSSVVAHEGGHSMAISELSKRITSEGWVDKY ENONKRSGAY SSGCYDSKPY I LLNYTGTL YDSSVVAHEGGHSMAISELSKRINGYTEADPELEAHSAAEQGIPLTEBEFFSGSYKKLQHIFYG DCYYFDELSSIEWAN I PHPYY NEYYVQYAGGIASLCFSEKILSKEAGAQEAYLTFLQ SGGSDPPIEILKKSGLDMTSSAPMLKAFSY I ERKLDELTNLL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKYCKNLTIIAREGKIJPVICRDEEIRTIQVISRRFKNNPMIGEPGVGKTAIAEGL
ALRIVOGDVPESLKDKHLYVLDMGALIAGAKYRGEPERKEKSVLKGYEASEGACILFI
DEWHTLVGAATDGAMDAANLIKPALARGILHCIGATTINEYQKYIEKDAALERRQP
IFVTEPSLEDAVFILKGLRKKYETEREALNAAVLSSYRITDRFLEDRAIDI
IDEAASLIRWOIGSLPLPIDEKERELSALIVKOEAIKREQAPAYQEEANEWOKAIDRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSREEKIIJASSSPALEVAYKIFSSLTDSEIPFGEAVDSEGKSHPLSHALSSLYMQSPD
RELRKSAYOKQCQRYHGYRLSLANLLNGKIQAHLFNAKAHNYKSCLEAALFQNNISTS
VYTTLIETVKQHTHLITKYFQLKQKALGLPDFHFYDVYAPIAASEFARHYSYEEAVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLVIKDVHGNLGLLTSAVDDALHREPTVVEGAAIPKPSPSLQQLLLNAQEEARSMGDE
YLSGDHLLLAFWKTTKEPFASWRKTVKTSPEALKELIIKLRQGSRMDSPSAEENLKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MEKFSDAVSEALEKAFELAKDAKHSYVTENHLLKSLLQNPGSLF
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DLKSITYLLTSFSEEISWIQPALIALPQKISEELLTSPELQTYHFYLKKIFRLAPHTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PID:1771208; identified by sequence similarity; putative" (codon start=1 /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (01 MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA On Jun 1, 2000 this sequence version replaced gi:7190428.
                                                                                                                                                                                                                                                                     Read, T.D., Brunham, R., Shen, C., Gill, S.R., Heidelberg, J.F., White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T., Berry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B., Bowman, C., Dodson, R., Gfunn, M., Nelson, W., DeBoy, R., Kolonay, J., McClarty, G., Salzberg, S.L., Elsen, J. and Fraser, C.M. Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Read, T.D., Brunham, R., Shen, C., Gill, S.R., Heidelberg, J.F., White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T., Berry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B., Bowman, C., Dadson, R., Gwinn, M., Nelson, W., DeBoy, R., Kolonay, J., McClarty, G., Salzberg, S.L., Elsen, J. and Fraser, C.M.
Chlamydia muridarum, section 37 of 85 of the complete genome.
AE002306 AE002160
AE002306.2 GI:8163215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 28 (6), 1397-1406 (2000)
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                                                                                                                                                                                                                                             (bases 1 to 12939)
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                                                                                                                                           Chlamydia muridarum.
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                                                                                                                                                                                                                                                                                  AUTHORS
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WDDSVVLFLSEQGYDGAFGARPLKRLIQQKVVTMLSKALLKGDIKSGMSVELTMAKDV
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9963 AGATCGTATTATTGTGCACTTTGAGGCAGC---AGAAAACCTTAAAGAAATTCTTGATTA 10019

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ELQOEVASLKEVNFLLKSVQKEFLGLSKDFATTSKDLSDVSLDFHNLLQDFGSSHQGF
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/note="hypothetical protein; identified by Glimmer2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="inclusion membrane localised protein IncA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T., Berry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B., Bowman, C., Dodson, R., Gwinn, M., Nelson, W., DeBoy, R., Koloaay, J., McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M. Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
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                                                                                                                                                                      Chlamydophila pneumoniae AR39, section 45 of 94 of the complete
                                                                                                                                                                                                                                                                                                                               Chlamydophila pneumoniae AR39
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
1 (bases 1 to 10150)
Read, T.D., Brunham, R.C., Shen, C., Gill, S.R., Heidelberg, J.F.,
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On Jun 1, 2000 this sequence version replaced gi:7189493.
Location/Qualifiers
10020 TATTCGAAAATGTGGAGTGCAGGGATCGCTTTTTCTCCAGAGAC 10067
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LICKKKFYFYERMYTR TQVERTY TEEVTOTDLVKROG THAVARKLIPMKOKTIBERSGHIT
OCR TNAEDPTINNES SPGRLDYYLPPAGPSTRVDGACYSGYA I PPYVDSMIAKVIAKG
KNREBAIAINKRALKEFHIGGVQST I PFHQFMLDNPKFLESNYDINY I DNLLAQGNSF
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AFARHAIKTLGLKOSCLIEVDGGIDQQSAPLCRDAGADILVTASYLFEADSLAMEDKI
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1742. .2431
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/gene="CP0586"
3498. .486.
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ICHEKDPDLSVLQYNILNYDENSFDRYMATYOGHREPGGTQNBEDLLLIFNNYLQQC
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QCLKERAPLGIILSGGPHSVYENKAPHLDPETYKLGIPILAICYGMQLMARDFGGTVS
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Marathe, R., Lammel, C., Fan, J., Olinger, L.,
Grimwood, J., Davis, R.W. and Stephens, R.S.
Direct Submission
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1765 AGTIGGCCCTTCGATTATGGGGGCAGATCTTACCTGTTTGGGTGTAGAAGCAAAAAACT 1824
                                                                          1885 CCTTACTTTTGGTCCAGGGATCATTGCTGCCATTAATAGATCTACGGATCTATTTTTAGA 1944
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                                       215 ttgtcaccttatggttacaaatcctcttgattatgttgaacccttggcaaaagctggtgc 274
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
1 (bases 1 to 12973)
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/gene="CPn0170"
complement(291. .1295)
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DYLIEVEDBYADSLDYQMLAGGTIYSDVIESSRSGHASEVIKSHHNVGGLPRNLKLKL
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EAVSTAELGYDDAVKYGIGPGSICTTRIVSGVGYPOITAITNVAKALKNSAVTVIADG
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SADRYFOTOGOOKKLYPOEGVASKGSVHDVLYQILGGIRSGMGYVGAETLKDLKTK
ASFVRITESGRAESHIHNIXKVQPTLNY
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LLSTIICFSVYGTSGETASLVFGILSLIVLVLLIIECRNRECCRRIS"
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GEFIEGLDTNSFPLEEVAIPILPGYHPKFYLSFIDRDDQGVHYEVLDGVFLKTVAACI
IENSFLTDSNSPELLSEVKEALKR"
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QVLKMSYLQVBELEKEKISISVAAASSLLKSRTSNAFEKGYSSYQSESSAQTVFLGGIGF
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FPTIKETSGAQPLSFVIRFDDIFEQONLVHUSTIIASTSVRLGFRGDSYRRYDALSF
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                                                                                                                                                                                                                                                                                                                                                                        /product="Inosine 5'-monophosphase dehydrogenase"
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                                                                                                                                                                complement(2706. .3446)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(3981, .4256)
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complement(3981, .4256)
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5555. .6790
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Shirai, M., Hirakawa, H., Kimoto, M., Tabuchi, M., Kishi, F., Ouchi, K.,
Shiba, T., Ishii, K., Hattori, M., Kuhara, S. and Nakazawa, T.
Comparison of whole genome sequences of chlamydia pneumoniae J138
from japan and CWL029 from USA
Nucleic Acids Res. 28 (12), 2311-2314 (2000)
/translation="MKKVLJANRGEJAVRIJTRACHDLGLSTVAVYSLADOEALHVLLA
DEAICIGEPQAAKSYLKISNILAACEITGADAVHPGYGFLSENANFASICESCGLTFI
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Submitted (04-JUL-2000) to the DDBJ/EMBL/GenBank databases.
Submitted (04-JUL-2000) to the DDBJ/EMBL/GenBank databases.
Mutsunori Shirai, Yamaquchi University School of Medicine,
Mutsunori Shirai, Yamaquchi University School of Medicine,
Department of Mcrobiology; 1-1-1 Minamikogushi, Ube, Yamaquchi
755-8905, Japan (B-mail:mshirai@po.cc.yamaguchi-u.ac.jp,
Tel:81-836-22-2227, Fax:81-836-22-2415)
AB033760-AB033781, AB033792-AB033799; Submitted (25-Oct-1999)
AB03376-AB038347: Submitted (14-Feb-2000)
AB036071-AB036078: Submitted (18-Dec-2000).
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Chlamydophila pneumoniae
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
                                                                                                    19.7%; Score 76.4; DB 1; Length 1: 54.7%; Pred. No. 2.5e-10; tive 0; Mismatches 126; Indels
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1. 300050
Acganism="Chlamydophila pneumoniae"
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complement
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Shirai, M.
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STVGSLMHPKSAALTLKTYRPHPIWINGYERSFNIDTGKYLKNGSRRRTSHDGPKNRA
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                                                                                                                                                                                                                                                                                                                         /translation="MKQPMSLIFSSVCLGLGLGSLSSCNQKPSWNYHNTSTSEEFFVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DESACSKEVLPVKGYYSLVWESVSSDSLNAFGDSFAEDYLRSTFLANGTSILCVHES
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CDS

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gene

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EDVALMMUVFSGRDFKDATSREFFROSFMSKLSTEVPKVIGVPRTFLEGLRDIRENF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIIRGGRIKAIVQGEERYFELAQTHIEDDAGMLKHFGEFAGVDYNRAGVPLIEIVSKP
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573. .87
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gene

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SLEDNKKTIMKEHAEMLESLSSYRKVFLALSDENVUDTPSDPKKWDLSGIPCRDALSE
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KAVFKGSLCCALASKAKPYFEEDPRFQDSDTGLRALTIRLQEAKASLEEEIKRFSNLE
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NYNEEKRRAKTRLVEMTQRYRDFKMALEAMQFNEEALLQEELSIQAPSE"
10975. ,11688
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7605. 11
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EIEMTLRMVELPLLEMKNTFEKASLOYNSCKEMLAKVEPOCKESPTYRSSGERLERLN BOLOTAYXTVOCBELGGESPUESKVRFCRDHLERDWRHFEVOGLNFINBELLWYGAELF TOARLDLVATVPYMEFLYEFLOYHNIKREKVRSOWMATTERYREIRQAFGGVMKEDLLAED TILKEEDYWLLRDDWLLRDERKNRORRLICONIAAAQORVKGF

RLEDCLETWSKKLTKAEESVFEMKFDATEKLGNKVLSDVTNRLEILCEDAEEMIFRIE

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Expression vector prices

artificial sequence; vectors.

I (bases 1 to 993)

E alonemistry 35, 9296 (1956)

E chart in 10 993)

E purification and characterization of recombinant problems rry 35, 9296 (1956)

E chart in 10 993)

E purification and properties of recombinant spinacia oleracea

ribulose-5-phosphate 3-epimerase from Spinacia oleracea

B prification and properties of recombinant spinach

ribulose-5-phosphate 3-epimerase

I plant physiol. (1969) In press

E a chart in 993)

E a chart in 993)

E a chart in 993)
                                                                                                                                                                                                                                                         /translation="Matsrvdkfsksdlivspsilsanfaklgeqvkavelagcdwih
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          220 accttatggttacaaatcctcttgattatgttgaacccttggcaaaagctggtgcttctg 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       327 ATCTGATGATTGTAGAACCAGAGCAGCGGGTCCCCAGACTTCATCAAAGCTGGTGCTGATA 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 gttttacatttcacgtagag---acatcaaaagataactggaaagaacttatccaaagaa 336
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                                                                                                                                                                             /product-"ribulose-phosphate 3-epimerase mature form"
/protein_1d="AAC24710.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 CTCCATCTATTCTCTCTGCTAACTTTGCAAAGTTGGGTGAGCAGGTAAAAGCAGGTTGAAT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267 CTATTGGACCTCTGGTGGTTGATGCCTTGCGACCTGTGACAGATCTCCCACTAGATGTGC 326
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Expression vector pFL505 for Spinacia oleracea chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 91; Length 849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 337 tcaagtcacatggcatgattcctggtgtagcattaaagcctgggaccc 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                447 TCAAGAGTTTGGGAGCTAAAGCTGGAGTTGTCTTAAACCCTGGAACCCC 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 75.4; DB 91; Length B Pred. No. 4e-10; 0; Mismatches 161; Indels
                        /note="synthetic tac (trp-lac) promoter"
                                                                                                                      /note="pentose-5-phosphate 3-epimerase"
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                                                                                           /EC_number="5.1.3.1"
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Best Local Similarity 53.0%;
Matches 185; Conservative
                                                                     /gene="RPE"
  /gene="RPE"
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                                                                                                                                                                                                                  /translation="MLLLISGALFLTLGIPGLSAAISFGLGIGLSALGGVLMISGLLC
                                                                                                                                                                                                                                           LLVKREIPTVRPEEIPEGVSLAPSEEPALQAAQKTLAQLPKELDQLDTDIQEVFACLR
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Submitted (06-JUN-1998) Life Sciences Division, Oak Ridge National
Laboratory, 1060 Commerce Park, Oak Ridge, IN 37831, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 222381 AGTTGGCCCTTCGATTATGGGGGCAGATCTTACCTGTTTGGGTGTAGAAGAAAAACT 222322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 222261 CCTTACTTTTGGTCCAGGGATCATTGCTGCCATTAATAGATCTACGGATCTATTTTAGA 222202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Expression vector FFL506 artificial sequence; vectors.

1 (Dases 10 849)
Larimer,F.W., Lu,T.-Y.S. and Stringer,C.D.
Construction, purification, and characterization of recombinant D-ribulose-5-phosphate 3-epimerase from Spinacia oleracea Biochemistry 35, 9296 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 tttaactattggcgctccagttattgaaagtttgagaaagcacacaaaaggcatatttgga 214
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                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                     35 aatagctccttcgatgctcttccgacttcgccaatttggcttccgagggctcagcgcat 94
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Chen, T. T., T. T.S., Hartman, F.C. and Larimer, F.W.
Purification and properties of recombinant spinach
ribulose-5-phosphate 3-epimerase
                                                                                                                                                                                                                                                                                                                                    0; Mismatches 126; Indels
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/db_xref="taxon:78122"
/lab_host="Escherichia coli"
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                                                                                                                                                                                                                                                                                       Score 76.4; DB 1;
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                                                                                                                                             /product="hypothetical protein"
/protein_id="BAA98220.1"
                                                                                                                                                                                                                                                                                                                Pred. No. 3e-10;
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Larimer, F.W. and Lu, T.-Y.S.
                                                                                                                                                                                            /db_xref="GI:8978383
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13434. .15758
/gene="CPj0010"
13434. .15758
/gene="CPj0010"
                                                                                                                      /transl_table=11
                                                                                                /codon_start=1
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1. .97
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/product="ribulose-phosphate 3-epimerase transit form"
/protein_id="AAC24709.1"
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SKRPEVVAV"
                                                                                                                                        /note="synthetic expression cassette for Spinacia oleracea
chloroplast ribulose-phosphate 3-epimerase transit form"
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Submitted (06-JUN-1998) Life Sciences Division, Oak Ridge National Laboratory, 1060 Commerce Park, Oak Ridge, TN 37831, USA
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19.4%; Score 75.4; DB 91; Length 993;
Best Local Similarity 53.0%; Pred. No. 4e-10;
Matches 185; Conservative 0; Mismatches 161; Indels 3
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98. .955
                                                                                                                                                                                                                                                                                                  /gene="RPE"
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                                             Location/Qualifiers
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/transl_table=11
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/gene="RPE"
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/SIDS6/gcgdata/geneseqq/geneseqn/NA1981.DAT:*
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| SIDS6/gcgdata/geneseg/genesegn/NA1996.DAT:*
| SIDS6/gcgdata/geneseg/genesegn/NA1997.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /SIDS6/gcgdata/geneseg/geneseqn/NA1994.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     960044
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  480022 segs, 187831343 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                  OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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Perfect score:
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Maximum DB seq
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS6/gcgdata/geneseg/genesegn/NA1998.DAT:*/SIDS6/gcgdata/geneseg/genesegn/NA1999.DAT:*/SIDS6/gcgdata/geneseg/genesegn/NA2000.DAT:*

Description	Staphylococcus aur Enterococcus faeca Streptococcus pneu Polynucleotide seq D-ribulose-5-phosp D-ribulose-5-phosp DNA encoding a S. S. pneumoniae deri Essential Staphylo DNA encoding a S. Plant microsatelli Streptococcus pneu
RIES	
SUMMARIES	V75460 X13166 V52282 X20515 Z45413 Z45412 T98644 Z96346 A26928 V65230 A31245
DB 1	18 20 20 20 21 19 19 19
Query Query Match Length DB	916 17082 12566 32768 1050 1260 1234 1542 1019 1040 459
% Query Match	21.5 20.1 20.0 19.1 17.8 17.0 16.9 14.9 13.7 11.2
Score	83.6 77.8 77.6 74.2 65.4 65.4 65.4 65.4 65.4 65.4 65.4 65.4
Result No.	C C C C C C C C C C C C C C C C C C C

(HUMA-) HUMAN GENOME SCI INC.

96US-0009861.

05-JAN-1996;

an parainflu nt microsate burgdorferi	B. burgdorferi ant Phosphate starvati Plant microsatelli Human transmembran	Cun encoung (180 L.lacts MG1363 Ad Enterococcus faeca Candida albicans p Enterococcus faeca	0 4 0 0	Campylobacter jeju Nicotiana plumbagi Human secreted pro PBR-associated pro Patinobacillus ple S. aureus nrdF pol Staphylococus aur Mycoplasma qenital	Nuclectide sequence Nuclet acid seque Thermoanaerobacter Thermoanaerobacter Rat tripeptidylpep Human prothrombina Rat brain homologu Thermoanaerobacter Thermoanaerobacter Thermoanaerobacter
13 Q27406 21 A31286 20 X61720 20 X61710			20 A2025/ 19 V02032 18 V74432 19 X14338 19 V65760	16 092525 21 257037 19 V05542 19 V05542 20 207815 18 V7431 18 T58840	20 X91990 18 X99556 18 X99556 20 Z19861 17 T72653 20 V84139 20 Z19859
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38.2 37.6 36.4	33.6 33.6 33.4	32.2 32.2 31.8 31.6	31.6 31.6 31.4 31.2	m	2000.000 2000.000 2000.000 2000.000 2000.000
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ALIGNMENTS

V75460 standard; DNA; 916 BP

V75460/c RESULT

V75460;

/*tag= a //*tag= a //*tag= a //*tag= a //*tag= Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds. Staphylococcus aureus contig SEQ ID #1149. Location/Qualifiers 16-MAR-1999 (first entry) Staphylococcus aureus. misc_feature 07-JAN-1997; EP786519-A2 30-JUL-1997. vaccine; attenuation; computer readable medium; ds.

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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (RAM), read-only memory (RAM), read-only memory (RAM), read-only memory (RAM), read-only memory (RAM), read-only memory (RAM), read-only memory (RAM), read-only memory (RAM), read-only memory (RAM), read-only memory (RAM), read-only memory (RAM), read-only memory (RAM), read-only searches using that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can also be used in a kit for the immunodetection of solypeptides can also be used in a kit for the immunodetection of scanned in a kit for the immunodetection of shock skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences can the used community of any of the S. aureus DNA sequences contained on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 tggattgtcaccttatggttacaaatcctcttgattatgttgaacccttggcaaaagctg 270\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gtgcttctggttttacatttcacgtagagacatcaaaagataactggaaagaacttatcc 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      685 GACTIGAAGAAGCAGGCGICGACGGAGTICATITIGAIGITATGGAIGGICAATITGIGC 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                625 CTAATATATCTATTGGTTTACCAATATTAGATGCAGTAAGAAAAGGCACAACATTACCTA 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               745 CAAAACTATATCCATCATTATTATCTGTTGATTTTTGGATTTACAACATGAATTAAAAC 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       565 TAGACGTACATTTGATGATTGAAAATCCAGAAAAGTATATTGCATCATTTGCAGAACATG 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 331 aaagaatcaagtcacatggcatgattcctggtgtagcattaaagcctgggaccccgt 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ж
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches 161; Indels
Fannon MR, Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 916 BP; 273 A; 165 C; 120 G; 291 T; 67 other;
                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 1854-1855; 3271pp; English.
   Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X13166 standard; DNA; 17082 BP
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                                                                                                                                                                                                                                                                   anti-S.aureus vaccines
       Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                      WPI; 1997-374922/35.
           Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                           Rosen CA;
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q δy g ò g ò Enterococcus faecalis; contig; detection; Enterococcal infection;

Enterococcus faecalis genome contig SEQ ID NO:229.

(first entry)

19-MAR-1999

x13166;

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A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcus infection in an animal and monitoring progression of disease, and for identifying agents which can be used to another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7132 ATCAATGCITITGCGGAAGCCGGTGCGGATATTATTACCGTCCATCAAGAAGCAACACCC 7073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7072 CATA---TICATCGTGCCTTACAAATGATTAAAAATGCGGGTGTGAAAGCTGGCGTAACC 7016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7192 CGTCCAGTGACAAAACTACCATTGGATGTTTGATTGTTGTACAACCTGAAAATTAT 7133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7312 AATTTAGAAAGAGATATCCGTTTAGTAGAAGAATTAGGAGCAGATTATATTCATGTTGAT 7253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309 gataactggaaagaacttatccaaagaatcaagtcacatggcatgattcctggtgtagca 368
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                                                                                                                                                                                                                                                                                                                                                               New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 77.8; DB 20; Length 17082; Pred. No. 1.5e-14; 0; Mismatches 177; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17082 BP; 4548 A; 3830 C; 3167 G; 5533 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 1149-1157; 2084pp; English.
                                                                                                                                                                                                                                                                                                Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 20.1%;
Best Local Similarity 52.3%;
Matches 197; Conservative (
                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                  97us-0066009.
                                                                                                                                                                                                    97US-0044031.
97US-0046655.
                                                                                                                                             98WO-US08985
                                                                                                                                                                                                                                                                                              Barash SC, Dillon PJ,
                               Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                 WPI; 1999-045171/04.
                                                                                                                                                                                                      06-MAY-1997;
16-MAY-1997;
                                                                      WO9850555-A2
                                                                                                                                                 04-MAY-1998;
                                                                                                                                                                                  14-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                infection.
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Gaps

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369 ttaaagcctgggacccc 385
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V52282 standard; DNA; 12566 BP 23-OCT-1998 (first entry) m

Streptococcus pneumoniae genome fragment SEQ ID NO:149.

Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay; computer readable medium; vaccine; pharmaceutical composition; ds Streptococcus

Streptococcus pneumoniae.

WO9818931-A2

97WO-US19588 30-OCT-1997;

96US-0029960. 31-OCT-1996; (HUMA-) HUMAN GENOME SCI INC

Dougherty BA, Fannon M; Dillon PJ, Rosen CA; Choi GH, Barash SC, Kunsch CA,

WPI; 1998-272225/24.

polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus Computer-readable medium with recorded Streptococcus pneumoniae pneumoniae

Claim 1; Page 998-1006; 1409pp; English.

The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (V52134 to V52524) recorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 premmoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating mRNA, DNA or CDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome of commercial importance, or expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and pharmaceutical vaccines for S. pneumoniae.

Sequence 12566 BP; 3602 A; 2488 C; 2984 G; 3492 T; 0 other;

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3; Gaps
 20.0%; Score 77.6; DB 19; Length 12566; 53.1%; Pred. No. 1.4e-14;
                                   0; Mismatches 164; Indels
                                     Conservative
             Local Similarity
                                  Matches 189;
Query Match
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33 aaaatagctccttcgatgctctctccgacttcgccaatttggcttccgaggctcagcg 92 ð

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4906 caaatcagititggtgcaggtgtggtcgaggccttcgtcctcatagtaagatggttttc 4965
                                                                                                                                                                                                               4966 gattgccacttgatggtgtcaaaccctgagcatcatctggaagattttgcgcgtgcaggt 5025
                                                                                                                                                                                                                                                                              5026 gcagacatcatcagtatccatgtaga---agcaacgcctcatattcatggcgccctccaa 5082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrelia infections in animals, and for the production of blosynthetic products such as enzymes.
                                               93 atgetecaetteggegeegattggeteeacatggacateatggatgggeattttgteece 152
                                                                                                             153 aatttaactattggcgctccagttattgaaagtttgagaaagcacacaaaggcatatttg 212
                                                                                                                                                                                213 gattgtcaccttatggttacaaatcctcttgattatgttgaacccttggcaaagctggt 272
                                                                                                                                                                                                                                                gcttctggttttacatttcacgtagagacatcaaaagataactggaaagaacttatccaa 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treponema pallidum infection; syphilis; Borrelia infection; animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, promoticand therapy of T. pallidum infections, particularly syphilis
                                                                                                                                                                                                                                                                                                                                        5083 aaaattcgttcactcggagttaagccttcagtcgttatcaatcctggcacatcagt 5138
                                                                                                                                                                                                                                                                                                               333 agaatcaagtcacatggcatgattcctggtgtagcattaaagcctgggaccccgt 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotide sequence from the genome of Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 32768 BP; 8253 A; 9783 C; 7257 G; 7433 T; 42 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 261-279; 1150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                   X20515 standard; DNA; 32768 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enzyme production; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-081273/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treponema pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9859034-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fraser CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X20515;
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Gaps

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Indels

Length 32768;

Query Match
Best Local Similarity 53.2%; Pred. No. 2.8e-13;
Matches 157; Conservative 0; Mismatches 138;

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The present sequence encodes a Rice D-ribulose-5-phosphate-3-eplmerase (RPE) nematode response protein. The enzyme is activated during the initial steages of nematode infestation of roots and is required for formation of the giant feeder cells on which the nematodes depend. Interfering with expression of the protein will thus inhibit nematode infestation. The RPE polynucleotide is used to produce transgenic plants (specifically potato, tomato, beet, rape and rice) that are resistant (or at least less susceptible) to nematode infestation. This is achieved by either expressing antisense sequences
                                                                                                                                                                                                                                                                                                                                         15093 TGCGTAGCAAAACGCACCTGCCGTTTGATGTTCACCTGATGGTCAGTAGGCCTGCCGACC 15034
                                                                 15273 AGCATGGACCTATGGAGCGGTCTTTACATTGGCACCTTCACTATAAGTGCAGATTTCT 15214
                                                                                                                                                                                                                 15213 CTGCGCTCGATAGGGCGCTGGTGTATTTGGAARSGCACGGCGCACAGTGGGTGCACCTGG 15154
                                                                                                                                                                                                                                                                                                                                                                                                                                              187 tgagaaagcacacaaaggcatatttggattgtcaccttatggttacaaatcctcttgatt 246
                                                                                                                                           67 ccaatttggcttccgaggctcagcgcatgctccacttcggcgccgattggctccacatgg 126
                                                                                                                                                                                                                                                                                               127 acatcatggatgggcattttgtccccaatttaactattggcgctccagttattgaaagtt 186
7 aqaaaqaaaqatgggaatgacaccgaaaatagctccttcgatgctctcttccgacttcg 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid encoding D-ribulose-5-phosphate-3-epimerase is used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D-ribulose-5-phosphate-3-epimerase, RPE; nematode response protein; mematode root infestation; giant feeder cell; transgenic plant; potato; tomato; beet; rape; rice; antisense sequence; promoter; anti-nematode protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DD 15033 TCATTGAGGATTTTGTGCAGGGGGGGGGGGACTTCTTAACTTTTCACATAGAGGC 14979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 atgitgaacccitggcaaaagciggtgctictggttttacaittcacgtagagac 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D-ribulose-5-phosphate-3-epimerase nematode response gene cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "D-ribulose-5-phosphate-3-epimerase
nematode response protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    increase resistance to root nematodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaucheret H, Tepfer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INRG ) INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Z45413 standard; cDNA; 1050 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-FR01398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09964613-A1
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100 acttoggcgccgattggctccacatggacatcatggatgggcattttgtccccaatttaa 159
                                                                                                                                                                                                                                                                                                                     ctattggcgctccagttattgaaagtttgagaaagcacacaaaggcatatttggattgtc 219
                                                                                                                                                                                                                                                                                                                                                                                                                    220 accttatggttacaaatcctcttgattatgttgaacccttggcaaaagctggtgcttctg 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                     434 atctgatgattgtggaacctgagcaacgagttccagattttatcaaggcaggtgctgata 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 gttttacatttcacgtagagacatcaaagataactggaaagaactta---tccaaagaa 336
                                                                                                                                                                                                                                          374 caatcggacctttggttgttgatgctctgcggccagtcactgatcttccgttggatgtgc 433
in the plant; or by using the promoter of the RPE gene to express an anti-nematode protein. Inhibition of the RPE protein or gene enables plant to mount an immediate response to the invasion of the nematode, consequently limiting the level of cellular damage and reducing the
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                     40 ctccttcgatgctctttccgacttcgccaatttggcttccgaggctcagcgcatgctcc 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D-ribulose-5-phosphate-3-epimerase; RPE; nematode response protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nematode root infestation; giant feeder cell; transgenic plant; potato; tomato; beet; rape; rice; antisense sequence; promoter; anti-nematode protein; ss.
                                                                                                                                                                                     3;
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                                                                                                                                                    17.8%; Score 69; DB 21; Length 1050; 51.9%; Pred. No. 2.4e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       337 tcaagtcacatggcatgattcctggtgtagcattaaagcctgggaccc 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      554 tcaaaagtcttggagcaaaggctggagttgttttgaatcctgcaacccc 602
                                                                                                                                                                                       165; Indels
                                                                                                     Sequence 1050 BP; 249 A; 234 C; 292 G; 272 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nematode response protein'
                                                                                                                                                                                         0; Mismatches
                                                                       complications of secondary infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaucheret H, Tepfer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INRG ) INST NAT RECH AGRONOMIQUE.
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/product=
                                                                                                                                                                                         Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana.
                                                                                                                                                                         Similarity
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                                                                                                                                                         Query Match
                                                                                                                                                                           Best Local
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3-epimerase (RPE) nematode response profein. The enzyme is activated during the initial stages of nematode infestation of roots and is required for formation of the giant feeder cells on which the nematodes depend. Interfering with expression of the protein will thus inhibit nematode infestation. The RPE polynucleotide is used to produce transgenic plants (specifically potato, tomato, beet, rape and rice) that are resistant (or at least less susceptible) to nematode infestation. This is achieved by either expressing antisense sequences in the plant; or by using the promoter of the RPE gene to express an anti-nematode protein. Inhibition of the RPE protein or gene enables plant to mount an immediate response to the invasion of the nematode, consequently limiting the level of cellular damage and reducing the complications of secondary infections.
                                                                            Nucleic acid encoding D-ribulose-5-phosphate-3-epimerase is used to increase resistance to root nematodes
                                                                                                                                                                                                         present sequence encodes an Arabidopsis D-ribulose-5-phosphate
                                                                                                                                                     Claim 1; Page 44-45; 62pp; French.
2000-097543/08
                            P-PSDB; Y54150
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Sequence 1260 BP; 365 A; 236 C; 288 G; 371 T; 0 other;

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1;
                                                             ctattggcgctccagttattgaaagtttgagaaagcacacaaaggcatatttggattgtc 219
                                                                                                                                                                  accttatggttacaaatcctcttgattatgttgaacccttggcaaaagctggtgcttctg 279
                                                                                                                                                                                                                           atctgatgatagtggaacccgagcagagtaccggatttcatcaaaagcaggtgcagata 526
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                                                 ctccttcgatgctcttccgacttcgccaatttggcttccgaggctccagcgatgctcc 99
                                                                                                                                                                                                                                                    gttttacatttca---cgtagagacatcaaaagataactggaaagaacttatccaaagaa
                           3;
 Length 1260;
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Score 65.8; DB 21; Length
Pred. No. 2.7e-11;
0; Mismatches 167; Indels
Query Match
17.0%;
Best Local Similarity 51.3%;
Matches 179; Conservative (
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Streptococcus pneumoniae protein; genetic immunisation; antagonist; immunological response; inoculation; antibody production; inhibitor; T cell immune response; antimicrobial compound; bacterial adhesion; extracellular matrix protein; protein mediated cell invasion; wound;
                                                                                                         DNA encoding a S. pneumoniae protein of unknown function.
              T98644 standard; DNA; 1234 BP
                                                                            (first entry)
                                                                                                                                                                                                    pathogenesis; ss.
                                                                            09-NOV-1998
                                              T98644;
T98644
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Streptococcus pneumoniae

Z96346 standard; DNA; 1542 BP

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This sequence encodes a Streptococcus pneumoniae protein of unknown function, and represents a DNA sequence of the invention.

The DNA sequences were isolated from Streptococcus pneumoniae strain 0100993 (NCIMB 40794). The Streptococcus pneumoniae proteins of the invention can be used to identify compounds which interact with and inhibit or activate the activity of the proteins. Antagonists can be used to treat diseases caused by 5. pneumoniae proteins, through genetic immunisation. They can also be used to induce an immunological response in a mammal by inoculation with the 5. pneumoniae proteins or delivery of the encoding nucleic acids in a vector adequate to produce antibody and/or T cell immune responses to protect the animal from disease. The proteins can also be used to identify antimicrobial compounds which are capable of inhibiting their bloactivity. In particular the proteins of the invention can be used to prevent adhesion of bacteria to mammalian extracellular matrix proteins on in-dwelling devices or in wounds, to block protein-mediated mammalian cell invasion, and to block the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or other surgical techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           956 aagattgctccgtcaattctggcagcagattatgccaactttgaacgtgaaatcaaacgt 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1076 caaatcagttttggtgcaggtgtggtcgagagccttcgtcctcatagtaagatggttttc 1135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 atgetecaetteggegeegattggetecaeatggaeateatggatgggeattttgteeee 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 aatttaactattggcgctccagttattgaaagtttgagaaagcacacaaaggcatatttg 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 aaaatagctccttcgatgctcttccgacttcgccaatttggcttccgaggctcagcgc 92
                                                                                                                                                                                                                                                                                                                                                                                                Novel Streptococcus pneumoniae proteins and related DNA - useful for diagnosing anti-microbial agents for treatment of bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                  Hodgson JE, Knowles DJC, Nicholas RO;
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Pred. No. 3.6e-11;
0; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Pages 167-168; 483pp; English.
Location/Qualifiers
55..933
                                                                                                                                                                                                                         (SMIK ) SMITHKLINE BEECHAM CORP (SMIK ) SMITHKLINE BEECHAM PLC.
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55.5%;
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Matches 126; Conservative
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                                                                        W09743303-A1
                                                                                                             20-NOV-1997
                                                                                                                                                                                                                                                                                                  Stodola RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Infections
                                                                                                                                                                                                                                                                                Black MT,
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 Key
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A26928 standard; DNA; 1019 BP.

A26928/c

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This invention describes novel isolated Streptococcus pneumoniae polynucleotides (see 29617-29694) and their encoded proteins (see 786792-886182). The DNA, vectors and host cells described in the method of the invention are useful for the recombinant expression of the polypeptides. The polypeptides are useful for treatment or prevention of disease, or diagnosis of disease related to expression or activity of such a polypeptide. They can also be used to screen for compounds which interact with and inhibit or activate such a polypeptide. The compounds which colypeptides (or DNA encoding them, via gene therapy) are also useful for inducing an immunological response in a mammal. The antagonists are useful to inhibit such bacterial polypeptides. The polypeptides are particularly useful to identify antimicrobial compounds and antibiotics. They are also useful to determine their role in pathogenesis of infection, dysfunction and disease.
                                                                                                                        Treatment; prevention; disease; diagnosis; gene therapy; screening; bacterial; antimicrobial; antibiotic; pathogenesis; infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                    Nicholas RO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae proteins and related DNA - useful for screening compounds for antibacterial activity
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                                                                                                                                                                                                                                                                                                                                                                                                    Lonetto MA,
                                                                                        S. pneumoniae derived DNA from ORF #174.
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                                                                                                                                                                                                                                                                                                                                                                                                    Knowles DJC,
                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM CORP.
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                                                    (first entry)
                                                                                                                                                                                 Streptococcus pneumoniae.
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                                                    10-APR-2000
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                                                                                                                                                          279 AAGATTGCTCCGTCAATTCTGGCAGCAGATTATGCCAACTTTGAACGTGAAATCAAACGT 220
                                                                                                                                                                                                                   93 atgetecaetteggegeegattggetecaeatggaeateatggatgggeattttgteeee 152
                                                                                                                                                                                                                                                                     219 CTAGAAGCAACTGGGGCAGAATATGCCCATATCGATATCATGGACAGTCATTTTGTACCG 160
                                                                                                                                                                                                                                                                                                                           153 aatttaactattggcgctccagttattgaaagtttgagaaagcacacaaaggcatatttg 212
                                                                                                                                                                                                                                                                                                                                                                                159 CAAATCAGTTTTGGTGCAGGTGTGGTCGAGAGCCTTCGTCCTCATAGTAAGATGGTTTTC 100
                                                     Gaps
                                                                                                        33 aaaatagctccttcgatgctcttccgacttcgccaatttggcttccgaggctcagcgc 92
                                                     ;
Score 65.4; DB 19; Length 1542; Pred. No. 4e-11; 0; Mismatches 101; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                      gattgtcaccttatggttacaaatcctcttgattatgttgaaccctt 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.9%;
ilarity 55.5%;
Conservative (
                         Similarity
                            Best Local Sim
Matches 126;
  Query Match
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The present sequence represents an essential Staphylococcus aureus gene. The invention relates to a method for screening for an antibacterial sepent. The method comprises determining if a test compound is active against the essential bacterial genes (A26850-A26956). The invention also includes a method for evaluating an agent for activity on the essential genes. Also included in the invention is the production of an antibacterial agent. The antibacterial agents of the invention are used to treat or prevent bacterial infections, particularly where caused by Staphylococcus aureus. The antibacterial agents are unlikely to be
                                                                                                                Essential gene; Staphylococcus aureus infection; screening; prevention; antibacterial agent; bacterial infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          283 ttacatttcacgtagagacatcaaaagataactggaaagaacttatccaaagaatcaagt 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 ggcgccgattggctccacatggacatcatggatgggcattttgtccccaatttaactatt 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 ggcgctccagttattgaaagtttgagaaagcacacaaaggcatatttggattgtcacctt 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             821 TTNCAATTCATGTCGAATCAACGCCTCATA--TTTCATCGTGCTATTCAAATGATTAAAC 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4:1 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1001 GGNTTCGACGGAGTTCATTTTGATGTATGGATGGTCAATTTGTCCCCTAATATCTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     941 GGTTTACCAATATTAGATGCAGTAAGAAAGGCACAACATTACNTATAGACGTACATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   881 ATGATTGAAAATTCCAGAAAGTATATTGCATCATTTGCAGAACATGGTGCCGATATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225 atggtt-acaaatcctcttgattatgttgaacccttggcaaaagctggtgcttct-ggtt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel methods for screening for antibacterial agents, useful for treatment or prevention of Staphylococcus infection, by testing compounds against, essential bacterial genes
                                                                                                                                                                                                                                                                                                                                                                                                                                  Malouin F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.9%; Score 58; DB 21; Length 1019; 56.9%; Pred. No. 7.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1019 BP; 314 A; 211 C; 151 G; 340 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sun D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Column 183-184; 256pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Schmid MB,
                                                                             Essential Staphylococcus aureus gene #79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          affected by known resistance mechanisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Martin PK,
                                                                                                                                                                                                                                                                                                                                    95US-0003798.
95US-0009102.
                                                                                                                                                                                                                                                                                                                                                                                               (MICR-) MICROCIDE PHARM INC.
                                        (first entry)
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                                                                                                                                                                             Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-282222/24.
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                                        29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                       22-DEC-1995;
                                                                                                                                                                                                                  US6037123-A.
                                                                                                                                                                                                                                                         14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                    Benton B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
  A26928;
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This sequence encodes a Streptococcus pneumoniae protein of unknown the direction. The invention provides DNA sequences (V65201 to V63304) from the Streptococcus pneumoniae genome and corresponding protein sequences (W80605 to W80728). A recombinant host containing a vector comprising any of the above nucleic acids can be used for the recombinant expression of the protein sequences. The invention also provides a DNA chip having arrayed on it at least 15 base pair fragment of any one or more of these bNA sequences. The DNA chip having methods for evaluating gene expression in S. pneumoniae and for identifying virulence genes in S. pneumoniae and the selectively bind to the above proteins or peptide fragments can be used to treat S. pneumoniae infection. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153 aatttaactattggcgctccagttattgaaagtttgagaaagcacacaaaggcatatttg 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               712 ctagaagcaactggggcagaatatgcccatatcg--attctggacagtcattttgtaccg 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 gattgtcaccttatggttacaaatcctcttgattatgttgaacccttggcaaaagctggt 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            652 aagattgctccgtcaattctggcagcacattatgccaactttgaacgtgaaatcaaacgt 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33 aaaatagctccttcgatgctcttccgacttcgccaatttggcttccgaggctcagcgc 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eptococcus pneumoniae nucleic acid sequences - used in DNA chips evaluating gene expression, and identification of virulence
                                                                                                                                                                           Streptococcus pneumoniae protein; recombinant; gene expression;
DNA chip; virulence; antibody; infection; detection; treatment; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dehoff BS, Hoskins JA, Jaskunas SR;
Peery RB, Rockey PK, Rosteck PR;
Solenberg PJ, Treadway PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibodies can also be used to detect S. pneumoniae cells,
                                                                                                                                         DNA encoding a S. pneumoniae protein of unknown function.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.7%; Score 53.2; DB 19;
52.5%; Pred. No. 2.6e-07;
Live 0; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 75; 333pp; English.
                               V65230 standard; DNA; 1040 BP.
                                                                                                                                                                                                                                                                                                                                         97WO-US22578
                                                                                                                                                                                                                                                                                                                                                                          96US-0036281
                                                                                                    24-DEC-1998 (first entry)
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Matches 187; Conservative
                                                                                                                                                                                                                               Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                            (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Norris FH,
, Smith MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Baltz RH, Burgett SG,
Mills BJ, Norris FH,
Skatrud PL, Smith MC,
Young Bellido ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-348529/30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus
                                                                                                                                                                                                                                                                                                                                     09-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                        13-DEC-1996;
                                                                                                                                                                                                                                                                                                     18-JUN-1998,
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                                                                    V65230;
RESULT 10
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                  V65230
                                                                 셤
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Sequences A31040-A32093 represent novel plant microsatellite sequences and associated flanking species. The sequences comprise a central core repeat sequence, especially selected from the sequences A32094-A32096 with left and right flanking sequences. The polynucleotide sequences can be used in the detection of DNA polymorphisms, in genome mapping, in positional cloning of genes, in variety identification and in evaluation of genetic variability within and between plant tissues, populations, cultivars, species and species groups. They may also be used to design hybridization probes for oligonucleotide fingerprinting and ilbrary screening and to design primers for microsatellite-primed PCR. Microsatellite markers are useful to locate specific economically useful genes in plant genomes.
                                                                                                                                                                                                                                                                                                                                                                                                      Plant microsatellite sequence; core repeat sequence; detection; probe; DNA polymorphism; genome mapping; physical mapping; fingerprinting; variety identification; genetic variability evaluation; primer; ss.
                                  273 gcttctggttttacatttcacgtagagacatcaaaagataactggaaagaacttatccaa 332
gattgccacttgatggtgtcaaaccctgagcatcatctggaagattttgcgcgtgcaggt 888
                                                                        889 gcagacatcatcagtatccatgtagaagcaacacctcatattcatggcgccc---tccaa 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 329 tatctccatcaattctatctgctaatttttcgaagctgggagatcaggtgaaagctgtgg 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 tagetecttegatgetetetteegaettegeeaatttggetteegaggeteagegeatge 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New plant microsatellite markers and associated flanking species for the detection of polymorphic genetic markers \cdot
                                                                                                                                                   946 aaaattegtteaeteggagttaageetteagtegttateaateetggeaeaeeagt 1001
                                                                                                               333 agaatcaagtcacatggcatgattcctggtgtagcattaaagcctgggacccccgt 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 459 BP; 121 A; 113 C; 120 G; 103 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENE-) GENESIS RES & DEV CORP LTD & FLETCHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (FLET-) FLETCHER CHALLENGE FORESTS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glenn M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 136; 392pp; English.
                                                                                                                                                                                                                                                                                                                                                                  Plant microsatellite marker #206.
                                                                                                                                                                                                                                                     BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-NZ00092
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                                                                                                                                                                                                                                                                                                                           05-JUL-2000 (first entry)
                                                                                                                                                                                                                                                  A31245 standard; DNA; 459
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Best Local Similarity
T6; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eucalyptus grandis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09967421-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JUN-1998;
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                                                                                                                                                                                                                                                                                       A31245;
  829
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Mismatches 142; Indels

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Conservative

127;

Matches

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The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (V52134 to V52524) recorded to it, or a representative fragment or a sequence at least 938 identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO: 1 pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members or (b) isolating mRNA, DNA or CDNA produced molecules from the members or (b) isolating mRNA, DNA or CDNA produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5. pneumoniae genome of commercial importance, or expression modulating
fragments of the S. pneumoniae genome. Products from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used in diagnosis kits and assays, and pharmaceutical
from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the fragment of the S. pneumoniae genome to prime the amplification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay; computer readable medium; vaccine; pharmaceutical composition; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fannon M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae genome fragment SEQ ID NO:49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dougherty BA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 445-451; 1409pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                            V52182 standard; DNA; 11443 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-OCT-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Choi GH,
Rosen CA;
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                                                                                                                       157 taactattgg 166
                                                                                                                                                                                                        449 ttacaatcgg 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9818931-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barash SC,
Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V52182;
                                                                                                                                                                                                                                                                                                                               RESULT 12
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Score 41.8; DB 19; Length 11443; Pred. No. 0.0037;

10.8%;

Best Local Similarity

Query Match

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                   7859 accttttgggtagatcaagttctcgatttacaatgtgagtatatttgtattcatgctgaa 7918
                                                                                                                                                                                                                                     7919 gitcigaaiggicitigcitticgittigaitgataaaaitcaigaigcaggictaaaggci 7978
                                                                                                   7799 caagaagttcaaaaaattagtgacacacctttatcagttcatctgatggtcacagaccca 7858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   269 tggtgcttctggttttacatttcacgtagagacatcaaaagataactggaaagaacttat 328
120 cacatggacatcatggatgggcattttgtccccaatttaactattggcgctccagttatt 179
                                                                    180 gaaagtttgagaaagcacacaaaggcatatttggattgtcaccttatggttacaaatcct 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vero cells were cultured in the presence of actinomycin D and infected with PIV-2. Poly(A)+ RNA was isolated from the infected cells and a cDNA library was prepared. The library was screened with a nucleocapsid RNA probe. A positive clone containing the PIV-2 ene was sequenced. The gene can be used for early diagnosis of PIV-2 infection and as a raw material for vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                      240 cttgattatgttgaacccttggcaaaagctggtgcttctggttttacatttcacgtagag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human para-influenza type 2 virus large protein gene – useful in
diagnosis and as a vaccine against para-influenza virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6866 BP; 2257 A; 1274 C; 1194 G; 2141 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human parainfluenza virus 2 large protein gene.
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55.7%; Pred. No. v...
0; Mismatches
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                                                                                                                                                                                                                                                                                         360 ggtgtagcattaaagcctgggacccccgt 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human parainfluenza virus-2
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                                                                                                                                                                                                                                                                                                                                                                                          Q27406 standard; DNA; 6866
                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-FEB-1993 (first entry)
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nes 73; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP04197179-A.
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X61720 standard; DNA; 573

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1911 TGTTATCTCGCGTATATCTCTCGCCTTTTCTGATATTATGCCAATTTGACTCATAGTAA 1852
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                                                                                                                                                                                                                                                                                           Plant microsatellite sequence; core repeat sequence; detection; probe; DNA polymorphism; genome mapping; physical mapping; fingerprinting; variety identification; genetic variability evaluation; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New plant microsatellite markers and associated flanking species for the detection of polymorphic genetic markers -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.7%; Score 37.6; DB 21; Length 439; 60.9%; Pred. No. 0.016; Live 0; Mismatches 49; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 439 BP; 122 A; 95 C; 119 G;·102 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENE-) GENESIS RES & DEV CORP LTD & FLETCHER. (FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glenn M;
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                                                                                                                                                                                                                                                              Plant microsatellite marker #247.
                                                                                                                                                           A31286 standard; DNA; 439 BP.
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                                                                               1851 GCAATGATTTA 1841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 cagttattgaaagtttgagaaagcacacaaaaggcatatttggattgtcaccttatggtta 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 caaaaattcgtgggttgaaatctcaggcaaaggatgatttcattttttatcctttgtttt 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 ttaataatetaagatatgagataataggtagaaaaaatatttetaagggetttgaatttg 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232 caaatcotottgattatgttgaaccottggcaaaagotggtgottotggttttacatttc 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                            Antigenic protein; vaccine; Lyme disease; infection; detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated Borrelia burgdorferi nucleic acids - used to develop products for the diagnosis, prevention and treatment of diseases caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 573;
                                                             B. burgdorferi antigenic protein coding sequence, t457.nt.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 573 BP; 208 A; 43 C; 97 G; 225 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81;
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51.2%; Pred. No. 0.045;
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                                                                                                                                                                                                                                                                                                                                                                              Lathigra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 165; 275pp; English.
                                                                                                                                                                                                                                                                                                                                                                              Erwin AL, Hanson MS,
                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                  97US-0057483.
97US-0050359.
                                                                                                                                                                                                                                                                               97US-0053344.
                                                                                                                                                                                                                     98WO-US12718
                              (first entry)
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                                                                                                                                                                                                                                                                                                                                              (MEDI-) MEDIMMUNE INC
                                                                                                                         Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-189980/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                      WO9859071-A1
                                                                                                                                                                                                                   18-JUN-1998;
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20-JUN-1997;
                             19-JUL-1999
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                                                                                                                                                                                                                                                                                                22-JUL-1997;
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Database :

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	US-09-014-969-1	US-08-465-795-1	IIS-08-306-601-1F	CT-STED-DOC DO CO	PCT-US93-06251-29	115-08-105-482-220	0/0-707 00 00	02-08-/03-209-370	US-08-458-101-370	0.0 101 000 000	02-08-042-TA3B-IB	US-08-743-637B-180	COT 0/20 07/ 00 01	1-6TF-8TT-60-co	PCT-US94-06430-25	27 00 100 1 EDG	FCI - 0534 - 06430-21	PCT-US93-10500-1	1 0000 101 00 01	6-6/0-760-20-50	US-08-417-080-5	C COO 177 00 01	02-08-1/2-7/08-14	IIS-08-726-525-5	070 077 00 01	02-08-48/-942-5	US-08-726-036A-5
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ALIGNMENTS

GENERAL INFORMATION:
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GENERAL INFORMATION;
GENERAL INFORMATION, Bret
APPLICANT: Benton, Francois
APPLICANT: Malouin, Francois
APPLICANT: Malouin, Patrick K.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
NUMBER OF SEQUENCES: 111
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 112
ADDRESSE: LOG & Lyon & Lyon
STREET: 633 West Fifth Street
STREET: 633 West Fifth Street
STREET: 634 West Fifth Street
CORRESPONDENCE ADDRESS:
ADDRESSE: LOS Angeles
STREET: Suite 4700
CITY: Los Angeles
STREET: Suite 4700
CITY: Los Angeles
STREET: Suite 500
STREET: Suite 666
COMPUTER: SEDAME: FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.996
COMPUTER: TBM Compatible
OFERRATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: MORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 60/009,102
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,103
FILING DATE: September 15, 1995
APTONEY/ABENT INPOMMATION
NUMBER: September 15, 1995
ATTONEY/ASENT INPOMMATION
NAME: WAPHINT PINANTION:
NAME: WAPHINT PINANTION: 32,327 32,327 32,327 Sequence 79, Application US/08714918; Patent No. 6037123 GENERAL INFORMATION: NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFRENCE/OCKET NUMBER: 222/(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-160
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARGES LENGTH: 1019 base pairs TYPE: nucleic acid RESULT 1 US-08-714-918-79/C

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                                                                                                                                                                                 225 atggtt-acaaatcctcttgattatgttgaacccttggcaaaagctggtgcttct-ggtt 282
                                                                                                                                                                                                                                                                                                                                                                                             283 tiacaittcacgtagagacaicaaaagataaciggaaagaactiaiccaaagaaicaagi 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    821 TINCAATICATGTCGAATCAACGCCTCATA--TTTCATCGTGCTATTCAAATGATTAAAC 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                            165 ggcgctccagttattgaaagtttgagaaagcacacaaaaggcatatttggattgtcacctt 224
                                                                                                                                                                                                                                                                                                                       941 GGTTTACCAATATTAGATGCAGTAAGAAAAGGCACAACATTACNTATAGACGTACATTIG 882
                                                                                                                                             4; Gaps
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APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Are
TITLE OF INVENTION: Members of The Mage-B Family and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match

8.8%; Score 34; DB 5; Length 3781;
Best Local Similarity 57.5%; Pred. No. 0.11;
Matches 61; Conservative 0; Mismatches 45; Indels
                                                                                             / Match 14.9%; Score 58; DB 5; Length 1019; Local Similarity 56.9%; Pred. No. 3.8e-10; hes 161; Conservative 0; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lefebvre, Daniel D.
APPLICANT: Malboobi, Mohammad A.
APLICANT: Malboobi, Mohammad A.
TITLE OF INVENTION: PHOSPHATE STARVATION-INDUCIBLE PROTEINS
FILE REFERENCE: PPL96-03
CURRENT APPLICATION UNBER: US/08/688,988B
CURRENT FILING DATE: 1996-07-31
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FASTERO for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327 atccaaagaatcaagtcacatggcatgattcctggtgtagcattaa 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15, Application US/08846111D Patent No. 6017705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 5, Application US/08688988B
; Patent No. 6096545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRGANISM: Arabidopsis Thaliana US-08-688-988-5
                                                                                                                                                    Matches 161; Conservative
STRANDEDNESS: single
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           ; TOPOLOGY: linear
US-08-714-918-79
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                                                                                                         Query Match
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Db 13954 AGATGTGGAGGTAGAAGACAGTGATATTGATGATCCTGACCTTGTGTAGGCCTAGGCTAA 14013
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APPLICANT: Mau, Shaio-Lim
APPLICANT: Du, He
APPLICANT: Gane, Alison M
APPLICANT: Bacic, Antony
APPLICANT: Bric, Adrienne E
APPLICANT: Bric, Adrienne E
APPLICANT: Plant Arabinogalactan Protein (AGP) Genes
NUMBER OF SEQUENCES: 91
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8.1%; Score 31.6; DB 5; Length 40352;
Best Local Similarity 54.2%; Pred. No. 2.9;
Matches 64; Conservative 0; Mismatches 54; Indels 0;
                                                                       STATE: New York
2IP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Greenlee and Winner, P.C.
5370 Manhattan Circle, Suite 201
                                                                                                                                                                                            SOFTWARE: Wordperfect For DOS 6.0b CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,111D FILING DATE: 25-APRIL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Hanson, No. 6017705man D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/658,578 FILING DATE: 5-MAY-1996 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/403,388
                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD E TELECOMOUNICATION INFORMATION: TELEPHONE: (212) 688-9200
TELERAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 14-MARCH-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40352 base pairs
               SEE: Felfe & Lynch
: 805 Third Avenue
New York City
                                                                                                                                                                               OPERATING SYSTEM: PC-DOS
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EDNESS: single
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PRIOR APPLICATION DATA:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                              IBM
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US-08-276-452A-25/C
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                     ADDRESSEE:
                                                                                                                                                                  COMPUTER:
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28, 30, 32-37 are identical to sequences obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 41..112
OTHER INFORMATION: /note= "Derived amino acid sequence
OTHER INFORMATION: corresponding to the peptide sequence by protein
OTHER INFORMATION: microsequencing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Amino acids 25, 27, 29, and
31 are hydroxylated proline residues; amino acid
26 can be T instead of A"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       992 TGTAGTICTCAGAGTAGGCATIGTIGTITTITGTIGTAATICTCAGAGAAAAGCAITGT 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                932 TGTTATTGTTTTTGTTGTAATTCTCGGAGAAACATTATTGTTGTTGTTGTTCTCGGAGA 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

8.0%; Score 31; DB 1; Length 1430;
Best Local Similarity 46.2%; Pred. No. 0.67;
Matches 103; Conservative 0; Mismatches 120; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by protein microsequencing"
                                                                         APPLICATION NUMBER: US/08/276,452A FILING DATE: 18-JUL-1994 CLASSIFICATION: 435
                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Caruthers, Jennie M.
REGISTRATION NUMBER: 34,464
REFERENCE/DOCKET NUMBER: 27-91A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303)499-8080
TELEFAX: (303)499-8089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25, Application US/08798744; Patent No. 5830747; GENERAL INFORMATION:
APPLICANT: Chen, Chao-Guang APPLICANT: Mau, Shaio-Lim
                                                                                                                                                                                                                                                                                                                    TELEX: 49617824
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1430 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: 41..112
OTHER INFORMATION: /note
OTHER INFORMATION: 28, 3
OTHER INFORMATION: by pr
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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28, 30, 32-37 are identical to sequences obtained
by protein microsequencing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Derived amino acid sequence corresponding to the peptide sequence by protein microsequencing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Amino acids 25, 27, 29, and
31 are hydroxylated proline residues; amino acid
26 can be T instead of A"
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APPLICANT: Du, He
APPLICANT: Gane, Alison M
APPLICANT: Bacic, Antony
APPLICANT: Bacic, Antony
APPLICANT: Clarke, Adrienne E
TITLE OF INVENTION: Plant Arabinogalactan Protein (AGP) Genes
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.0%; Score 31; DB 3; Length 1430; Best Local Similarity 46.2%; Pred. No. 0.67; Matches 103; Conservative 0; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,744
FILIG DATE: 13-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION: 435
APPLICATION DATA:
APPLICATION NUMBER: 08/276,452
FILIG DATE: 18-UUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                      ADDRESSEE: Greenlee and Winner, P.C. STREET: 5370 Manhattan Circle, Suite 201 CITY: Boulder
                                                                                                                                                                                                                                                                     United States of America
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Caruthers, Jennie M. REGISTRATION NUMBER: 34,464
REFERENCE/DOCKET NUMBER: 27-
TELECOMMUNICATION: TELEPHONE: (303)499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (303)499-8089
TELEX: 49617824
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1430 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: 41..112
OTHER INFORMATION: /not
OTHER INFORMATION: 28,
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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US-08-798-744-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                              STATE: Colorado
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 tgagaaagcacacaaaaggcatatttggattgtcaccttatggttacaaatcctcttgatt 246
                                                     263 aaaagctggtgcttctggttttacatttcacgtagagacatcaaaagataactggaaaga 322
                                                                                       872 AAGCATTGTTGTTATTGTTGTTGTTATTCTCGGAGAAACATTATTGTTATTATTGTTGT 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 acatcatggatgggcattttgtccccaatttaactattggcgctccagttattgaaagtt 186
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                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Inzana, Thomas J.
APPLICANT: Ward, Christine
TITLE OF INVENTION: RECOMBINANT VACCINE FOR DISEASES CAUSED
TITLE OF INVENTION: BY ENCAPSULATED ORGANISMS
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,814,
FILING DATE: 27-JUN-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69;
                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Whitham, Curtis, Whitham & McGinn STREET: 11800 Sunrise Valley Dr., Suite 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Whitham, Michael E.
REFERENCE/DCOKET NUMBER: VIIP 95-067
TELECOMUNICATION INFORMATION:
TELEPHONE: 703-391-2510
TELEFRAX: 703-391-9035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 5, Application US/08673814
; Patent No. 6086894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 283072
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
2743..3150
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1586..2740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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376..1557
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Best Local Similarity
'-haq 72; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 27 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1180(
CITY: Reston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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LOCATION:
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US-08-673-814-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
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1618 ITCTGTCGGACTTGCCGTAATAGTTGTTTCCATATTTTATCCTTATAAATTCAATATATT 1559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       275 ttctggttttacatttcacgtagagacatcaaaagataactggaaagaacttatccaa 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Davis, Maria
APPLICANT: Davis, Maria
APPLICANT: Davis, Maria
APPLICANT: To Davis, Maria
APPLICANT: TO SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5;
                                                                                                                                                                                                                                             APPLICANT: John, Maliyakal
TITLE OF INVENTION: FIBER-SPECIFIC PROMOTERS
WHERE OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   score 30; DB 5; Pred. No. 1.9; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Baker, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 670513.90244
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                             E: Quarles & Brady
411 East Wisconsin Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23, Application US/08766014
Patent No. 5744312
                                                                                                                                                                             Sequence 6, Application US/08749522
Patent No. 6096950
GENERAL INFORMATION:
APPLICANT: JOHN, Maliyakal
                                                                              1558 AATAGGCACGAATAGCATTAG 1538
                                        247 atgttgaacccttggcaaaag 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: DNA (genomic)
US-08-749-522-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (414) 277-5709
TELEFAX: (414) 277-552
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 2168 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                STREET: 411 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                              US-08-749-522-6/c
                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                           STATE: WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.7%; Score 29.8; DB 2; Length 2622; Best Local Similarity 55.2%; Pred. No. 2.4; Matches 58; Conservative 0; Mismatches 47; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 atcctcttgattatgttgaacccttggcaaaagctggtgcttctg 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 AACTIATCGAGGAGAAAACCTGATTACATAGCTATTGCTTTTG 175
                                                                                                                                                                                                                                                                                                                                                       CLASSIFTCATION: 435

CLASSIFTCATION: 435

PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,688

FILING DATE: December 15, 1995

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327

REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Mamooe, Joseph A.
APPLICANT: Davis, Maria
APPLICANT: Sha, Dan
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASE
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                             DOS 5.0
                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.(
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,014
FILING DATE: Herewith
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STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08766014
Patent No. 5744312
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (213) 489-1600
TELERAX: (213) 955-0440
TELER: 67-3510
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2622 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                               Los Angeles: California
RY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                    90071-2066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-766-014-23
                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-766-014-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 tggcttccgaggctcagcgcatgctccacttcggcgcccgattggctccacatggacatca 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: MISHRA, LOPA
TITLE OF INVENTION: GENES CODING PROTEINS FOR EARLY LIVER DEVELOPMENT.
FILE REFERENCE: XX/PO3470US0
CURRENT APPLICATION NUMBER: US/08/841,349B
CURRENT FILING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 29.8; DB 2; Length 5300;
Pred. No. 3.6;
0; Mismatches 47; Indels 0
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                                                                                                                                                                                       One
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,014
CLASSIFICATION 1435
PILING DATE: Herewith
CLASSIFICATION DATA:
PRIOR APPLICATION DATA: Including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 60/008,688
FILING DATE: December 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: WASTUNG, RICHARD 3.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 tggatgggcattttgtccccaatttaactattggc 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08841349B Patent No. 5955594
                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.7%;
Best Local Similarity 55.2%;
Matches 58; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 5300 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) NAME/KEY: CDS
; LOCATION: (333)...(6794)
US-08-841-349-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
US-08-766-014-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-841-349-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 6960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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Query Match 7.5%; Score 29; DB 1; Length 4182; Best Local Similarity 57.0%; Pred. No. 5.9; Matches 53; Conservative 0; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-08-257-073-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                       US-07-973-257-1
       STRAIN:
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                                                                                                                                                                            APPLICANT: MISHRA, LOPA
TITLE OF INVENTION: GENES CODING PROTEINS FOR EARLY LIVER DEVELOPMENT. . .
TITLE OF INVENTION: GENES CODING PROTEINS FOR EARLY LIVER DEVELOPMENT. . .
TITLE REFERENCE: XX/PO4470050
CURRENT APPLICATION NUMBER: US/08/841,349B
CURRENT FILING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4006 TCGCTCACCAGTCTTCGGCCAGTCTCCACAACAGCATTGATCTTCTCCTCGTTGGCATCC 3947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 tggcttccgaggctcagcgcatgctccacttcggcgccgattggctccacatggacatca 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACHERAL INCRMATION:
APPLICANT: Keeler, Jr. Calvin L.
APPLICANT: Dohms, John E.
TITLE OF INVENTION: Gene Encoding Cytadhesin
TITLE OF INVENTION: Protein of Mycoplasma Gallisepticum and Its Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 29.4; DB 4; Length 8176;
Pred. No. 6.4;
0; Mismatches 41; Indels 0
  3946 AFGGTGGTCATGAAGTCCTCCTGCTTTTTAATGGC 3912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3946 ATGGTGGTCATGAAGTCCTCCTGCTTTTTAATGGC 3912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Wordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/973,257
FILING DATE: 19921109
CLASSIFICATION: 435
PRIOR APPLICATION DATA: No. 5378820e
INFORMATION FOR SEQ ID No: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4182 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mycoplasma Gallisepticum
                                                    RESULT 11
US-08-841-349-5/c
; Sequence 5, Application US/08841349B
"-+ant No. 5955594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM/PC or Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 4182 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-07-973-257-1/c
; Sequence 1, Application US/07973257
; Patent No. 5378820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Connolly and HussTREET: 1220 Market Street CITY: Wilmington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.6%;
Best Local Similarity 56.8%;
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: Genomic DNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Mus musculus US-08-841-349-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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COUNTRY: U.S.A.
ZIP: 19899
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 5
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                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,073
FILING DATE: 09-JUN-1994
CLASSIFICATION 1424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,783
FILING DATE: 11-JUN-1993
PRIOR APPLICATION NUMBER: US 07/852,305
FILING DATE: 18 WAR-1992
PRIOR APPLICATION NUMBER: US 07/852,305
FILING DATE: 18 WAR-1992
PRIOR APPLICATION NUMBER: US 07/672,183
FILING DATE: 20-MAR-1991
ATTONING NUMBER: US 07/672,183
FILING DATE: 20-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.5%; Score 29; DB 2; Best Local Similarity 53.0%; Pred. No. 6.7; Matches 62; Conservative 0; Mismatches 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue, 25th Floor
CITY: New York
                                                                                                                         4042 AGCTGGTGCTTTTGCTCCTGGAGCAGA 4010
                                                                                                266 agctggtgcttctggttttacatttcacgtaga 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Frommer, William S.
REGISTARION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2570
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                   Sequence 10, Application US/08257073;
Patent No. 5766597;
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: de Taisne, Charles
APPLICANT: Tine, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212) 840-3333
TELERAX: (212) 840-0712
TELEX: 425066 CURTMS
INFORMATION FOR SED ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5181 base pairs
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STRANDEDNESS: single
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0652.0980004
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G tz, Friedrich
Schnell, No. 5843709bert
Augustin, Johannes
Engelke, Germar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/466,961A FILING DATE: 06-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/392,625
FILING DATE: 22-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/876,791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/876,791
FILING DATE: 30-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/784,234
FILING DATE: 31-OCT-1991
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                           Sequence 16, Application US/08466961A Patent No. 5843709 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 065
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosenstein, Ralf
Kaletta, Cortina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
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EDNESS: single
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MEDIUM TYPE: Floppy
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US-08-466-961A-16/C
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US-08-466-961A-16
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APPLICANT:
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APPLICANT:
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224 tatggttacaaatcctcttgattatgttgaacccttggcaaaagctggtgcttctggttt 283
                                                                                                3105 TACAGGTTTGACCGAAACACAAAAAAATGCATTAAATGATGAAATTAAAAAATTAAA 3161
                                                                            284 tacatttcacgtagagacatcaaaagataactggaaagaacttatccaaagaatcaa 340
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kupke, Thomas
APPLICANT: Jung, G nther
APPLICANT: Fellner, Roland
TITLE OF INVENTION: Blosynthetic Process For The Preparation
TITLE OF INVENTION: Of Chemical Compounds
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.5%; Score 29; DB 3; Length 8700; 47.5%; Pred. No. 9; tive 0; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Sterne, Kessler, Goldstein & Fox 1100 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0652.0980002
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CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION DATE:
APPLICATION DATE: 30 APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W
REGISTRATION NUMBER: 32,893
REFERNEK/DCOKET NUMBER: 0652.09800
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
TEMETHY FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                     Entian, Karl-Dieter
G tz, Friedrich
Schnell, No. 5837485bert
Rugustin, Johannes
Engelke, Germar
Rosenstein, Ralf
Raletta, Cortina
Klein, Cora
                                                                                                                                                                                                                 Sequence 16, Application US/08392625
Patent No. 5837485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 8700 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 47.59
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1100 New CITY: Washington STATE: D.C.
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                                                                                                                                                                            RESULT 14
JS-08-392-625-16/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT
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4514 AGATAAAACAAATTTTTCTTTTTCAGGATTAATACCGAATATTCTATTACAACGCATGTT 4455
296 agagacatcaaaagataactggaaagaacttatccaaagaatcaagtcacatggcatgat 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Klein, Cora
APPLICANT: Wieland, Bernd
APPLICANT: Kupke, Thomas
APPLICANT: Jung, G nther
APPLICANT: Kellner, Rolland
TITLE OF INVENTION: Biosynthetic Process for the Preparation of
TITLE OF INVENTION: Chemical Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Sterne, Kessler, Goldstein & Fox STREET: 1100 New York Avenue, NW CITY: Washington
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                         0; Gaps
Query Match
7.5%; Score 29; DB 3; Length 8700;
Best Local Similarity 47.5%; Pred. No. 9;
Matches 86; Conservative 0; Mismatches 95; Indels
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Search completed: November 4, 2000, 13:33:58 Job time: 16674 sec

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November 4, 2000, 11:52:10 ; Search time 4352.3 Seconds (without alignments) 551.186 Million cell updates/sec
                                                                                                             14379728
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                           7189864 seqs, 3091403243 residues
                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                 OM nucleic - nucleic search, using sw model
                                                                                                                                IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                            US-09-300-482-298
                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
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em_estba:*
em_estfun:*
em_estfun:*
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gb_est11:*
gb_est12:*
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gb_est37:*
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	37973 sa3 12302 AV4	42690 sa85b04	2881 NFUUIC 5053 NF119G	3508 GM210002	25192 AV425192	1120 MtBA42A	3286 HVSMEg00	1347 WHE0441	864 WHE1258_	100 B AUSSAOA	023 EST24836	355 EST25345	1337 EST27479	23738 EST30054	I896020 EST26546	5338	2294 EST24359	13/3 EST2524/	386U AV33386U 47 RTC	EST2440	3 EST26839	A071P71U	A061P33	A015P26	A001P55U	283 DG1_27_G	WHE0443	ICS4145	ICR2840A	ST03D04	AU / 2p4 3u	GM210	7/5 LODI	2000	1101/45 AUU0F2	5543 AU85p48u	V5451/4 AV5451	To	34120 MG03C03	288722 Mou	
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ALIGNMENTS

Strategiers of IIISC Strate Synthesis Partner, and Strategiers of IIISC Strates Synthesis, the CDNA ends were 'polished' with Cone Pt' DNA polymerase.' ligated to EcoRI adapters, with cone Pt' DNA polymerase.' ligated to EcoRI adapters, and phosphorylated. The XDIS site within the first-strand synthesis primer was restricted by digestion with XDOI; all XNOI sites in the CDNA would be protected by their hemimethylated status. The CDNA constructs were size-fractionated with a 500bp cutoff, using GibcoBRL Life Technologies' CDNA Size Practionation column. The column eluent was then ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+) that had been digested with EcoRI and XDOI, and phosphorylated). Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts. Blue colonies 9m-15) have been sequenced, and possess putative cDNA inserts. This library was constructed by Dr. Paul Kelm & Viiginia H. Coryell, paul Keim), 520-523-1078 (Dr. Paul Keim), 520-523-1078 (Dr. Paul Keim), 520-523-1078 (Dr. Paul Keim), 60-523-1070 (miversity, Fax: /note="Vector: pBluescript II XR; Site_I: EcoRI; Site_2: XhoI: Root cDNA. The mRNA was isolated from entire roots of 8 day old 'Williams' seedlings which were propagated on paper towels with distilled water. Stratagene's cDNA Synthesis Kit (catalog #200401) was used to synthesize the CDNA. First strand Synthesis was performed with 5-methyl dCTP, hence the ligated cDNA is hemimethylated. Stratagene's first-strand synthesis primer was used Shoemaker, R. Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Thelsing, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Kitter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R. Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (3314) 427-3222 FAX:(888) 919-3324 or (334)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
Insert Length: 945 Std Error: 0.00
Seq primer: -40RP from Gloco
High quality sequence stop: 414 A1437973 418 bp mRNA EST 18-APR-2000 a334012.71 Gm-C1004 Glycine max CDNA clone GENOME SYSTEMS CLONE ID: Gm-C1004-1199 5' similar to TR:014105 O14105 RIBULOSE-PHOSPHATE 3-EPIMERASE.;, mRNA sequence. Glýcine max Bukaryota; Viridiplantae; Embryophyta; Tiacheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine. 18-APR-2000 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 /clone="GENOME SYSTEMS CLONE ID: Gm-c1004-1199" /clone_lib="Gm-c1004" Unpublished (1999) Contact: Shoemaker R/Public Soybean EST Project 1. 418 /organism="Glycine max" /db_xref="taxon:3847" /tissue_type="root" /lab_host="XL10-Gold" Location/Qualifiers Public Soybean EST Project A1437973.1 GI:4289768 POLYA-No. soybean. source DEFINITION ORGANISM ACCESSION JOURNAL VERSION KEYWORDS REFERENCE AUTHORS FEATURES TITLE COMMENT

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Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids I;
Fabales, Fabaceae, Papilionoideae, Lotus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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/clone="lime"Lotus japonicus young plants (two-week old)"
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/note="Vector: pBluescriptII SK-; Site_l: EcoRI; Site_2:
XhoI; isolate=Miyakojima MG-20"
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Generation of 7137 non-redundant expressed sequence tags from a legume, Lotus japonicus
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                   113
                                                                                        Score 365.4;
virginia.coryell@nau.edu"
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Unpublished (1999)
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Glycine.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               caaaagataactggaaagaacttatccaaagaatcaagtcacatggcatgattcctggtg
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                                               32;
  Score 320.8; DB 1
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Fax: 314 286 1810
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High quality sequence stop: 395

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                                                                                      ACCESSION
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                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                            AUTHORS
                               AW682881
                                                                                                              KEYWORDS
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XhoI; Root cDNA. The mRNA was isolated from entire roots
Apol "Williams' seedlings which were propagated on
paper towels with distilled water. Stratagene's cDNA
Synthesis Kit (catalog #200401) was used to synthesize the
CDNA. First- strand synthesis was performed with 5-methyl
dCTP, hence the ligated cDNA is hemlmethylated.
Stratagene's first-strand synthesis primer was used
[GAGGAGAGAGAGAACTACTCGAG(T).18]. After
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aatttggetteegaageeteagegeatgeteeaetteggegeegattggeteeacatggae 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 atcatggatgggcattttgtccccaatttaactattggcgctccagttattgaagtttg 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 ATCATGGATGGGCATTTTGTCCCCCAATTTAACTATTGGCGCTCCAGTTATTGAAAGTTTG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 agaaagcacacaaaggcatatttggattgtcaccttatggttacaaatcctcttgattat 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 AGAAAGCACACAAAGGGATATTTGGATTGTCACCTTATGGTTACAAATCCTCTTGATTAT 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            309 gataactggaaagaacttatccaaagaatcaagtcacatggcatgattcctggtgtagca 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Indels 21; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.0%; Score 310.4; DB 10; Length 405; 91.6%; Pred. No. 1.1e-82; tive 0; Mismatches 11; Indels 21;
                                                              /clone="GENOME SYSTEMS CLONE ID: Gm-c1004-6056"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 t
                                   /organism="Glycine max"/db_xref="taxon:3847"
                                                                                                      /lab_host="XL10-Gold"
                                                                           /clone_lib="Gm-c1004"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96
9
         Location/Qualifiers
                                                                                            /tissue_type="root"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                340 TTAAAGCCTGGGACCCCCAT 359
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POLYA=No.
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            FEATURES
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Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula leaf library
Unpublished (2000)
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
Fer: 580 221 7391
Fex: 580 221 7380
                                                                                                                                                                                          Medicago truncatula
Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bagnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Medicago.
AW682881 641 bp mRNA EST 15-JUN-2000 NF001C10LF1F1081 Developing leaf Medicago truncatula cDNA clone NF001C10LF 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 gccaatttggettccgaggetcagcgcatgetccacttcggcgccgattggctccacatg 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: Lambda Zap; Contains a mixture of very young, developing, mature and senescing leaves." 130 c 139 g 171 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 AAAAGAAGAAAGATGGGAGTGACACCGAAAATAGCTCCTTCGATGCTATCATCAGATTTT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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79.3%; Score 307.8; DB 23; Length 641;
Best Local Similarity 87.7%; Pred. No. 7e-82;
Matches 336; Conservative 0; Mismatches 47; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="Pooled developmental"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Medicago truncatula"
/db_xref="taxon:3880"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Developing leaf"
/tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FdA: gdmay@noble.org
Email: gdmay@noble.org
Insert Length: 641 Std Error: 0.00
Plate: 001 row: C column: 10
Seq primer: TCACACAGAAACAGCTATGAC.
Location/Qualifiers
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Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
Magnoliophyta; eudicotyledons; core eudicots, Rosidae; eurosids I;
Fabales, Fabaceae, Papilionoideae; Medicago.
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                                                                                                                                         NF119G01ST1F1006 Developing stem Medicago truncatula cDNA clone
                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 633)
He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 gecaatttggettccgaggetcagcgcatgetccacttcggcgccgattggctccacatg 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: Lambda Zap; Contains a mixture of internodal stem segments"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Medicago Genome Initiative accession: MGI:S:15815
Insert Length: 633 Std Error: 0.00
Plate: 119 row: G column: 01
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="Pooled developmental"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Medicago truncatula"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="NF119G01ST"
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                                                                                                                                                                                                                                                                                                                                                                                                                Medicago truncatula stem library Unpublished (2000)
                                                                                                                                                          NF119G01ST 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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366 gcattaaagcctgggacccccgt 388
| |||||||||||||||||
                                   486 TCGATAAAGCCTGGAACATCCGT 508
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                                                                                                                                                                                                 BE325053.1 GI:9198914
                                                                                                                              633 bp
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Fax: 580 221 7380
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                                                                                                         BE325053
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//note="Vector: paluescript II XR; Site_1: EcoRI; Site_2:
XhoI; Library Gm-r1021 is a sequence-driven, reracked set
of the original library Gm-c1004 which was prepared from
root CDNA. The mRNA was isolated from entire roots of 8
day old 'Williams' seedlings which were propagated on
paper towels with distilled water. Stratagene's cDNA
Synthesis Kit (catalog #20040I) was used to synthesize
the cDNA. The Gm-c1004 library was constructed by Dr.
Paul Keim & Virginia H. Coryell, Department of Biology,
Box5640, Northern Arizona University, Flagstaff, Az 86011
'email: paul keim@eau.edu, virginia.coryell@nau.edu. The
contig analysis to select unique genes was performed by
the laboratory of Ernest Retzel, Computational Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids I,
Fabales, Fabaceae, Papilionoideae, Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vodkin, L., Keim, P., Shoemaker, R., Retzel, E., Khanna, A., Coryell, V., Erpelding, J., Raph, C., Shoop, E., Pardinas, J., Liu, L. and Lewin, H. A Functional Genomics Program for Soybean (NSF 9872565)
Unpublished (1999)
Contact: Vodkin, L.O., PI, A Functional Genomics Program for Soybean (NSF 9872565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA 1217, 244-6147
Fax: (217) 244-6147
Fax: (217) 334-458
Email: 1-vodkineuluc.edu
This clone is available through: Genome Systems, Inc. 4633 World
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parkway Circle St. Louis, Missouri 63134. For further information call: (800) 430-0030 or (314) 427-3222 FAX:(888)919-3324 or (314) 427-3324 or contact:clones@genomesystems.com_or_info@genome
                                               306 aaagataactggaaagaacttatcc-aaagaatcaagtcacatggcatgattcctggtgt 364
                                                                                                                                                                                                                                                                                                                     AW348508 736 bp mRNA EST 01-FEB-200
GW210002B12C3R Gm-r1021 Glycine max cDNA 3', mRNA sequence.
AW348508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ystems.com web site:www.genomesystems.com
Seq primer: 5. TTTTTTTTTTTTTTTT(A/C/G)-3V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Glycine max"
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/db_xref="taxon:3847"
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                                                                                                                        365 agcattaaagcctgggaccccgt 388
                                                                                                                                                             464 ATCGATAAAGCCTGGAACATCCGT 487
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tegecaatttggetteegaggeteagegatgeteeactteggegegegattggeteeaca 123 74 GTAACAAACAAACGATGGGAGTGACACCCAAAATTGCTCCGTCGATGCTCTCATCGGACT 133

304 caaaagataactggaaagaacttatc 329

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Bukaryota, Viridiplantae, Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Lotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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/db_xref="teaxon:34305"
/clone="MRMG5007_r"
/clone=lib="Lotus japonicus young plants (two-week old)"
/dev_stage="young plants (two-week old)"
/note="Vector: pBluescriptII SK.; Site_1: EcoRI; Site_2:
XhoI; isolate=Miyakojima_MG-20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Generation of 7137 non-redundant expressed sequence tags from a legume, Lotus Japonicus
DNA Res. 7 (2), 127-130 (2000)
                                                                                                                                                                                                              69 aatttggcttccgaggctcagcgcatgctccacttcggcgccgattggctccacatggac 128
                                                                                                                                           129 atcatggatgggcattttgtccccaatttaactattggcgctccagttattgaaagtttg 188
                                                                                                                                                                             676 ATCATGGATGGGCATTTTGTCCCCAATTTAACTATTGGCGCTCCAGTTATTGAAAGTTTG 617
                                                                                                                                                                                                                                                                                   gttgaaccettggcaaaagetggtgettetggttttacatttcacgtagagacatcaaaa 308
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                                     Gaps
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AV425192 Lotus japonicus young plants (two-week old) Lotus
japonicus cDNA clone MWM050b07_r 5', mRNA sequence.
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Best Local Similarity 91.4%; Pred. No. 6.1e-74;
Matches 298; Conservative 0; Mismatches 28; Indels 0;
DB 21; Length 736;
Score 285.4; DB 21; Length
Pred. No. 3.9e-75;
0; Mismatches 31; Indels
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Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
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Kazusa DNA Research Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Yasukazu Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                 369 ttaaagcctgggaccccgt 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTAAAGCCTGGGACCCCCAT 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AV425192
AV425192.1 GI:7782868
 Query Match 73.6%;
Best Local Similarity 90.3%;
Matches 289; Conservative
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Eukaryóta; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillionoideae; Medicago.

1 (bases 1 to 448) Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O., Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Gianinazzi-Pearson

,V. and Gamas,P. Medicago truncatula ESTs from nitrogen-starved roots

Contact: Genoscope Unpublished (2000)

JOURNAL

TITLE

AUTHORS

Contact: remoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmall: sequefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Contact: Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Emall:
Mt-estétoulouse.inra.fr Website:
Location/Qualifiers

.448

source

MtBA42A06F1 MtBA Medicago truncatula cDNA clone MtBA42A06 T3, mRNA

AL371120.1 GI:9670873

sednence. AL371120

Medicago truncatula

ORGANISM

barrel medic.

mRNA

448 bp

03-AUG-2000

EST

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directionally lighted into Uni-zapXR vector from Stratagene and packaged using Gigapack Gold packaging Stratagene and packaged using Gigapack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using ExAssit helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de sequencing was performed by the Centre National de sequences (Genoscope, Evry, France)."
                                                                                                                                                                                                                                /dev_stage="harvested after 3 days of N-starvation"
/note="Vector: pBluescript pSK; Site_1: EcoRI; Site_2:
XhoI; Plants were grown in an aeroponic chamber for 14
days on nitrogen-rich medium followed by 3 days on N-free
medium. RNA was extracted from root tips (1-3 cm). cDNA
was prepared from polyA+ enriched RNA. The cDNA was
/organism="Medicago truncatula"
/cultivar="Jemalong"
/db_xref="taxon:3880"
/clone="MtBA42A06"
                                                                                                                                                                                              /tissue_type="root tips"
                                                                                                                                                         /clone_lib="MtBA"
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gaaagaaagaaagaatgggaatgacaccgaaaatagctccttcgatgctcttccgact 63

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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.

(bases 1 to 825)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu., Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, Y., Saski, C., Schwartzbeck, J., Simmons, J., Chol, D.W., Main, D. and Wood, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Development of a genetically and physically anchored EST resource for barley genomics Unpublished (2000)
                                                                                                                                    AW981286 825 bp mRNA EST 25-JUL-2000 HVSME90010B10f Hordeum vulgare pre-anthesis spike EST library HVCNDA0008 (white to yellow anther) Hordeum vulgare cDNA clone HVSME90010B10f, mRNA sequence.
                                                                                                                                                                                                                                                                            185 tttgagaaagcacacaaaggcatatttggattgtcaccttatggttacaaatcctcttga 244
                                                                                                                                                                                                                                                                                                 305 aaa-----agataactggaaagaacttatccaaagaatcagaagtcacatg 348
                                                                                                                                                                                                                                                                                                                                                                                                                                           5 aaagaaagaaagatgggaatgacaccgaaaatagctccttcgatgctcttccgactt 64
                                                                                                   15 AAAAGAGAAAGATGGGAGTGACACCGAAAATAGCTCCTTCGATGCTATCATCAGATTT 74
       DB 14; Length 448;
72.5%; Score 281.2; DB 14; Length 84.0%; Pred. No. 6.3e-74; tive 0; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wing RA
Clemson University Genomics Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:4513"
/clone="HVSMEg0010B10f"
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High quality sequence stop: 484.
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                                 Matches 336; Conservative
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                Best Local Similarity
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/clone_lib="Hordeum vulgare pre-anthesis spike EST library
HYCDNAD008 (white to yellow anther)"
/tissue_type="pre-anthesis spike"
/lab_host="SQL"
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Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.
The structure and function of the expressed portion of the wheat
                                                                            /note="Vector: lambda2AP; Site_1: EcoR1; Site_2: Xho1" 225 c 231 g 178 t 1 others
                                                                                                                                                                                                                                                                                                                                     146 tgtccccaatttaactattggogctccagttattgaaagtttgagaaagcacacaaaggc 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206 atatttggattgtcaccttatggttacaaatcctcttgattatgttgaacccttggcaaa 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266 agctggtgcttctggttttacatttcacgtagagacatcaaaagataactggaaagaact 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       326 tatccaaagaatcaagtcacatggcatgattcctggtgtagcattaaagcctgggaccc 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE404347 494 bp mRNA EST 21-JUL-2000 WHE0441_B06_C11ZS Wheat etiolated seedling root cDNA library Triticum aestivum cDNA clone WHE0441_B06_C11, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Strategene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               232 TGTTCCTAATTTAACTATTGGAGCTCCAGTGATTGAGAGCTTGAGGAAGCACCAAGGC
                                                                                                                                                                          Query Match 63.0%; Score 244.6; DB 25; Length 825; Best Local Similarity 79.6%; Pred. No. 7e-63; Matches 289; Conservative 0; Mismatches 74; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum
1 (bases 1 to 494)
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800 Buchanan Street, Albany, CA 94710, USA
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Triticum aestivum
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Fax: 5105595818
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meiosis to late meiosis. The tissue, total RNA, and poly(A) RNA were prepared (Butler, Ross and Gustafson) at University of Missouri, Columbia. A cDNA library was made, and the DNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Amberson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: EcoRI; Site_2: XhoI; Plants were grown in the greenhouse. Anthers were harvested and pooled from early meiosis to late meiosis. The tissue, total RNA, and
                                                                                                        US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
The structure and function of the expressed portion of the wheat genomes - Anther cDNA library from rye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 atatttggattgtcaccttatggttacaaatcctttgattatgttgaacctttgcaaa 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 CGTTCCTAATTTAACTATTGGAGCTCCAGTGATTGAGAGCTTGAGGAAGCACACAAAGGC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 GECGGCGAAGATAGCGCCGTCCATGCTCTCGTCGGACTTCGCCAACCTCGCCGCAGAGGC 71
                                                                                                                                                                                                                                                                          Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 tgtccccaatttaactattggcgctccagttattgaaagtttgagaaagcacacaaaggc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:4550"
/clone="WHE1258_D10_H20"
/clone_lib="Secale cereale anther cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
61.4%; Score 238.2; DB 36; Length 526;
Best Local Similarity 78.5%; Pred. No. 5.3e-61;
Matches 285; Conservative 0; Mismatches 78; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Anther"
/dev_stage="Adult plant before anthesis"
/lab_host="E. coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Secale cereale"/cultivar="Blanco"
                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                         Email: oandersn@pw.usda.gov
                                                                                             Contact: Olin Anderson
                                                           Unpublished (2000)
                                                                                                                                                                                                Tel: 5105595773
Fax: 5105595818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123
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AU069503
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                                                                                                                                                                 /dev_stage="Five day old etiolated seedling"
/dab_host="E. coli SOLR"
/dab_host="E. coli SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRn: Site_2: Nho!: Seeds were surface-sterilized
site_1: EcoRn: Site_2: Nho!: Seeds were surface-sterilized
, germinated and grown aseptically in the dark at room
temperature on filter paper with water, nystatin and
cefotaxime in covered crystallization dishes. Roots were
harvested. The tissue, total RNA, and poly(A) RNA were
prepared, a cDNA library was made, and the cDNA clones
were in vivo excised to give pBluescript phagemids in the
TJ Close lab (Choi, Close, Fenton) at the University of
California, Riverside. Plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab (all
other authors)."
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WHE1258_D10_H202S Secale cereale anther cDNA library Secale cereale
cDNA clone WHE1258_D10_H20, mRNA sequence.
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Magnoliophyta; Liliopsida; Poales; Poaceae; Secale.
1 (bases 1 to 526)
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Anderson.O.D., Butler,E., Chao,S., Choi,D.W., Close,T.J., Fenton
,R.D., Gustafson,J.P., Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R.,
Miller,R., Rausch,C.J., Ross,K., Seaton,C.L. and Tong,J.C.
                                       /cultivar="Chinese Spring"
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/clone=IWHE0441=Wheat etiolated seedling root cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           266 agetggtgcttctggttttacatttcacgtagagacatcaaaagataactggaaagaact 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 GGGGGGAAGATAGCGCCGTCCATGCTGTCGGACTTCGCCAACCTCGCCTCGGAGGC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.6%; Score 243; DB 35; Length 494; 79.3%; Pred. No. 1.9e-62;
              /organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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Bukaryotta, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Oryza.
Magnollophyta: Liliopsida; Poales; Poaceae; Oryza.
Yamamoto, K. and Sasaki, T.
Rice cDNA from callus (1998)
Unpublished (1998)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="cultivar Nipponbare, sub_species Japonica"
/db_xref="taxon:4530"
/clone="c62255_11A"
/clone="lib="Rice callus"
/note="Vector: pBluescript II SK+; Site_1: SalI; Site_2:
NotI; cDNA prepared from rice callus mRNAs by using
oligo(dT) as a primer and ligating to the SalI-NotI site
of pBluescript II SK+ phagemid. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AV554048 483 bp mRNA EST 23-JUL-2000 AV554048 Arabidopsis thaliana roots Columbia Arabidopsis thaliana CDNA clone RZ79e04R 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 tgtccccaatttaactattggcgctccagttattgaaagtttgagaagcacacaaaggc 205
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AU069503 407 bp mRNA EST 07-JUN-1999
AU069503 Rice callus Oryza sativa cDNA clone C62255_11A, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.2%; Score 237.4; DB 15; Length 407; 78.8%; Pred. No. 8.7e-61; Live 0; Mismatches 76; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                               Email: tsasaki@abr.affrc.go.jp
                                                                                                                                                                                                                                                                                                                                                                                         KGF.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 g
                                                                                                                                                                                                                                                                                   2-1-2 Kannondai, Tsukuba
                                                                 AU069503.1 GI:5004354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283; Conservative
                                                                                                                                                                                                                                                                                                                                  Tel: 0298-38-7441
Fax: 0298-38-7468
                                                                                                                                                                                                                                                                                                                                                                                                                   .407
                                                                                                                                                                                                                                                                                                                                                                                  PROJECT = 'RGP'
                                                                                                    Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                  Oryza sativa
                                                                                                                                                                                                                                                                                                                  Japan 305
                                  sequence.
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JOURNAL
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bugaryota; Viridiplantae; Embryophyta; Tracheophyta; Bagandicotyledons; core eudicots; Rosidae; eurosids II;
Lassicales; Brassicaceae; Arabidopsis.

(bases 1 to 483)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana; Generation of 12.028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                               Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon.3702"
/clone="RX79e04R"
/clone="RX79e04R"
/clone_lib="Arabidopsis thaliana roots Columbia"
/tissue_type="roots"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI490023 497 bp mRNA EST 29-JUN-1999
EST248362 tomato ovary, TAMU Lycopersicon esculentum cDNA clone
cLED19K11, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             255 cccttggcaaaagctggtgcttctggttttacatttcacgtagagacatcaaaagataac 314
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Kazusa DNA Research Institute
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   AV554048
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                                         Lycopersicon esculentum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
I; Solanales; Solanaceae; Solanum; Lycopersicon.
I (bases 1 to 497)
Alcala,J., Verbalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E.
Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman
,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley
,S.D. and Giovannoni,J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     1...497

/organism="Lycopersicon esculentum"

/cultivar="TA496"

/db_xref="taxon:4081"

/clone="CLED19K11"

/clone=lib="tomato ovary, TAMU"

/tissue_type="carpel"/dev_stage="5 days pre-anthesis to 5 days post-anthesis"

/lab_host="X11-Blue MRF"

/lab_host="X11-Blue MRF"

/lab_host="X11-Blue MRF" | Strong Site 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 GCAAGTGAGGAAGATGGTGAAGGCAATCATAGCACCGTCGATGCTGTCATCGGACTTTGC 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95; Indels
                                                                                                                                                                                                                               Generation of ESTs from tomato carpel tissue
                                                                                                                                                                                                                                                                                                               Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                            Clemson University Genomics Institute
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                                                                                                                                                                                                                                                                                                                                                                                                Email: dfrisch@CLEMSON.EDU.
Location/Qualifiers
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                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: David Frisch
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RESULT 15

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/note_rvector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xho1; cLER - Tomato Pseudomonas Resistant EST Library.
Directionally cloned cDNAs inserted into pBlueScript SK(-) at 5' end with EcoR1 and 3' end with XhoI site."

1 122 c 144 g 141 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Lycopersicon esculentum"
/cultivar="R11-12 (35S::Pto in Rio Grande x Money Maker)"
                  EST253455 tomato resistant, Cornell Lycopersicon esculentum cDNA clone cLER2M16, mRNA sequence.
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29-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="cLER2M16"
/clone_lib="tomato resistant, Cornell"
  EST
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Clemson University
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/dev_stage="4-week old"
/lab_host="SOLR"
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  mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 Jordan Hall, Clemson, S
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                                                                                    Lycopersicon esculentum
                                                                                     AI772355.1 GI:5270396
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  552 bp
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- 368 attaaagcctgggaccc 385 || || || || || || || || 406 TTTGAAGCCTGGTACACC 423 Q Q

Search completed: November 4, 2000, 11:52:13 Job time: 18250 sec

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		Match Length DB	1246	1050	1260	533	613	667	2930	3669	3693	3639	5511	1149	
ď	Query	Match	14.6	14.0	11.3	10.9	10.9	10.9	10.8	10.8	10.8	10.7	10.6	10.4	
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Cahoon RE, Hitz WD, Shen JB, Williams ME;

WPI; 2000-072184/06. P-PSDB; Y44220.

(DUPO) DU PONT DE NEMOURS & CO E I.

Mycobacterium tube Nucleotide sequenc Mycobacterium tube Nucleotide sequenc BCG deletion regio Chimeric gene cons Polynucleotide seq Human 5' EST isola Human Colon cancer Protein regulating Streptococcus pneu	Zea mays pathogene Microspore-specifi Brassica napus mic Enterococcus faeca Borrelia burgdorfe Sequence encoding Genomic DNA of pot Genomic DNA encodi	Murine embryo macr EST clone DF971. ORF 8 from MYMV co MYMV strand (b). Essential Staphylo Rat von Ebner's gl Human prostrate-sp Human prostrate-sp Human prostrate-sp	a -c -⊣
	005749 T48867 X13166 X20249 Q21453 Z50264 V52282	2 2	
20 20 10 10 10 10 10 10 10 10 10 10 10 10 10			
500 500 2050 2050 16885 5511 9848 341 300 6138 622	8586 8586 17082 116277 10329 10329	8793 232 249 2723 3305 4360 5836 5836 5836	7646 997 1803 756
100.1 100.1 100.1 100.1 100.1 100.0 99.6 99.6		0,000000000000000000000000000000000000	8.8 8.7 8.7 8.7
32 32 32 32 32 32 32 32 32 32 32 32 32 3	28.3 28.3 28.3 28.3 28.3 28.3 28.3 28.3	28 27.8 27.8 27.8 27.8 27.8 27.8	
13 14 16 17 18 19 20 22 23	25 27 27 33 33 33 33 33	33 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	4 4 4 4 2 6 4 4 3
000 000 0	U U	0 0 0 0	υυ

ALIGNMENTS

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Location/Qualifiers
2..949
/*tag= a
/product= "Zeaxanthin epoxidase C-terminal half"
                                                                                 Corn; zeaxanthin epoxidase; carotenoid biosynthetic enzyme; chimeric gene; transformed cell; inhibitor; antibody; ds.
                                                                Corn zeaxanthin epoxidase C-terminal half encoding cDNA.
               229148 standard; cDNA; 1246 BP.
                                                                                                                                                                                                       99WO-US08789.
                                                                                                                                                                                                                      98US-0083042.
                                               21-FEB-2000 (first entry)
                                                                                                                                                                     WO9955889-A2.
                                                                                                                                                                                                                     24-APR-1998;
                                                                                                                                                                                                     22-APR-1999;
                                                                                                                                                                                     04-NOV-1999.
                                                                                                           Zea mays.
                                 229148;
RESULT
Z29148/C
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                                                                         The present cDNA sequence encodes the C-terminal half of corn zeaxanthin epoxidase which is a carotenoid biosynthetic enzyme. The sequence comprises a contig derived from clones crln.pk0033.d8 (from corn root cDNA library), p0110.c9smp011. p0012.cglae05r and p0088.clrim55r (last three clones from corn leaf tissue cDNA libraries). The present sequence is used for construction of chimeric gene to alter expression of the enzyme in transformed cell. The enzyme can be used to raise cantibodies and identify compounds that inhibit the activity of carotenoid biosynthetic enzyme. The polynucleotide also serves as a source of probes and primers which are useful for genetic mapping and to isolate homologous sequences from other species.
                                                                                                                                                                                                                                                                                                                                                                                                             240 tttttttattcgtcgcgttttagttcaaacatgaactagcggacgactgatattcgagaa 299
Novel carotenoid biosynthesis enzyme polynucleotides and polypeptides used to identify inhibitors and to mödulate expression of the enzyme
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid encoding D-ribulose-5-phosphate-3-epimerase is used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D-ribulose-5-phosphate-3-epimerase; RPE; nematode response protein; nematode root infestation; giant feeder cell; transgenic plant; potato; tomato; beet; rape; rice; antisense sequence; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D-ribulose-5-phosphate-3-epimerase nematode response gene cDNA.
                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                         Score 46.2; DB 21; Length 1246; Pred, No. 1.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "D-ribulose-5-phosphate-3-epimerase
                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                           Sequence 1246 BP; 365 A; 269 C; 304 G; 306 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nematode response protein"
                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  increase resistance to root nematodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaucheret H, Tepfer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INRG ) INST NAT RECH AGRONOMIQUE.
                                                    Claim 7; Paqe 50; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245413 standard; cDNA; 1050 BP.
                                                                                                                                                                                                                                                                                                                                n
Similarity 76.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-FR01398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anti-nematode protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1044 CGAGTGTATCCTTTC 1030
                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 tggagggagtacttc 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ...918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; Y54151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berthome R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09964613-A1
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                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                     Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245413;
                                                                                                                                                                                                                                                                                                                                                                 Matches
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The present sequence encodes a Rice D-ribulose-5-phosphate-3-epimerase (RPE) nematode response protein. The enzyme is activated during the initial stages of nematode infestation of roots and is required for formation of the giant feeder cells on which the nematodes depend. Interfering with expression of the protein will thus inhibit nematode infestation. The RPE polynucleotide is used to produce transgenic plants (specifically potato, tomato, beet, rape and rice) that are resistant (or at least less susceptible) to nematode in the plant; or by using the promoter of the RPE gene to express an in the plant; or by using the promoter of the RPE protein or gene enables plant to mount an immediate response to the linvasion of the nematode, consequently limiting the level of cellular damage and reducing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 tagaogiggcogcatctgctggggccaattgcatcgtcgctggaagctctatatttggcg 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         791 cctacaaggtcattgaagctggggccaacgccattgttgctggttcagccgttttcgggg 850
                                                                                                                                                                                                                                                                                                                                                                                                                                   17 tgagaaagaagtaccettccettgacatagaggttgatggtggtctaggtcettcaacca 76
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D-ribulose-5-phosphate-3-epimerase; RPB; nematode response protein; nematode root infestation; giant feeder cell; transgenic plant; potato; tomato; beet; rape; rice; antisense sequence; promoter; anti-nematode protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D-ribulose-5-phosphate-3-epimerase nematode response gene CDNA.
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0
                                                                                                                                                                                                                                                                                                                                                            14.0%; Score 44.2; DB 21; Length 1050; 54.7%; Pred. No. 4.8e-05; Live 0; Mismatches 73; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "D-ribulose-5-phosphate-3-epimerase
nematode response protein"
                                                                                                                                                                                                                                                                                                          Sequence 1050 BP; 249 A; 234 C; 292 G; 272 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137 ctgcggacccaggagccatcatatctgtgctgaggaagagc 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                851 ctccagactatgcagaagctatcaagggaatcaagaccagc 891
                                                                                                                                                                                                                                                                          complications of secondary infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaucheret H, Tepfer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INRG ) INST NAT RECH AGRONOMIQUE.
         Claim 1; Page 45-46; 62pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245412 standard; cDNA; 1260 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-FR01398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAR-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                       88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106..951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09964613-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245412;
                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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during the initial stages of nematode incertain. The enzyme is activated during the initial stages of nematode infestation of roots and is depindent of for formation of the giant feeder cells on which the nematodes required for formation of the giant feeder cells on which the nematodes of nematode infestation. The RPE polynuclectide is used to produce transgenic plants (specifically potato, tomato, beet, rape and rice) that are resistant (or at least less susceptible) to nematode infestation. This is achieved by either expressing antisense sequences in the plant; or by using the promoter of the RPE gene to express an anti-nematode protein. Inhibition of the RPE protein or gene enables consequently limiting the level of cellular damage and reducing the complications of secondary infections.
                                                                    Nucleic acid encoding D-ribulose-5-phosphate-3-epimerase is used to increase resistance to root nematodes
                                                                                                                                                                                  present sequence encodes an Arabidopsis D-ribulose-5 phosphate-
                                                                                                                                       Claim 1; Page 44-45; 62pp; French.
WPI: 2000-097543/08
                              P-PSDB; Y54150
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Sequence 1260 BP; 365 A; 236 C; 288 G; 371 T; 0 other;

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                                                 43 atagaggttgatggtggtctaggtccttcaaccatagacgtggccgcatctgctggggcc 102
                                                               103 aattgcatcgtcgggaagctctatatttggcgctgcggacccaggagccatcatatct 162
                                                                                                                    850 aatgototagtggctggttcagctgtatttggagctaaggactacgcagaagctataaaa 909
                                  0; Gaps
                                                                                                                                                                                                                                                                                                               Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
    11.3%; Score 35.8; DB 21; Length 1260; Score 35.8; DR 21; Length 1260; Conservative 0; Mismatches 62; Indels 0;
                                                                                                                                                                                                                      T20487 standard; cDNA to mRNA; 533 BP.
                                                                                                                                                                                                                                                                                           Human gene signature HUMGS01693.
                                                                                                                                                                                                                                                                   19-JUL-1996 (first entry)
                                                                                                                                          163 gtgctgaggaaggc 177
                                                                                                                                                               910 ggaattaaggccagc 924
Query Match
Best Local Similarity
Matches 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                  WO9514772-A1.
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                            T20487;
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94WO-JP01916. 93JP-0355504

11-NOV-1994; 12-NOV-1993;

01-JUN-1995

Matsubara K, Okubo K;

WPI; 1995-206931/27

(MATS/) MATSUBARA K.

OKUBO K.

(OKUB/)

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A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences quiven in T19001-T25837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed CDNA libraries prepared from various human tissues; synthesis of CDNA was initiated from the untranslated sequence is unique to a particular mRNA species, almost length or contented cDNA hybridise with specific mRNA species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 tggtctaggtccttcaaccatagacgtggccgcatctgctgggggccaattgcatcgtcgc 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
                         - e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monahan JE;
              Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; gene expression product; diagnosis; tumour; colon cancer; colorectal adenocarcinoma; cell line SW480; cell proliferation; cytostatic; sarcoma; breast cancer; neoplasia; dysplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bushnell ŚE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human colon cancer cell line SW480 cDNA clone SEQ ID NO:389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

10.9%; Score 34.4; DB 16; Length
Best Local Similarity 63.1%; Pred. No. 0.065;
Matches 53; Conservative 0; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 533 BP; 126 A; 102 C; 134 G; 158 T; 13 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endege WO, Steinmann KE, Astle JH, Burgess CC, Bus
Carroll E, Catino TJ, Derti A, Ford DM, Lewis ME,
                                                                                                Claim 1; Page 647; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 tggaagctctatatttggcgctgc 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 tggcagccttatcattggttatgc 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280305 standard; cDNA; 613 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-IB01062.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hyperplasia; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09964576-A2.
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                                                                  tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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                                                                                                                                                                                                          human colorectal adenocarcinoma (colon cancer) cell line SW480. The cDNA clones can be used to generate antisense oligonucleotides which can be used for antisense therapy. Methods and products from the present invention can be used for identifying and/or classifying cancerous cells present in a human tumour, particularly in solid tumours, e.g. carcinomas and sarcomas, e.g. breast or colon cancers. The cDNA clones can be used for developing agents for the diagnosis and treatment of disorders in the colon cancers in the colon cancers.
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                                                                                                                                                                                       279917 to 280766 represent double stranded cDNA clones isolated from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 tggtcttaggtccttcaaccatagacgtggccgcatctgctggggccaattgcatcgtcgc 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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Novel nucleic acids, used to develop products for the diagnosis and treatment of disorders involving unwanted cell proliferation, particularly cancers, especially colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E, Astle JH, Burgess CC, Bushnell SE;
Derti A, Ford DM, Lewis ME, Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; gene expression product; diagnosis; tumour; colon cancer; colorectal adenocarcinoma; cell line SW480; cell proliferation; cytostatic; sarcoma; breast cancer; neoplasia; dysplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.9%; Score 34.4; DB 21; Length 613; llarity 63.1%; Pred. No. 0.069; Conservative 0; Mismatches 31; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human colon cancer cell line SW480 cDNA clone SEQ ID NO:388.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 613 BP; 188 A; 151 C; 128 G; 137 T; 9 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 15; Page 286-287; 469pp; English.
                                                                                                                                 Claim 15; Page 287; 469pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 tggaagctctatatttggcgctgc 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294 TGGCAGCCTTATCATTGGTTATGC 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         280304 standard; cDNA; 667 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-IB01062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-APR-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Catino IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-087220/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hyperplasia; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09964576-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-DEC-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hyperplasia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endege WO,
Carroll E,
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                                                     present in a human tumour, particularly in solid tumours, e.g. carcinomas and sarcomas, e.g. breast or colon cancers. The cDNA clones can be used for developing agents for the diagnosis and treatment of disorders involving unwanted cell proliferation, such as neoplasia, dysplasia or
human colorectal adenocarcinoma (colon cancer) cell line SW480. The CDNA clones can be used to generate antisense oligonucleotides which can be used for antisense therapy. Methods and products from the present invention can be used for identifying and/or classifying cancerous cells
                                                                                                                                                                                                                                         352 regrecaderecaacaacaeradeaereecreerreregrecregrariegaacaerer 293
                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= c
/note= "nucleotides 1 through at least 1890
are transcribed (possibly through 2150)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= d
/mote= "nucleotides 1 through at least 1890
/mote= are transcribed (possibly through 2150)"
                                                                                                                                                                                     Length 667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= e
/note= "the Ds2 transposon insertion occurs
at nucleotide 168"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maize; Zea mays; Id; id*; transposon; transposable element; Ds2; flower evocation; zinc-finger regulatory protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             įs
                                                                                                                                                                                  Score 34.4; DB 21; Length Pred. No. 0.071; 0; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "the DNA strand given in T42175 complementary to this fragment"
                                                                                                                                          Sequence 667 BP; 192 A; 171 C; 153 G; 150 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (complement)1..410
                                                                                                                                                                                                                                                                                                     117 tggaagctctatatttggcgctgc 140
                                                                                                                                                                                                                                                                                                                    292 TGGCAGCCTTATCATTGGTTATGC 269
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TD T42174 standard; DNA; 2930 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Colasanti JJ, Sundaresan V;
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                                                                                                                                                                                       Query Match 10.9%;
Best Local Similarity 63.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176..1600
/*tag= b
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1..1890
                                                                                                                                                                                                                    53; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prim_transcript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maize Id gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAR-1995;
                                                                                                                        hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays.
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                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                             The Id gene controls flower evocation in maize plants. The maize nucleic acid is similar to that of genes encoding zincfinger regulatory proteins in animals.

Transposons Ac and Ds constitute a family of related transposable elements present in maize. A derivative of Ds, Ds2, can be used to produce a new mutant of the Id gene. The Ds2 (in the presence of active Ac) is excised from a nearby gene on chromosome 1 and inserted into the Id gene to produce id*.
                                                                                                                                                                                                 ö
                          New isolated plant Id gene - used to develop prods. for use in altering the induction of flowering in plants
                                                                                                                                                                           Query Match 10.8%; Score 34; DB 17; Length 2930; Best Local Similarity 74.1%; Pred. No. 0.19; Matches 43; Conservative 0; Mismatches 15; Indels (
                                                                                                                                                  Sequence 2930 BP; 850 A; 664 C; 643 G; 771 T; 2 other;
                                                                                                                                                                                                                                                                                                                                              ss; maize; Id; floral induction; transgenic plant.
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/number= 2
380..442
/*tag= e
/note= "Zinc finger motif"
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/oote= "Zinc finger motif"
                                                    Claim 6; Fig 2 and Fig 3; 58pp; English.
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/product= "Id protein"
12..228
                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                          V41721 standard; DNA; 3669 BP
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729..902
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/*tag= j
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WPI; 1996-497621/49.
           P-PSDB; W03698
                                                                                                                                                                                                                                                                                                                             Maize Id gene.
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                                                                                                                                                                                                                                                                                                                                                                Sea mays.
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V41721/C
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The maize Id gene controls floral induction and is useful in the production of transgenic plants with altered floral induction times, i.e. earlier, delayed or inhibited floral induction. The Id gene and zinc finger regulatory regions are useful to identify these genes in maize and isolate similar genes in other plants. The polypeptides and antibodies are also useful in Id detection e.g. to locate activity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                         Id gene controlling floral induction in maize - useful to create transgenic plants with earlier, delayed or inhibited floral induction e.g. to extend geographical range of crops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 10.8%; Score 34; DB 19; Length 3669; 1 Similarity 74.1%; Pred. No. 0.21; 43; Conservative 0; Mismatches 15; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indeterminate gene; Id gene; maize; corn; flower induction; floral evocation; transgenic plant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3669 BP; 1011 A; 922 C; 851 G; 884 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/note= "contains introns"
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                                                                                                                                                                              (COLD-) COLD SPRING HARBOR LAB.
                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 2; 68pp; English.
                                                                                                                                     97US-0000640.
97US-0804104.
                                                                                                                                                                                                        Colasanti JJ, Sundaresan V;
                                                                                                           98WO-US03161
/number= 4
3179
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241..329
                           /*tag= k
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330..627
/*tag= d
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                                                                                                                                                                                                                                  WPI; 1998-467564/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                P-PSDB; W59836
                                                    WO9837201-A1
                                                                                                           18-FEB-1998;
                                                                                                                                     30-DEC-1997;
                                                                                                                                                  20-FEB-1997;
                                                                               27-AUG-1998
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             polyA_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                              plants.
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Z34479/c
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T06481 standard; cDNA; 3639 BP.

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This sequence represents the maize chromosome 1 indeterminate (Id)

ce gene. Ds2 transposon insertion occurs at nucleotide 914 of the

ce gene. The Id gene encodes a regulatory protein (see Ya2114) that

plays a crucial role in the switch from vegetative to reproductive

ce plays a crucial role in the switch from vegetative to reproductive

chevelopment, controlling the expression of other genes required for

floral development. Iloss of Id function causes prolonged vegetative

ce development. Understanding the mechanism of this regulation

crowides a basis for producing specialized plants designed to flower

ce nowironmental effects. Methods are provided for producing plants

ce nowironmental effects. Methods are provided for producing plants

ce nowironmental effects. Methods are provided for producing plants

ce nowironmental effects. Methods are provided for producing plants

ce nowironmental effects. Methods are provided for producing plants

ce with selected times of transition from the vegetative to the

crow egetative growth and initiation of flowering, or in later

consecuting or the absence of floral induction. The plants can be

consecuted to flower and set seed prior to adverse weather. Similarly,

cflower induction can be prolonged for short-season plants grown in

areas with long periods of warm weather. As a result of the extra

consecutive mass and carbohydrate, these plants can produce more and/or

larger flowers and, consequently, more seed. Plants can even be

consecuted from flowering, thus providing nutritious silage blomass.

consecution of hybrids.

consecution of hybrids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated floral induction gene, used for producing plants with selected times of transition from the vegetative to the flowering stage
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"site of Ds2 transposon insertion"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (COLD-) COLD SPRING HARBOR LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 2; 80pp; English.
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                                                                                                     /number= 2
747..920
/*tag= f
'number= 2
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/number=
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                                   ..746
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211 tgtttctgctgtaaagtactccctccgtttttttttttattcgtcgcgttttagttcaaaca 270
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                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid encoding plant cystathionine gamma synthase - used to increase the methionine content of seeds for improvement of animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Four chimeric genes encoding (1) a plant cystathionine gamma synthase (CS); (2) a feedback insensitive aspartokinase (lysc), operably linked to a chloroplast transit sequence; (3) a bifunctional feedback insensitive aspartokinase homoserine dehydrogenase (AK-HBH), operably linked to a chloroplast transit sequence; and (4) a methionine rich storage protein (HSZ); all being operably linked to plant seed specific regulatory sequences, are used for increasing the methionine content of the seeds of plants. Plants having increased methionine content may be used to produce improved animal feeds.
                                                                                Methionine; lysine; aspartokinase; lysC; homoserine dehydrogenase; cystathionine gamma synthase; chloroplast; transit sequence; seed; storage protein; animal feed; CS; AK-HDH; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 3639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric gene construct glb1::HT12::glb1 designated PHP7999..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3639 BP; 957 A; 806 C; 781 G; 1095 T; 0 other;
                                                        Cystathionine gamma synthase (CS) XbaI gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33.8; DB Pred. No. 0.24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 tgaactagcggacgactgatattcgagaatg 301
                                                                                                                                                                                                                                                                                                  (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    claim 21; Page 66-68; 80pp; English.
                                                                                                                                                                                                                                                                                                                                 Falco SC, Guida AD, Locke ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.7%;
68.1%;
                                                                                                                                                                                                                                                                       94US-0242408.
                                                                                                                                                                                                                                         95WO-US05545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Z08718 standard; DNA; 5511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-OCT-1999 (first entry)
                             22-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-010939/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                       13-MAY-1994;
                                                                                                                                                                              WO9531554-A1.
                                                                                                                                                                                                                                          12-MAY-1995;
                                                                                                                                                                                                           23-NOV-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62;
                                                                                                                                                    Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
T06481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z08718/c
 δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        XEXEXEX
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Gaps ö

DB 20; Length 3693;

10.8%; Score 34; DB 20; Length 36 74.1%; Pred. No. 0.21; tive 0; Mismatches 15; Indels

Conservative

Local Similarity hes 43; Conserva

Matches

δλ

Query Match

22-NOV-1999 (first entry)

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The present invention describes a clausionmew cereat plant, seculose and operated lavel of at least one preselected amino a coid (aa) compared to a seed from a corresponding untransformed plant, where the aa is selected from lysine, cysteine, threonine, tryptophan, carginine, laucine, laoleucine, histidine or their combinations, and optionally methionine. Plants transformed to express a heterologous protein that has an elevated content of a preselected amino acid can be content of the preselected amino acid, and therefore having an increased content of the preselected amino acid, and therefore having an increased noutritional value. The transformed cereals can be used in feed formulations for animals. Transforming plants to have an elevated lavel of a preselected amino acid in the endosperm of its seed is advantageous of a preselected amino acid in the endosperm of its seed is advantageous of a preselected amino acid in the endosperm of its seed is advantageous cupplementation with specific amino acids to provide animals with content of the seeds without derrimental side increase the nutritional content of seeds without derrimental side cutritional content of the seeds is increased whilst maintaining a high cleast 10-20% by weight to about 10 times greater compared to a corresponding untransformed seed. The present sequence represents a chierry derived from the barley (Hondem vulgare) alpha hordothionin content of the area (The present sequence represents a chierry derived from the barley (Hondem vulgare) alpha hordothionin content of the reads (The present sequence represents a chierry derived from the barley (Hondem vulgare) alpha hordothionin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant seeds containing elevated preselected amino acid levels, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Hordeum vulgare; alpha hordothionin; HT12; modification; plant seed;
alteration; endosperm; nutrition; cereal; barley; chimeric gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention describes a transformed cereal plant seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene and introduces 12 lysine residues into the mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33.4; DB 20; Length 5511;
Pred. No. 0.39;
0; Mismatches 41; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5511 BP; 1463 A; 1256 C; 1310 G; 1482 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                     Dress VM, Ertl DS, Higgins RK, Jung R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 attcgtcgcgttttagttcaaacatgaactagcggacga 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 37-39; 49pp; English.
                                                                                                                                                                                                                                                                                                          (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Z21189 standard; DNA; 1149 BP
                                                                                                                                                                                                                                                                  98US-0020716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 10.6%;
Best Local Similarity 58.6%;
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-508509/42.
                                                               Synthetic.
Hordeum vulgare.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to grow cereals
                                                                                                                              WO9940209-A1
                                                                                                                                                                                                                    27-JAN-1999;
                                                                                                                                                                                                                                                               09-FEB-1998;
                                                                                                                                                                            12-AUG-1999
                                                                                                                                                                                                                                                                                                                                                     Beach LR,
Ranch JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Z21189;
                                                                                                                                                                                                                                                                                                                                                     Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Z21189
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isolated from a family of maize (Zea mays) genes encoding pathogenesis related (PR-1) proteins. The promoters are useful for expressing heterologous genes (including genes for disease resistance) in plants, especially diccts, or monocots i.e. maize. The promoters are useful for the genetic manipulation of plants to exhibit specific phenotypes, particularly enhanced resistance to pathogen caused disease. Pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223 aaagtactccctccgtttttttttttttcgtcgcgttttagttcaaacatgaactagcgga 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             include viruses such as tobacco or cucumber mosaic virus, ringspot virus, necrosis virus, and maize dwarf virus, and viroids, bacteria, insects, nematodes and fungi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221186 to 221190 represents the nucleotide sequences for promoters
                                                                           regulation; expression; disease resistance; genetic manipulation; tobacco mosaic virus; cucumber mosaic virus; ringspot virus; necrosis virus; maize dwarf virus; viroid; bacterial; insect;
                                                                                                                                                                                                                                                                                                                                                                                                                                             New promoter sequences from pathogenesis-related genes of maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.4%; Score 32.8; DB 20; Length 1149; 68.2%; Pred. No. 0.31;
                                                              maize; pathogenesis-related class I; PR-1; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \label{eq:mycobacterium} Mycobacterium \; tuberculosis; \; antigen; \; vaccine; \; immunological; \; infection; \; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis antigen RD1-ORF8 encoding DNA
                               Zea mays pathogenesis-related class I PR-1#83 promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1149 BP; 361 A; 229 C; 214 G; 345 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                283 cgactgatattcgagaatggagggagta 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               764 tgaccaatatttaagaatagatgtagta 791
                                                                                                                                                                                                                                                                                                                                              (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 64; 86pp; English.
                                                                                                                                                                                                                                                                                                               98US-0079648.
                                                                                                                                                                                                                                                               99WO-US03011.
                                                                                                                                                                                                                                                                                               98US-0076100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.4°
Best Local Similarity 68.2°
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V63934 standard; DNA; 500
                                                                                                                               nematode; fungal; ss
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-527621/44.
                                                                                                                                                                                             WO9943819-A1.
                                                                                                                                                                                                                                                               11-FEB-1999;
                                                                                                                                                                                                                                                                                              26-FEB-1998;
27-MAR-1998;
                                                                                                                                                                                                                                02-SEP-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JAN-1999
                                                               Zea mays;
                                                                                                                                                                Zea mays.
                                                                                                                                                                                                                                                                                                                                                                               Crane VC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V63934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V63934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes a Mycobacterium tuberculosis protein. Products from the present invention, which describes protein fragments and nucleic acid fragments derived from M.tuberculosis, can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the diagnosis of or vaccination against tuberculosis caused by M. tuberculosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 ccggcgatgggcatggggggtgtgggtgtttagatgcggccggttccggcgagggcggc 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 cettecettgacatagaggttgatggtggtetaggtecttcaaccatagacgtggccgca 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunogenic; Mycobacterium tuberculosis; immune response; infection; tuberculosis; fusion polypeptide; T'eall epitope; ESAT'6; MPT59; TB; pharmaceutical; vaccination; M. africanum; M. bovis; CFP7A; CFP30A; CFP7B; CFP19; CFP19; CFP23, CFP7B; CFP19; CFP19; CFP23, CFP23, CFP23, CFP10A; CFP10A; CFP10B; CFP23; CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP23, CFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated mycobacteria polypeptides and nucleic acids - used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                   Nielsen R, Oettinger T, Rasmussen PB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              products for the diagnosis of or vaccination against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 tetgetgggggccaattgcatcgtcgctggaagetctatatttggcgctgcgg 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.1%; Score 32; DB 19; Length 500; 55.4%; Pred. No. 0.39; tive 0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 500 BP; 54 A; 111 C; 235 G; 100 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mycobacterial infections, particularly tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of antigen RD1-ORF8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 23; Page 178-179; 163pp; English.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X81041 standard; DNA; 500 BP
                                                                                                                                                                                                                                              97DK-0000376.
97US-0044624.
                                                                                                                                                                               98WO-DK00132
                                                                                                                                                                                                                         98US-0070488
                                                                                                                                                                                                                                                                                           97DK-0001277
                                                                                                                                                                                                                                                                                                                                                                                                      Rosenkrands I, Weldingh K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                       (STAT-) STATENS SERUM INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-SEP-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M. africanum or M. bovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62; Conservative
                       49..468
                                                                                                                                                                                                                                                                                                                                                                                   Florio W,
                                                 /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-542705/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; W72910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9924577-A1
                                                                                        WO9844119-A1
                                                                                                                                                                               01-APR-1998;
                                                                                                                                                                                                                                                                                           10-NOV-1997;
                                                                                                                                                                                                                         05-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                   Andersen P,
                                                                                                                                     08-OCT-1998
                                                                                                                                                                                                                                                02-APR-1997
18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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The invention describes a substantially pure immunogenic polypeptide fragment (1) from Mycobacterium tuberculosis that is able to evoke a protective immune response against infections by mycobacteria belonging to the tuberculosis complex. The invention provides a (1) fusion to the tuberculosis complex. The invention provides a (1) fusion to the tuberculosis complex. The invention provides a (1) and at least one polypeptide fragment comprising a T-cell epitope from M. tuberculosis protein ESAFF, or MPT59 and a second different amino acid sequence from M. tuberculosis, protein ESAFF, or MPT59 and a second different amino acid sequence from In vivo a sequence which protects the first amino acid sequence from in vivo degradation or post-translational processing; (3) a nucleic acid fragment that encodes the above polypeptides. The polypeptides and nucleic acid fragment cuestul as pharmaculicals, for diagnosis of and as antigens for vaccination against TB caused by Mycobacterium tuberculosis, africanum or bovis. The polypeptides are also useful for diagnosis of as antigens for tuberculosis complex. The invention also describes the use of CFP7A or CFP3AAFF, or a frong immune composition in amimal with bacteria belonging to the tuberculosis complex. The invention also describes the use of CFP7A or CFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3AAFF, cFP3A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis; antigen; vaccine; immunological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.1%; Score 32; DB 20; Length 500; 55.4%; Pred. No. 0.39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis antigen RDI-ORF9B encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New immunogenic fragment of Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 500 BP; 54 A; 111 C; 235 G; 100 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 0.39;
0; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 197-198; 265pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V63935 standard; DNA; 2050 BP
                                                                                                                                                     98WO-DK00132.
97DK-0001277.
98US-0070488.
                                                                              98WO-DK00438.
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                                                                                                                                                                                                                                                                                                                       (STAT-) STATENS SERUM INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JAN-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                  Andersen P, Skjot R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-347282/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; Y21927
                                                                              08-OCT-1998;
                                                                                                                                                                                                                                        05-JAN-1998;
                                                                                                                                                         01-APR-1998;
10-NOV-1997;
20-MAY-1999
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The present sequence encodes a Mycobacterium tuberculosis protein. Products from the present invention, which describes protein fragments and nucleic acid fragments derived from M.tuberculosis, can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the diagnosis of or vaccination against tuberculosis caused by M. tuberculosis, M. africanum or M. bovis.
                                                                                                                                                                                                                                                                                                                               New isolated mycobacteria polypeptides and nucleic acids - used for developing products for the diagnosis of or vaccination against mycobacterial infections, particularly tuberculosis
                                                                                                                                                                                                                                                Florio W, Nielsen R, Oettinger T, Rasmussen PB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2050 BP; 404 A; 774 C; 582 G; 290 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                     Claim 23; Page 180-183; 163pp; English.
             Location/Qualifiers
22..2022
/*tag= a
                                                                                                                                                  98US-0070488.
97DK-0000376.
97US-0044624.
97DK-0001277.
                                                                                                                        98WO-DK00132
                                                                                                                                                                                                                                                              Rosenkrands I, Weldingh K;
                                                                                                                                                                                                                    (STAT-) STATENS SERUM INST.
                                                                                                                                                                                                                                                                                        WPI; 1998-542705/46.
P-PSDB; W72911.
                                                                                                                                                05-JAN-1998;
02-APR-1997;
18-APR-1997;
                                                                  WO9844119-A1
                                                                                                                        01-APR-1998;
                                                                                                                                                                                          10-NOV-1997;
                                                                                                                                                                                                                                                Andersen P,
                                                                                            08-OCT-1998
             Key
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278 δ

31 ccttcccttgacatagaggttgatggtggtgtcttaggtccttcaaccatagacgtggccgca 90

qq

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Ouery Match
10.1%; Score 32; DB 19; Length 2050;
Best Local Similarity 55.4%; Pred. No. 0.74;
Matches 62; Conservative 0; Mismatches 50; Indels

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Gaps

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Search completed: November 4, 2000, 13:45:01 Job time: 16428 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on:

November 4, 2000, 13:33:34; Search time 189.35 Seconds (without alignments) 252.402 Million cell updates/sec

US-09-300-482-225 Perfect score:

1 gataaggtgcgcacactgag......gaatggagggagtacttcga 316 Sednence:

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

262060 seqs, 75620727 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

1: /cgg2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/5C_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/5D_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/6_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/2/ina/pcaycomB.seq:* Issued_Patents_NA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	face 30 endemons	9	Sequence 30 April	2	· –	Sequence 76 April	<u> </u>	ì -	Segmence 1 Appli	ì	ìσ	ìσ	ìσ	ìo	ìσ	` ~	Segmence 3, appli	À -	Sequence 1. Appli	ì	ì	i (, ,			'n
SUMMARIES	ID	US-08-737-524B-26	US-08-390-878-16	US-08-581-148C-30	\sim	US-07-960-389-1	US-08-714-918-76	US-08-470-350B-1	US-08-380-916-1	US-08-721-690-1	US-08-458-922-2	US-08-468-853-9	US-08-468-855-9	US-08-310-357-9	US-08-468-852-9	US-08-468-857-9	US-08-616-392C-3	US-08-377-440A-2	US-07-705-490-1	US-08-455-073A-1	US-08-592-874-1	US-09-096-942-2	US-09-096-867-2	US-08-781-891-207	US-08-253-155A-15	5-429-1	US-08-996-621-1
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dЮ	Query	10.7	10.1	•	9.1	8.9	8.8	8.8	8.8	•	•	9.8	8.6	•	•		8.5	8.5	8.5				8.5		8.4	8.4	8.4
	Score	33.8	3	29.5	28.8	28.3	27.8	27.8	27.8	27.8	27.6		27.2	27.2	27.2	27.2	27	26.8	26.8	26.8	26.8	26.8	26.8	26.8	26.6	26.4	26.4
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Sequence 15, Appliance 15, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 1, Appliance 10, Appliance	Sequence 9, Appli
US-08-846-111D-15 US-08-088-633-3 US-08-245-756-3 US-08-441-750-3 US-08-441-750-3 US-08-441-751-3 US-08-441-751-3 US-08-618-16-1 US-08-618-16-1 US-08-618-16-2	PCT-0894-01/82-9
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ALIGNMENTS

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GENES AND METHODS FOR INCREASING
THE METHIONINE CONTENT OF THE SEEDS
OF PLANTS
                                                                                                             APPLICANT: CARL SAVERIO FALCO
APPLICANT: CARL SAVERIO FALCO
APPLICANT: MARY ELIZABETH HARNETT LOCKE
TITLE OF INVENTION: GENES AND METHODS FOR INCREASING
TITLE OF INVENTION: THE METHIONINE CONTENT OF THE SEE
TITLE OF INVENTION: THE METHIONINE CONTENT OF THE SEE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER TO THE STATES OF AMERICA
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: MCROSOFT WINDOWS 95
SOFTWARE: MCROSOFT WINDOWS 95
SOFTWARE: MCROSOFT WINDOWS 95
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/O8/737,524B
FILING DATE:
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                           ADDRESSE: E. I. DU PONT DE NEMOURS AND COMPANY STREET: 1007 MARKET STREET CITY: WILMINGTON STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: BB-1059-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-5481
TELEPAX: 302-773-0164
                                              Sequence 26, Application US/08737524B Patent No. 5912414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: LYNNE M. CHRISTENBURY
REGISTRATION NUMBER: 30,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 3639 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 835420
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                           GENERAL INFORMATION:
RESULT 1
US-08-737-524B-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-737-524B-26
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10.7%; Score 33.8; DB 4; Length 3639; 68.1%; Pred. No. 0.033; Query Match Best Local Similarity

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APPLICANT:
APPLICANT:
                                    APPLICANT:
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APPLICANT: Stover, Gregory G.
TITLE OF INVENTION: VIRULENCE-ATTENUATING GENETIC DELETIONS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESSS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Street Tower, 20th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.1%; Score 32; DB 2; Length 16885; Best Local Similarity 55.4%; Pred. No. 0.34; Matches 62; Conservative 0; Mismatches 50; Indels (
27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,878
FILING DATE: 17-FEB-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
  0; Mismatches
                                                                                                                15371A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-581-148C-30
; Sequence 30, Application US/08581148C
Patent No. 6060644
; GENERAL INFORMATION:
                                                                                                                                                                                                                                    US-08-390-878-16/c
; Sequence 16, Application US/08390878
Patent No. 5700683
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 1537.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/543/9600
TELEFAX: 415/543/5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . APPLICANT: Schnable, Patrick S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415/543/5043
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic) US-08-390-878-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 16885 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
    62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94105
    Matches
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Gaps
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US-08-3
US-08-3
Sequence 3, Application US/08030096
Patent No. 542604
GENERAL INFORMATION:
APPLICANT: Fabijanski, Steven F.
APPLICANT: Arnison, Paul G.
TITLE OF INVENTION: BINARY CRYPTOCYTOTOXIC METHOD OF HYBRID ITILE OF INVENTION: SEED PRODUCTION
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 5; Length 6343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: ISOLATION AND USE OF CUTICULAR LIPID ITLE OF INVENTION: GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 9.2%; Score 29.2; DB 5; Length 6
Best Local Similarity 74.0%; Pred. No. 2;
Matches 37; Conservative 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMFUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,148C
FILING DATE: 29-DEC-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Zea mays
INDIVIDUAL ISOLATE: Z.mays Glossy2 locus DNA
                                                                                                                                                       NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Larcher, Carol
REGISTRATION NUMBER: 35243
REPRENCE/POCKET NUMBER: 7138
TELECOMMUNICATION:
Robertson, Donald S.
Hansen, Joel D.
Nikolau, Basil J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington, D.C.
                                                               APPLICANT: Xu, Xiaojie
APPLICANT: Xia, Yiji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 6343 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                  60601-6780
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ORIGINAL SOURCE:
                                                                                                                                                                                                                         STREET: Two Pr
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                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: join(308..370, 1136..1261, 6369..6428, 7198..7353)
US-08-030-096-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
9.1%; Score 28.8; DB 1; Length 8585;
Best Local Similarity 52.5%; Pred. No. 3.3;
Matches 63; Conservative 0; Mismatches 57; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INCOMMATION:
APPLICANT: HAYASHIDA, Kasuhiro;
APPLICANT: HAYASHIDA, Kasuhiro;
TITLE OF INVENTION: Human GM-CSF Receptor Component
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STRRET: 2000 Galloping Hill Road
CITY: Renilworth
STRATE: USA
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/030,096
FILING DATE: 22-MAR-1993
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                           33229/164/PIHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disc
COMPUTER: Apple Machincsh
OPERATING SYSTEM: System Software 7.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DARM:
                                                                                            PRIOR APPLICATION DATA

APPLICATION NUMBER: US 07/556,917
FILING DATE: 20-7UL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA91/00255
FILING DATE: 22-7UL-1991
ATOMES BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERNICE/DOCKET NUMBER: 33229/164/PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
mprev. 0.4132
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APPLICATION NUMBER: 554,745
FILING DATE: 18-JUL-1990
APPLICATION NUMBER: PCT/US 91/04846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/07/960,389
FILING DATE: 07-JAN-1993
CLASSIFICATION: 800
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Patent No. 5705611
                                                                                                                                                                                                                                                                                                                                            TELEFAX: (Zuz,c.
TELEFAX: (Zuz,c.
TELEFAX: 904136
; INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8585 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 cttcaaccatagacgtggccgcatctgctggggccaattgcatcgtcgctggaagctcta 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 tatttggcgctgcggacccaggagccatcatatctgtgctgaggaagagcgtcgagggct 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: DNA sequence encoding Human GM_CSF receptor US-07-960-389-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 8.9%; Score 28.2; DB 2; Length 3475; Best Local Similarity 49.7%; Pred. No. 3.3; Matches 72; Conservative 0; Mismatches 73; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Benton, Bret
APPLICANT: Lee, Ving
APPLICANT: Malouin, Francois
APPLICANT: Malouin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Schmid, Molly B.
TILLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
                                    NAME: Blasdale, John H. C.
REGISTRATION NUMBER: 31,895
REFERNE/COCKET NUMBER: DX0143Q
TELEPHONE: (908) 298-2902
TELEPHONE: (908) 298-5388
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGALH: 3475 base pairs
TYPE: nucleotides
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIF: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
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FILING DATE: September 13, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 ctcagaacaaaaactgattttggtg 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 76, Application US/08714918 Patent No. 6037123
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700
FILING DATE: 16-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA
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: California
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ORIGINAL SOURCE:
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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RECISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: FP-60058-PC
TELECOMONICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/182,247
FILING DATE: 13-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: DNA (genomic)
US-08-380-916-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 5836 base pairs
                                                                                                                    ORGANISM: Rattus rattus
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 55.6%
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3747 AACATCCACCTTT 3735
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 aaaaactgatttt 208
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                                                                                                                                                                         94..3963
                          MOLECULE TYPE: CDNA
                  linear
                                                                                                                                                        NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                               ORIGINAL SOURCE:
                                                       HYPOTHETICAL: NAMI-SENSE: NO
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US-08-470-350B-1
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                                                                                                                                      FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                      Query Match 8.8%; Score 27.8; DB 5; Length 3305; Best Local Similarity 51.2%; Pred. No. 4.5; Matches 65; Conservative 0; Mismatches 62; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: L1, Xiao
APPLICANT: Snyder, Solomon H
TITLE OF INVENTION: Ebnerin: A Secreted von Ebner's Gland
TITLE OF INVENTION: Protein Associated with Taste Buds
NUMBER OF ENDURENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,350B
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                                                       NAME: Warburg Richard J.
REGISTRATION NUMBER: 32,327
REGISTRENCE/DOCKET NUMBER: 222/005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 3305 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSEE: Banner & Witcoff, Ltd.:
1: 1001 G Street, N.W.
Washington
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08470350B Patent No. 5684126 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: WOLFE, Susan A
REGISTRATION NUMBER: 33,568
REFERENCE/DOCKET NUMBER: 0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEPHONE: 202-508-9100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-470-350B-1/c
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TOPOLOGY:
US-08-714-918-76
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78 agacgiggccgcatcigctggggccaattgcatcgicggcaggctctatatttggcgc 137
                                                  2; Gaps
8.8%; Score 27.8; DB 1; Length 4360; 55.6%; Pred. No. 5.2; tive 0; Mismatches 57; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08380916
Patent No. 5648478
GENERAL INFORMATION:
TITLE OF INVENTION: Tissue-Specific Enhancer Active in TITLE OF INVENTION: Prostrate
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcardero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUBER: US/08/380,916 FILING DATE: 12-JAN-1995 CLASSIFICATION: 424
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                                                                                                   4839 CIGGGIGACAGAGIGAGACICIGICICAAAAAAAAAAAITITITITITITITITGIAGA 4898
                                                                             166 ctgaggaagagcgtcgagggctctcagaacaaaaactgattttggtgtttctgctgtaaa 225
                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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0
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'Match 8.8%; Score 27.8; DB 1; Length 5836; Local Similarity 53.2%; Pred. No. 6.1; es 59; Conservative 0; Mismatches 52; Indels 0;
                                                                                                                                                                                     4899 GATGGATCTTGCTTGTTTGTTTGTTGGTTGGAACTCCTGGCTTCAAGT 4949
                                                                                                                                                               226 gtactccctccgtttttttttttttttqttcgtttagttcaaacatgaact 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.8%; Score 27.8; DB 5; Length 5836; 53.2%; Pred. No. 6.1; tive 0; Mismatches 52; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226 gtactccctccgtttttttttttttcgtcgcgttttagttcaaacatgaact 276
                                            52; Indels
                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Henderson, Daniel R.
TITLE OF INVENTION: ITSSUE-SPECIFIC ENHANCER ACTIVE
TITLE OF INVENTION: IN PROSTATE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FSEASEED for Windows Version 2.0
SOFTWARE: FSEASEED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/721,690
FILING DATE: 27-SEP-1996
CLASSIPICATION 514
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 08/380,916
FILING DATE: 30-JAN-1995
APPLICATION NUMBER: US 08/182,247
FILING DATE: 13-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Catherine, Polizzi M
REGISTRATION NUMBER: 40,130
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08721690 Patent No. 6057299
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TELEX: 706141
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5836 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 53.28
Matches 59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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ZIP: 94304-1018
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US-08-721-690-1
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Query Match
                                     Matches
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1736 CITCGTCCGGCTGAGATGTTCCCGATGGTGGCGCCCCCCCCTCTCATGCCGGTTCTCCAT 1677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 cttcccttgacatagaggttgatggtggtcttaggtccttcaaccatagacgtggccgcat 91
                                                                                                                                   Cloning and expression of a protein antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.7%; Score 27.6; DB 5; Length 1803;
49.3%; Pred. No. 3.8;
tive 0; Mismatches 74; Indels 0;
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APPLICANT: VCK, Jacobus Johannus
APPLICANT: VERMEULEN, Arnoldus Nicolaas
TITLE OF INVENTION: COCCIDIOSIS POULTRY VACCINE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Akzo No. 5670362el Patent Department
                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O8/458,922
FILING DATE: 02-June-95
CLASSIFICATION: 435
                                                                                                                                                                                                                      ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                             of toxoplasma gondii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1616 TCTCCATGCCTTGCAATGGGAGGAGC 1591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B3125C2
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                       Sequence 2, Application US/08458922
Patent No. 6077690
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Patent No. 5670362
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: B3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5019
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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NAME: Jervis, Herbert
REGISTRATION NUMBER: 31,1
                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1803 base pairs
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Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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; MOLECULE TYPE: CDNA
US-08-458-922-2
                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                     GENERAL INFORMATION:
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RESULT 10
US-08-458-922-2/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 8.6%; Score 27.2; DB 1; Length 2375; Best Local Similarity 52.7%; Pred. No. 6.1; Matches 59; Conservative 0; Mismatches 53; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: van den BOOGAART, Paul
APPLICANT: VOK, Jacobus Johannus
APPLICANT: VERNEULEN, Arnoldus Nicolaas
APPLICANT: VERNEULEN, Arnoldus Nicolaas
TITLE OF INVENTION: COCCIDIOSIS POULTRY VACCINE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,357
APPLICATION NUMBER: US 08/310,357
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,865
FILING DATE: 06-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/604,075
FILING DATE: 18-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91.201.523.7
ATTONEY AGGNT INFORMATION:
NAME: MATY E. GOTTLLEY
REGISTANTION NUMBER: 34,409
                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/468,853
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08468855 Patent No. 5780289
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1300 Piccard Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (301) 258-5200 INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 2375 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                     COMPUTER READABLE FORM:
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                          Rockville
                                               Maryland
                                                                       U.S.A.
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CLONE: Eam100E
                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                        20850
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US-08-468-853-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-468-855-9
                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE
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47 aggitgaiggiggictiaggiccitcaaccalagacgiggccgcatcigcigggggccaait 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 8.6%; Score 27.2; DB 2; Length 2375; Best Local Similarity 52.7%; Pred. No. 6.1; Matches 59; Conservative 0; Mismatches 53; Indels 0
                                                                                                                                                 PatentIn Release #1.0, Version #1.25
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APPLICANT: Van den BOOGAART, Paul
APPLICANT: KOK, Jacobus Johannus
APPLICANT: VERMEULEN, Arnoldus Nicolaas
TITLE OF INVENTION: COCCIDIOSIS POULTRY VACCINE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Organon Teknika Corporation
ADDRESSEE: Biotechnology Research Institute
STREET: 1330-A Piccard Drive
                                                                                                                                                                                                                                                                           PAPLICATION NUMBER: US 08/310,357
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,865
FILING DATE: 06-AUG-1993
PRIOR APPLICATION NUMBER: US 07/604,075
FILING DATE: 18-UNN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: EP 91.201.523.7 FILING DATE: 18-Jun-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,855
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                               PC-DOS/MS-DOS
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; Patent No. 5789233
                                                                                                          COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34,409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (301) 258-5200 INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 2375 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA to mRNA
                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 34
REFERENCE/DOCKET NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Mary E. Gormley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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3..1859
                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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Maryland: U.S.A.
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CLONE: Eam100E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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                                        20850
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; LOCATION:
US-08-468-855-9
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US-08-310-357-9
                      COUNTRY:
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1576 AGATIGAAGCIGIIGCAGGACGIACAACGAAAAACAAGGCAAAGIAICIGGAICIAAGG 1635
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PatentIn Release #1.0, Version #1.25
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Patent No. 592534
GENERAL INCOMATION:
APPLICANT: Van den BOOCAART, Paul
APPLICANT: KOK, Jacobus Johannus
APPLICANT: VERMEULEN, Arnoldus Nicolaas
TITLE OF INVENTION: COCCIDIOSIS POULTRY VACCINE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                   APPLICATION NUMBER: US/08/468,852
CLASSIPLICATION 1435
CLASSIPLICATION ATA:
CLASSIPLICATION ATA:
APPLICATION NUMBER: US 08/310,357
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,865
FILING DATE: 06-AUG-1993
PRIOR APPLICATION NUMBER: US 07/604,075
FILING DATE: 18-JUN-1992
PRIOR APPLICATION NUMBER: US 07/604,075
FILING DATE: 18-JUN-1992
PRIOR APPLICATION NUMBER: EP 91.201.523.7
FILING DATE: 18-JUN-1991
                                                                                                                                                                                                                                                                                                                                         EP 91.201.523.7
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                  ATTOKNE,

RAME: MARY E. ST.

REGISTRATION NUMBER: ST.

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPONE: (301) 258-2200

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 2375 base pairs

TYPE: nucleic acid

TYPE: "NEVES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1300 Piccard Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA to mRNA
                   CURRENT APPLICATION DATA
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STATE: Maryland
COUNTRY: U.S.A.
ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eam100E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
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LOCATION:
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8.6%; Score 27.2; DB 2; Length 2375;
Best Local Similarity 52.7%; Pred. No. 6.1;
Matches 59; Conservative 0; Mismatches 53; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 gcatcgtcgctggaagctctatatttggcgctgcggacccaggagccatcat 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Akzo No. 5792644el Patent Department STREET: 1300 Piccard Drive CITY: Rockville STATE: Maryland
                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/310,357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: van den BOOGAART, Paul
APPLICANT: KOK, Jacobus Johannus
APPLICANT: VERWEULEN, Arnoldus Nicolaas
TITLE OF INVENTION: COCCIDIOSIS POULTRY VACCINE
                                                                                                                                                                                                                                                                                                                           FILING DATE: APPLICATION NUMBER: EP 91.201.523.7
                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/904,075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/08468852
Patent No. 5792644
                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: William M. Blackstone
REGISTRATION NUMBER: 29,772
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ 1D NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH: 2375 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: CDNA tO MRNA
IMMEDIATE SOURCE:
CLONE: EAM100E
                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 18-Jun-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: CONUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: 3..1859
US-08-310-357-9
                            U.S.A.
         Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                     FILING DATE:
                                                  20850
                               COUNTRY:
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,857
CLASSIFICATION: 6-JUN 1995
CLASSIFICATION: 6-JUN 1995
CLASSIFICATION: 6-JUN 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/10,357
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/10,865
FILING DATE: 06-MG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,075
FILING DATE: 18-JUN-1992
PRIOR APPLICATION NUMBER: EP 91.201.523.7
FILING DATE: 18-JUN-1991
APPLICATION NUMBER: 34,409
REGISTRATION NUMBER: 34,409
REGISTRATION NUMBER: 34,409
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA IMMEDIATE SOURCE: CLONE: Bam100E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
; LOCATION: 3..1859
US-08-468-857-9
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Query Match 8.6%; Score 27.2; DB 4; Length 2375; Best Local Similarity 52.7%; Pred. No. 6.1; Matches 59; Conservative 0; Mismatches 53; Indels 0;

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Search completed: November 4, 2000, 13:33:43 Job time: 16659 sec

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November 4, 2000, 13:40:30 ; Search time 320.8 Seconds (without alignments) 480.118 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                      480022 seqs, 187831343 residues
                                                                          OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                         IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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                                                                                                                     Run on:
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1: /SIDS6/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /SIDS6/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /SIDS6/gcgdata/geneseq/geneseqn/NA1981.DAT:*
4: /SIDS6/gcgdata/geneseq/geneseqn/NA1983.DAT:*
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8: /SIDS6/gcgdata/geneseq/geneseqn/NA1987.DAT:*
8: /SIDS6/gcgdata/geneseq/geneseqn/NA1987.DAT:* /SIDS6/gcgdata/geneseq/geneseqn/Nal989 DAT:*
/SIDS6/gcgdata/geneseq/geneseqn/Nal990 DAT:*
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/SIDS6/gcgdata/geneseq/geneseqn/Nal995 DAT:* /SIDS6/gcgdata/geneseq/geneseqn/NA1998.DAT:*/SIDS6/gcgdata/geneseq/geneseqn/NA1999.DAT:* /SIDS6/gcgdata/geneseq/geneseqn/NA2000.DAT:* /SIDS6/gcgdata/geneseq/geneseqn/NA1997.DAT:* N_Geneseq_36:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES		Ð	18 T88035	2.01425	X06748	256375	V60943	X20537	V42965	X16683	V52287	Z30047	V74364	V21187	
		DB	18	20	20	21	_	20	19	20		20		19	
		Match Length DB ID	1916	1038602	14516	14516	4487	2450	2025	2025	1953	2087	16592	53789	
æ	Query	Match	24.2					16.0	13.9	13.9	13.8	13.8	12.1	9.6	
		Score	99.2	91.2	69.2	69.2	66.2	65.6	57	57	56.4	56.4	49.6	39.5	
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ALIGNMENTS

RESULT

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a X	T88035 stand	T88035 standard; DNA; 1916 BP.
AC	T88035;	
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占:	22-DEC-1997	(first entry)
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X DE	Brevibacteri	Brevibacterium flavum 6-phosphogluconate dehydrogenase DNA.
KW	Brevibacteri	Brevibacterium flavum: 6-phosphoglucopate debudrocommon.
XX XX	recombinant p	recombinant production; coryneform; bacterium; bacteria; ds.
SO XX	Brevibacterium flavum.	ım flavum.
FH	Key	Location/Onalifiers
ΕŢ	cos	3741852
FT		/*tag= a
F X		/product= 6-phosphogluconate_dehydrogenase
PN	JP09224662-A	
XX		
PD	02-SEP-1997.	
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XX	23-FEB-1996;	96JP-0036346.
PR	23-FEB-1996;	96JP-0036346
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PA XX	(MITU) MITSUBISHI CHEM	BISHI CHEM CORP.
DR	WPI; 1997-484097/45.	097/45.
Z X	P-PSDB; W27613	3.
ΡŢ	6-phospho:qlu	6-phospho:qluconate dehydrogenase - can be recombinantly broof
ΡŢ	transforming	끍

6-phospho:gluconate dehydrogenase - can be recombinantly produced by transforming coryneform bacteria with DNA molecule encoding it

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Griffais R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            677 gacgecatggacgacgacateateategacggeggeaacgeeetetaeacegacaee 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312 gagaggagagaaggccatggaggagcgcggcctnctgtatcttggcatgggtgtctct 371
                                                                                                                                                                                                                                                                                              132 ettecegtetaeggettecatgaeecegegteetttgtgaagteeatteagaageeaegg 191
                                                                                                                                                                                                                                tacaacaggacaacctccaaggtggacgagaccgtgcagcgtgccaaggcagaaggaaac 131
                                                                                                                                                                                                                12 goggtcatggggcagaaccttgccctcaacattgcagagaaagggttccccatctctgtg 71
                                                                                                                                                                                        Gaps
                                     The present sequence encodes the Brevibacterium flavum JM-233 6-phosphogluconate dehydrogenase (6-PD). The 6-PD can be recombinantly produced by transforming coryneform bacteria with the DNA molecule encoding it.
                                                                                                                                                                                                                                                                                                                                                                                         563 ttcatcccttccgcaaccgtcgaagag-----ttcgtagcatccctggaaaagccacgc
                                                                                                                                                                                                                                                                                                                                                                                                                     617 egegecateateatggtteaggetggtaaegecaeegaegeagteateaaeeagetggea
                                                                                                                                                                                       9
                                                                                                                                                          24.2%; Score 99.2; DB 18; Length 1916; 54.9%; Pred. No. 5.3e-17;
                                                                                                                 Sequence 1916 BP; 425 A; 596 C; 507 G; 388 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete genome sequence of Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 ggaggaaaggaggtgccgcaacggcccgtccttgatg 410
                                                                                                                                                                                       0; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             797 ggcggcgaagaaggcgcactcaacggcccatccatcatg 835
               Claim 1; Pages 5-7; 8pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Z01425 standard; DNA; 1038602 BP
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97FR-0015041.
97FR-0016034.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-OCT-1999 (first entry)
                                                                                                                                                                            Best_Local Similarity 54.9
Matches 219; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydia trachomatis.
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trachomatis open reading frames (ORFS) of the genome encode polypeptides y36754-Y37949. The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microcorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and veneral lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 397222 ccrrrcrrcgaagagagagararrcrcarrgarggggggaaragcrarrarragarrcr 397163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 397162 GAGCGACGCTATGTCGACCTGAAAAAAGAAGGAATTCTATTTGTTGGGATGGGAGTCTCT 397103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 397456 GCCGTGATGGGCAAAAACCTTGTATTGAACATGGTGGATCATGGTTTTTCTGTTTCTGTC 397397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 397336 CTGC-----AAGGATTTACTACGATTCAAGAGTTTGTTCAATCTTTGAAGCGTCCTCGT 397283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1038602 BP; 304265 A; 214645 C; 214259 G; 305001 T; 432 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 tacaacaggacaacctccaaggtggacgagaccqtgcagcgtgccaaggcagaaggaaac 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 397282 AAGATCATGATCATGATTAAAGCGGGGGGCTCCTGTTGATGAAATGATTGCCTCCTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252 gctcacttggagcagggcgactgcatcatcgatgggggaacgagtggtacgagaacacg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 91.2; DB 20; Length 1038602; Pred. No. 3.3e-14;
                                                                                                                                                                 present sequence represents the complete genome of Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                    Genome sequence of Chlamydia trachomatis
                                                                                                            Claim 1; Page 373-656; 1755pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E. coli 0111 antigen gene cluster.
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Best Local Similarity 53.6%;
Matches 214; Conservative
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WPI; 1999-371125/31.
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/product= O_antigen_flippase
/note= "wzx gene (ORF8), this region is
Specifically claimed in Claim 6; encodes W88307"
                                                                                                                                                                                                                                                                                                                                                 /product= O_antigen_polymerase
/note= "wzy gene (ORF9), this region is
specifically claimed in Claim 6; encodes W88308"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= colitose or glucose transferase
/note= "wbdM gene (ORF11), this region is
specifically claimed in Claim 6; encodes W88310"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; W88300, W88301, W88302, W88303, W88304, W88305, W88306, W88307, W88308, W88309, W88300, W88310, W88311.
                                  it= galactosyl_transferase
    "wbdH gene (ORFI), this region is
    specifically claimed in Claim 6, and encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= 1
/note= "gnd gene (partial sequence); encodes W88311"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid molecules specific for bacterial polysaccharide antigens – useful for detecting specific strains in, e.g. food, faeces or patient samples
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                                                                                                                                                                                                                                                                                                                                                                                                      /product= colitose_or_glucose_transferase
/note= "wbdL gene (ORF10); encodes W88309°
11821..12945
                                                                                                                                                                                                                                                     '*tag= g
'note= "wbdK gene (ORF7); encodes W88306"
                                                                                                                               "wbdI gene (ORF3); encodes W88302"
                                                                                                                                                                                               "manB gene (ORF5); encodes W88304"
                                                                                                                                                                                                                             "wbdJ gene (ORF6); encodes W88305"
                                                                                                                                                              "manc gene (ORF4); encodes W88303'
                                                                                                "gmd gene (ORF2); encodes W88301"
  Location/Qualifiers
739..1932
                                                                W88300
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97AU-0006545
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 Key
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gene cluster was isolated from a cosmid gene bank of E. coli M92 cfromosomal DNA by screening with E. coli Olll antiserum. Open reading frames within the gene cluster were identified on the basis of homology to known sequences. The genes encode proteins is case M88100-11) involved the synthesis of sugars present in the polysaccharide antigen, and in the transport or processing of polysaccharide or ollosaccharide units. The use of nucleic acid molecules derived from particular assembly and transport genes, particularly wbd (transferase), wax (flippase) and wzy (polymerase) genes, within O antigen gene clusters improves the specificity of methods for the detection and identification of O antigens. Esting food- or faecal-derived samples, or samples from patients. The O antigen is a major virulence factor of enteropathogenic E. coli strains that cause diarrhoea and haemorrhagic colitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13157 gcagigatggggggggaaccigggggctcaacatcgaaagccggggttataccgtctccatc 13216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13217 ttcaaccgctcccgcgagaaaactgaagaagttgttgccgagaacccggataagaactg 13276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 tacaacaggacaacctccaaggtggacgagaccgtgcagcgtgccaaggcagaaggaac 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 cttcccgtctacggcttccatgaccccgcgtctttgtgaagtccattcagaagccacgg 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               252 getcaettggagcagggcgaetgcatcatcgatggggggaacgagtggtacgagaacaeg 311
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                                                                                                                                                                                                                                                                                                                                                                                Length 14516;
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                                                                                                                                                                                                                                                                                                                                                                       16.9%; Score 69.2; DB 20; 50.4%; Pred. No. 5.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 189;
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                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 50.49
Matches 201; Conservative
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                                                                                                                                                                                                                                                                                                                             256331 to 256398 represent nucleic acid molecules (I) encoding all or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Gaps
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                                                                                                                                                                         Novel nucleic acid molecule useful for the detection of flagellated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 giggigateatgetegteaaggeeggegegecagtigaecagaecategegaegetegea
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Pred. No. 5.7e-09;
0; Mismatches 189; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14516 BP; 4582 A; 2221 C; 2971 G; 4742 T; 0 other;
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                                                                                                                                                                                                            bacterial strains in food, faeces, etc.
                                                                                                                                                                                                                                                                        Claim 3; Page 216-221; 245pp; English.
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16.9%;
Best Local Similarity 50.4%;
Matches 201; Conservative 0
(UNSY ) UNIV SYDNEY.
                                                                                                                    WPI; 2000-072598/06
                                                           Reeves PR, Wang L;
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4163 ttgcttgaagaaggcgacgtcatcatggacggaggaaactcccactatgaagacacagaa 4222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4043 teteteagecegtattacgagettgaggaetttgtteaategttagaaaaaecaagaaaa 4102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3932 gtaatgggaagcaacatcgccttaaacatggcaaataaaggcgaaaacgtcgctgtctat 3991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  315 aggagggagaaggccatggaggagggcctnctgtatcttggcatggtgtctctgga 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 aacaggacaacctccaaggtggacgagaccgtgcagcgtgccaaggcagaaggaaaggaaactt 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 cccgtctacggcttccatgaccccgcgtcctttgtgaagtccattcagaagccacgggtg 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 greatggggcagaaccttgcctcaacattgcagagaaagggttccccatctctgtgtac 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence may be used in the expression of hetrogenous sequences, without catabolite repression, inducible with the action of gluconic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 cacttggagcagggcgactgcatcatcgatggggggaacgagtggtacgagaacacgggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195 gtgatcatgctcgtcaaggccggcgccagttgaccagaccatcgcgacgctcgcagct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gluconic acid operon and its promoter of Bacillus subtilis - in DNA fragment, which is controlled by catabolite repression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 4487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4487 BP; 1308 A; 991 C; 1065 G; 1123 T; 0 other;
                                                        Sequence encoding gluconic acid promoter and operon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 66.2; DB 7;
Pred. No. 2.6e-08;
0; Mismatches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4283 ggtgaagtcggtgcgttaacagggccttccatcatg 4318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    375 ggaaaggagggtgcccgcaacggcccgtccttgatg 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 499; 10pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MITK ) MITSUI TOATSU CHEM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X20537 standard; DNA; 2450 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 16.1%;
Best Local Similarity 50.0%;
Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    84JP-0221192
                                                                                                                                                                                                                                                                                                                                                                                                                                             84JP-0221192
07-OCT-1991 (first entry)
                                                                                                                              Catabolite repression; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1986-166561/26.
                                                                                                                                                                                          Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                    23-OCT-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                23-OCT-1984;
                                                                                                                                                                                                                                                      JP61100194-A
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V42965 standard; DNA; 2025

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 tacaacaggacaacetecaaggtggacgagaccgtgcagcgtgccaaggcagaaggaaac 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 cttcccgtctacggcttccatgaccccgcgtcctttgtgaagtccattcagaagccacgg 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 aagcgaatcaccggcgcccactccattgcagaacttgtttcacttttggcacgtccacgc 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252 gctcacttggagcagggcgactgcatcatcgatgggggaacgagtggtacgagaacacg 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 cccttctagaaaagggggacctcgttatcgacggtggcaactctcattaccaggatacc 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      312 gagaggaggaggagggccatggaggaggggcctnctgtatcttggcatgggtgtctct 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              329 atccggcgcatgcatgcgctagaggccgcaggtattcatttcattggcacaggagtttcg 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 gctgtcatgggagagaatctggttctcaaca-tgagcgcaacgkttttccktcgcagtt 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis
                                                                     Treponema pallidum infection; syphilis; Borrelia infection; animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 ttcaatcgcaccaccamggtggtcga----ccgatttcttgcagggcgcgctcatggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polynucleotide sequence from the genome of Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.0%; Score 65.6; DB 20; Length 2450; 50.9%; Pred. No. 3.1e-08; Live 2; Mismatches 187; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2450 BP; 553 A; 643 C; 631 G; 617 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            production of biosynthetic products such as enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ggaggaaaggatgcccgcaacggcccgtccttgatg 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                          98WO-US13041
                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0050667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-081273/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                  enzyme production;
                                                                                                                                                                 reponema pallidum
                                                                                                                                                                                                                         WO9859034-A2
                                                                                                                                                                                                                                                                                                                                                          23-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUN-1997;
                                                                                                                                                                                                                                                                                           30-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fraser CM;
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conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema, endocarditis or infection of the cerebrospinal fluid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 ttcccgtctacggcttccatgaccccgcgtcctttgtgaagtccattcagaagccacggg 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 taccaagct-----atgacgttgaaagttttgtaaactcaatcgaaaaacctcgtc 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 tggtgatcatgctcgtcaaggccggcgccagttgaccagaccatcgcgacgctcgcag 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 ctcacttggagcagagggactgcatcatcgatggggggaacgagtggtacgagaacacgg 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 gtatcatgctgatggttcaagctggacctggtacagatgctactatccaagcccttcttc 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  products for diagnosis, prevention and treatment of infections e.g. pneumonia, bacteremia, meningitis or endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence is that of a Streptococcal polypeptide coding region. The polypeptide can potentially be used for the diagnosis and prevention of bacterial infections, especially SP infection. It may be used for the treatment of diseases such as otilis media,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ccgtaatgggtcgtaaccttgcccttaatattgaatcacgtggttacacaattgctatct
                                                                                                                                                                                                                                                                                                                                                                                                                                            Black MT, Hodgson JE, Knowles DJC, Lonetto MA, Nicholas RO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2025;
                                                                                                                     Polypeptide; ORF; open reading frame; infection; bacterial; streptococcal; bacteremia; diagnosis; prophylaxis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 13.9%; Score 57; DB 19; Length 20 Best Local Similarity 48.5%; Pred. No. 5.2e-06; Matches 193; Conservative 0; Mismatches 196; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2025 BP; 593 A; 413 C; 461 G; 557 T; 1 other
                                                                                        Streptococcus pneumoniae polypeptide coding region.
                                                                                                                                                                                                               complement (1697..1843)
/*tag= a
/note= "polypeptide"
                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 59; 181pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                   96US-0031879.
                                                                                                                                                                                                                                                                                                                                     97WO-US21976
                                                          (first entry
                                                                                                                                                                   Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zarfos PN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-322654/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; W62685
                                                                                                                                                                                                                                                                         WO9823631-A1
                                                                                                                                                                                                                                                                                                                                   24-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                 27 -NOV - 1996;
                                                          09-NOV-1998
                                                                                                                                                                                                                                                                                                       04-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reid RH,
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The present sequence encodes a bacterial response regulator (RR) protein which is a component of the two component signal transduction system (TCSTS). RR Polynuclectides and proteins are useful for diagnosing susceptibility to diseases by detecting mutations or polymorphisms in the RR gene or analysing for the presence of amount of RR protein expressed in a patient sample. RR PCR probes are useful for diagnosing diseases, and can characterise the response of the infectious organism to drugs. RR proteins and polynucleotides are also useful for screening for antagonists, agonists and drugs against infectious micro-organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           microbial diseases, especially Streptococcus pneumoniae diseases including ottits media, bacteraemia, conjunctivitis, pneumonia, sinusitis, pleural empyema, endocarditis and especially meningitis. Epitopes of RR proteins and polynucleotides are useful immunogens for producing anti-RR antibodies for prevention of bacterial infections, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cus pneumoniae; response regulator; antibacterial; infection; bacteraemia; meningitis; otitis media; conjunctivitis; pleural empyema; endocarditis; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RR agonists and antagonists are bacteriostatic and bacteriocidal compounds which can be used in treatment to enhance (agonist) or block
                                                                            agaggaggagaaggccatggaggagcgcggcctnctgtatcttggcatgggtgtctctg 372
                                                                                                                                                292 tocgtogtaatgaagaattggcaaactcaggtatcaactttatcggtactggagtttctg 351
232 cacacettgacaagggtgatatettgattgacggtggaaataetttetacaaagatacea 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polynucleotides - useful as diagnostic reagents and for prevention and treatment of Streptococcus pneumoniae infections, especially pneumonia, bacteraemia and meningitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (antagonist or antisense sequence) RR activity, therefore treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae response regulator polypeptides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae response regulator ORF DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shilling LK, Throup J,
                                                                                                                                                                                                                                     373 gaggaaaggaggtgcccgcaacggcccgtccttgatg 410
                                                                                                                                                                                                                                                                                                         352 gtggtgaaaaaggtgcccttgaaggtccttctatcatg 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/note= "no stop codon given"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 5-6; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X16683 standard; DNA; 2025 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-083574/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; W94667.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP892057-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pneumonia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sinusitis;
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NAME OF THE PROPERTY OF THE PR

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RR polynucleotides can be used in genetic immunisation (gene therapy) to prevent infections. RR proteins, polynucleotides and their (ant)agonists can prevent adhesion of bacteria to matrix proteins, and are useful for use on wounds and body implants to prevent bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ctcacttggagcagggcgactgcatcatcgatggggggaacgagtggtacgagaacacgg 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   313 agaggaggagaaggccatggaggagggcggcctnctgtatcttggcatgggtgtctctg 372
                                                                                                                                                                                                                                                                                73 acaacaggacaacetecaaggtggacgagaccgtgcagcgtgccaaggcagaaggaaace 132
                                                                                                                                                                                                                                                                                                                   121 taccaagct-----atgacgttgaaagttttgtaaactcaatcgaaaaacctcgtc 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 gtatcatgctgatggttcaagctggacctggtacagatgctactatccaagcccttcttc 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 tocgtogtaatgaagaattggcaaactcaggtatcaactttatcggtactggagtftctg 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, and
                                                                                                                                                                                                              13 cggtcatggggcagaaccttgccctcaacattgcagagaaagggttccccatctctgtgt 72
                                                                                                                                                                                                                                               1 ccgtaatgggtcgtaaccttgcccttaatattgaatcacgtggttacacaattgctatct 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay; computer readable medium; vaccine; pharmaceutical composition; ds.
                                                                                                                                                                                                                                                                                                                                                      133 ttcccgtctacggcttccatgaccccgcgtcctttgtgaagtccattcagaagccacggg
                                                                                                                                                                                                                                                                                                                                                                                                                            193 tggtgatcatgctcgtcaaggccggcgcgccagttgaccagaccatcgcgacgctcgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232 cacaccttgacaagggtgatatcttgattgacggtggaaatactttctacaaagatacca
                                                                                                                                                                           6
                                                                                                                                        Length 2025;
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                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae genome fragment SEQ ID NO:154.
                                                                                      Sequence 2025 BP; 592 A; 413 C; 463 G; 557 T; 0 other;
                                                                                                                                                                           0; Mismatches 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dougherty BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         373 gaggaaaggaggtgcccgcaacggcccgtccttgatg 410
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                                                                                                                                                          5.2e-06;
                                                                                                                                          DB 20;
                                                                                                                                          Score 57;
                                                                                                                                                            Pred. No.
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                                                                                                                                        13.9%;
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                                                                                                                                                                             Matches 193; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae.
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Rosen CA;
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                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-OCT-1997;
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Kunsch CA,
                                                                                                                                            Query Match
                                                                                                                                                              Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V52287;
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V52287
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pharmaceutical compositions and vaccines for Streptococcus pneumoniae

Claim 1; Page 1020-1021; 1409pp; English.

The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (V52134 to V52524) recorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391 (V52134 to V52524) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced genome (SEW 1D NO:1 to 31) where the nutting and missions to process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences to 391, identifying members of the library which contain sequences to 391, identifying members; or (b) isolating the nucleic acid molecules from the members; or (b) isolating mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome. Products from the present fragments of the S. pneumoniae genome. Products from the present used in diagnosis kits and assays, and pharmaceutical compositions and vaccines for S. pneumoniae.

Sequence 1953 BP; 568 A; 404 C; 443 G; 538 T; 0 other;

ä 44 gccgtaatgggtcgtaaccttgcccttaatattgaatctcgtggttacacagttgctatc 103 72 tacaacaggacaacctccaaggtggacgagaccgtgcagcgtgccaaggcagaaggaaac 131 132 cttcccgtctacggcttccatgaccccgcgtcctttgtgaagtccattcagaagccacgg 191 164 gtaccaagct-----atgacgttgaaagttttgtaaactcaatcgaaaacctcgt 214 192 giggigateaigetegicaaggeeggegegeeagitgaeeagaeeategegaegetegea 251 215 cgtatcatgctgatggttcaagctggacctggtacagatgctactatccaagccttctt 274 252 gctcacttggagcagggcgactgcatcatcgatgggggaacgagtggtacgagaacacg 311 275 ccacaccttgacaagggtgatatcttgattgacggaggaaatactttctacaaagatacc 334 335 atccgtcgtaatgaagaattggcaaactctggtatcaactttatcggtactggggtttct 394 gagaggaggagagaggccatggaggagcgcgcctnctgtatcttggcatgggtgtctct 371 12 goggtcatggggcagaaccttgccctcaacattgcagagaaagggttccccatctctgtg 71 6 13.8%; Score 56.4; DB 19; Length 1953; 48.4%; Pred. No. 7.3e-06; tive 0; Mismatches 197; Indels 9; 372 ggaggaaaggaggtgcccgcaacggcccgtccttgatg 410 395 ggtggtgaaaaaggtgcccttgaaggtccttctatcatq 433 Best Local Similarity 48.49 Matches 193; Conservative Query Match g g οy q ò q QQ ò ά ö a δ

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DNA encoding S. pneumoniae 6-phosphogluconate dehydrogenase protein.
                        Z30047 standard; DNA; 2087 BP
                                                                        26-JAN-2000 (first entry)
RESULT 10
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ij

6

13.8%; Score 56.4; DB 20; Length 2087; 48.4%; Pred. No. 7.5e-06; tive 0; Mismatches 197; Indels 9;

Best Local Similarity 48.4 Matches 193; Conservative

δ a

g ò

δλ

Query Match

Sequence 2087 BP; 610 A; 424 C; 474 G; 572 T; 7 other;

12 geggtcatggggcagaaccttgccctcaacattgcagagaaagggttccccatctctgtg 71

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The present sequence encodes a 6-phosphogluconate dehydrogenase protein from Streptococcus pneumoniae. The protein induces an immune response against bacteria, causing production of antibodies that interfere with bacterial adhesion. The 6-phosphogluconate dehydrogenase, its fusion proteins and cells (or their membranes) are used to screen for specific as antibacterials and to raise antibodies. Antibodies are used as antibacterials and to raise antibodies. Antibodies are used as immunosasay reagents; for isolation or identification of therapeutic antibacterials. Conditions that can be treated include bacterial infections, by Helicobacter pylori, or especially by capterial infections, by Helicobacter pylori, or especially by protein or mutations in gene sequences encoding it can be used for the diagnosis, staging or monitoring treatment of infections, or determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               susceptibility to them, particularly in standard immunoassays or hybridisation and amplification tests. Nucleic acids encoding the protein may also be used for chromosomal mapping and identification, for genetic immunisation or the rational design of (ant)agonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New 6-phosphogluconate dehydrogenase from Streptococcus pneumoniae, and related proteins, used to screen for antibacterial agents, to treat infections and to raise diagnostic antibodies
               6-phosphogluconate dehydrogenase; bacterial adhesion; antibaction; bacterial infection; Helicobacter pylori; meningitis; chromosomal mapping; genetic immunisation; ss.
                                                                                                                                                                                    /product= "6-phosphogluconate dehydrogenase"
                                                                                                                               Location/Qualifiers
11..1435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 3-4; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                        (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                      98US-0058692.
                                                                                                                                                                                                                                                                                                 99WO-US07782.
                                                                                                                                                                   /*tag= a
                                                                                            Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-620409/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; Y43524
                                                                                                                                                                                                                        WO9953020-A1.
                                                                                                                                                                                                                                                                                               09-APR-1999;
                                                                                                                                                                                                                                                                                                                                    10-APR-1998;
                                                                                                                                                                                                                                                             21-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                               Warren RL;
                                                                                                                               Key
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given in the specification for this DNA sequence"

/*tag= c //note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence 10921..10980
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/*tag= b
/note= "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "these bases represent a line of missing text in
the sequence listing in the specification. They
215 cgtatcatgctgatggttcaagctggacctggtacagatgctactatccaagcccttctt 274
                                                                 275 ccacaccttgacaagggtgatatcttgattgacggwggaaatactttctacaaagatacc 334
                                                                                                    312 gagaggaggagaaggccatggaggaggagcctnctgtatcttggcatgggtgtctct 371
                                                                                                                                     335 atccgtcgtaatgaagaattggcaaactcwggtatcaactttatcggtactggrgtttct 394
                                    gctcacttggagcagggcgactgcatcatcgatggggggaacgagtggtacgagaacacg
                                                                                                                                                                            ggaggaaaggaggtgcccgcaacggcccgtccttgatg 410
                                                                                                                                                                                                Staphylococcus aureus contig SEQ ID #53.
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121..180
                                                                                                                                                                                                                                                                                                   V74364 standard; DNA; 16592 BP
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                                                                                                                                                                                                                                                                                                                                                                         16-MAR-1999 (first entry)
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/note= "t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus.
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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access medium, preferably selected from a floppy or hard disk, random access the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial; therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, coalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for the polypeptides. The new DNA sequences can the transformed as primers or probes for isolating chomologues of any of the S.aureus DNA sequences contained on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ï
                                                                                             the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
                                                                                                                                                                                          "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
                                                                                                                                                                                                                                                                                                           "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
                                                                               "these bases represent a line of missing text in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus
in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.1%; Score 49.6; DB 18; Length 16592; 47.1%; Pred. No. 0.00075;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches 201; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fannon MR, Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotide(s) and proteins derived from stored on computer readable medium and used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 403-413; 3271pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
                                            12721..12780
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nes 188; Conservative
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7779 CATCCAACGTATTCATTGGAAGA-----ATTTGTTAATTCTTTAGAAAACCACGT 7729
                                                                                       '668 CCTTTATTAGATGATGAGATATTTAATTGATGGTGGTAATACAAACTATCAAGATACT 7609
                                                                                                                                                                          7608 ATCAGACGTAATAAAGCATTWRCACAAAGTGCAATCAACTTTATTGGTATGGGCGTTTCT 7549
                                132 etteccgtetacggettecatgaccecgcgtectttgtgaagtecatteagaagecaegg 191
                                                                       gctcacttggagcagggcgactgcatcatcgatgggggaacgagtggtacgagaacacg 311
                                                                                                                                                        312 gagaggaggagagaggccatggaggagcgcctnctgtatcttggcatgggtgtctct 371
                                                                                                                                                                                                                                                                                                                                     Amycolatopsis mediterranei rifamycin synthesis gene cluster fragment.
                                                                                                                                                                                                                                                                                                                                                          Amycolatopsis mediterranei; rifamycin; synthesis; gene cluster; polyketide synthase; actinomycete; ansamycin; ds.
                                                                                                                                                                                                              372 ggaggaaaggaggtgcccgcaacggcccgtccttgatg 410
                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/label= ORP_A
/product= "polyketide synthase"
15550..30759
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|Product= "polyketide synthase"
| 16259..41325
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41373..51614
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1825..15543
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                                                                                                                                                                                                                                                                                                                    (first entry)
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The present sequence represents a Amycolatopsis mediterranei rifamycin synthesis gene cluster DNA fragment from the present invention. The DNA fragment comprises a DNA region involved directly or indirectly in the gene cluster responsible for rifamycin synthesis, including the adjacent DNA regions to the right and left which, by reason of their function in connection with rifamycin biosynthesis, qualify as constituents of this rifamycin gene cluster, and functional fragments, derivatives or constituents of these. The Amycolatopsis mediterranei rifamycin synthesis gene cluster DNA fragment can be used for producing rifamycin, rifamycin analogues or precursors. It can also be used for inactivating or modifying genes involved in ansamycin or rifamycin biosynthesis. The DNA can be used for constructing mutant actinomycetes strains from which the natural rifamycin or ansamycin biosynthesis gene cluster has been partly or completely deleted. The DNA can be used for assembling a library of polyketide synthases, which can be used for assembling a library of polyketide synthases, which can be used for assembling a library of polyketide synthases, which can be used for assembling a library of polyketide synthases, which can be used for assembling a library of polyketide synthases, which can be losed for assembling a library of polyketide synthases, which can be losed for assembling a library of polyketide synthases, which can be losed for assembling a library of folyketide synthases, which can be losed for assembling a library of polyketide synthases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 agaagccacgggtggtgatcatgctcgtcaaggccggcgccagttgaccagaccatcg 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ccatctctgtgtacaacaggacaacctccaaggtggacgagaccgtgcagcgtgccaagg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 cagaaggaaaccttcccgtctacggcttccatgaccccgcgtcctttgtgaagtccattc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 acgagaacacggagagaggagaaggccatggaggagcgcgcctnctgtatcttggca 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 cccacgcgtccgcggtcatggggcagaaccttgccctcaacattgcagagaaagggttcc 60
                                                                                                                                                                                       Amycolatopsis mediterranei rifamycin synthesis gene cluster - used to produce rifamycin and rifamycin analogues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
9.6%; Score 39.2; DB 19; Length 53789;
Best Local Similarity 45.2%; Pred. No. 0.52;
Matches 183; Conservative 0; Mismatches 219; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 53789 BP; 6707 A; 19183 C; 20504 G; 7395 T; 0 other;
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                                                                                                                                                                                                                                                                  Claim 4; Page 53-102; 205pp; English.
                                                          Toupet C;
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ID T63571 standard; DNA; 1524 BP.
                                                                                                     WPI; 1998-169172/15.
P-PSDB; W52845-W52850.
(NOVS ) NOVARTIS AG.
                                                    Schupp T,
                                                    Engel N,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         595 cgcgcgatgggcagcgggtacatcgccgacgcgtgcgcacgcgcacgccgccgaccc 654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         xylanase\ gene\ sequences - obtd. by recovering DNA from soil samples and PCR amplification using primers based on xylanase\ genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rice; beta-glucanase; Gns; promoter; plant resistance; expression; fungal infection; transgenic monocotyledon; growth; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A DNA sequence (T63571) codes for a novel xylanase (W09777). It was isolated from a phagemid in a soil DNA library using as probe a gene fragment (T63568) obtd. by amplification of soil DNA using degenerate primers (T63548-49) based on conserved portions of family F cellulases. It was sequenced by primer walking over the phagemid insert using the same degenerate primers as initial extension primers. Subsequent extension primers were constructed by examining the previously generated sequence data. The novel xylanase gene can be used for prodn. of xylanase for industrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           309 acggagagaggagaaggccatggaggagcggcctnctgtatcttggcatggg 364
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Pred. No. 0.61;
0; Mismatches 87; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1524 BP; 281 A; 537 C; 507 G; 199 T; 0 other;
                                               Xylanase gene obtained by soil DNA amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yap WH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rice beta-glucanase Gns8 encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Warren RAJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; Page 24-26; 34pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TERR-) TERRAGEN DIVERSITY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.1%;
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30-JUN-1997 (first entry)
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                                                                                                             Xylanase; soil DNA; ds.
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Best Local Similarity
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                                                                                                                                                                  Not identified.
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                                                                                                                                                                                                                                                                                                                                                                                               22-SEP-1995;
                                                                                                                                                                                                                          WO9712991-A1
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The present invention describes isolated polynotrocuses (FW) comprises the present invention described are: (A) a chimeric gene (CGI) used to produce a transgenic monocot plant, comprising: (I) a transcriptional regulatory region which hybridises under high stringency with a rice beta glucanase promoter; and (ii) a DNA sequence heterologous to the regulatory region, and encoding a protein to be produced by the plant; cand (iii) a second DNA sequence encoding a signal polypeptide operatively linked 5 to 3', so that the signal polypeptide is in translation frame with the protein, and is effective to facilitate secretion of the protein are plant; (B) a monocot plant stably transformed with CGI; (C) seeds from the above plant; (D) a method of enhancing the stably transformed of a monocot plant to fungal infection by stably transforming it with CGI; (E) seeds from the above plant; (D) a method of enhancing the restsing stably transforming a plant with CGI, obtaining the protein, comprising stably transformed plant, germinating the seeds and obtaining the protein from the seed endosperm; (F) an isolated protein having the draracteristics of a rice beta-glucanase enzyme, corresponding to beta-glucanases 2.9 a rice beta-glucanase enzyme, corresponding to beta-glucanases 2.9 a rice beta-glucanase resistance of fungal infection, improved growth corresponding to heterologous proteins in contact plants. The polynucleotides and the proteins produced may also provide increased resistance to fungal infection, improved growth contact relations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes isolated polynucleotides (PN) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 561 CCCGAGCTGCACGCTGCTCCGCGCCCCTACGCAAGTAGGGGGTACACGTTCACCAG 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        501 CAGCGGCGCCCCTGGACGCGAGGTAGGCGACGATCGCCCAGTGTACGGCGACGCGCC 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggtggacgagaccgtgcagcgtgccaaggcagaaggaaaccttcccgtctacggcttcca 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                             New polynucleotides which hybridise with rice beta-glucanase genes useful for transforming monocot plants for various characteristics including increased resistance to fungal infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           621 GGTGTATGTCACGCCGCCGTCGGTCACCGACGCCGACTGCCACCCCGACAGCAGGGGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152 tgaccccgcgtcctttgtgaagtccattcagaagccacgggtggtgatcatgctcgtcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212 ggccggcgccagttgaccagaccatcgcgacgctcgcagctcacttggagcagggcga
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Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 939 BP; 144 A; 345 C; 307 G; 143 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   various tissues obtained from the plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 55-56; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 8.7%;
Best Local Similarity 45.9%;
                                                                                                            98WO-US13525
                                                                                                                                                       97US-0050675
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                                                                                                                                                                                                       (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                 WPI; 1999-105620/09.
                                                                                                                                                                                                                                                                                                                      P-PSDB; Y09297
                                                                                                                                                                                                                                                     Rodriguez RL;
                                                                                                                                                          25-JUN-1997;
                   W09859046-A1
                                                                                                            25-JUN-1998;
                                                                 30-DEC-1998.
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ggaggagcgcggcctnctg 350 381 GGTGGTGACCGGGATGCCG 363

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The present invention describes isolated polynucleotides (PN) comprising a sequence which hybridises under high stringency with a rice beta-glucanase gene. Also described are: (A) a chimeric gene (CGI) used to produce a transgenic monocot plant, comprising: (i) a transcriptional regulatory region which hybridises under high stringency with a rice beta glucanase promoter: and (ii) a DNA sequence heterologous to the regulatory region, and encoding a protein to be produced by the plant; and (iii) a second DNA sequence encoding a signal polypeptide operatively linked 5' to 3', so that the signal polypeptide is in translation frame with the protein, and is effective to facilitate secretion of the protein caross aleurone or scutellar epithelium layers into the endosperm of seeds obtained from the plant; (b) a monocot plant stably transformed with CGI; (C) seeds from the above plant; (D) a method of enhancing the transforming the transforming the carbot stans of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides which hybridise with rice beta-glucanase genes useful for transforming monocot plants for various characteristics including increased resistance to fungal infection
                                                                                                                                                                                                                                                                                                      Rice; beta-glucanase; Gns; promoter; plant resistance; expression; fungal infection; transgenic monocotyledon; growth; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 74-75; 90pp; English
                                                       X33570 standard; DNA; 1020 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US13525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0050675
                                                                                                                                                                             07-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (REGC ) UNIV CALIFORNIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; Y09305
                                                                                                                                                                                                                                              Rice Gns8 CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rodriguez RL;
                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-DEC-1998.
                                                                                                                     X33570;
RESULT 15
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Sequence 1020 BP; 172 A; 360 C; 320 G; 168 T; 0 other;

702 GGIGTATGTCACGCCGCCGTCGGTCACCGACGCCGACTGCGACCCCGACAGCAGCGCGTA 643 92 ggtggacgagaccgtgcagcgtgccaaggcagaaggaaaccttcccgtctacggcttcca 151 ŏ Ω

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Gaps

; 0

0; Mismatches 140; Indels

DB 20; Length 1020;

1 8.7%; Score 35.6; Similarity 45.9%; Pred. No. 1.6

Matches 119; Conservative

Query Match Best Local S

152 tgaccccgcgtcctttgtgaagtccattcagaagccacgggtggtgatcatgctcgtcaa 211 642 CCCGAGCTGCACGCTCCGCGCCCGCGCGAAAGTAGGGGTACACGTTCACCAG 583 ggccggcgccagttgaccagaccatcgcgacgctcgcagctcacttggagcagggcga 271 582 CAGCGGCGCCCCTGGACGCGAGGTAGGCGACGATCGGCGAGTGTACGGCGACGCGCC 523 272 ctgcatcatcgatggggggaacgagtggtacgagaacacggagagggggggagggcat 331 332 ggaggagcgcgcctnctg 350 462 GGTGGTGACCGGGATGCCG 444 q q δ q ογ ò

Search completed: November 4, 2000, 13:43:19 Job time: 16326 sec

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

November 4, 2000, 13:33:21; Search time 189.35 Seconds
(without alignments)
327.483 Million cell updates/sec
Perfect Score: 410
Sequence: 1 cccacgcgtccgggtcatg......gcaacggcccgtccttgatg 410
Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0
Searched: 262060 seqs, 75620727 residues
Total number of hits satisfying chosen parameters: 524120
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries Database : Issued_Patents_NA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

l, Appli 5, Appli 5, Appli 5, Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Sequence 24, Appl Sequence 2, Appli Sequence 1, Appli Sequence 47, Appl Sequence 13, Sequence 5, Sequence 3, Sequence 7, Sequence 13, Patent No. 52 Sequence 3, Sequence 1, Sequence 5, Sequence 5, Sequence 5, Description Sequence Sequence US-08-572-951.1 US-08-572-951.1 US-08-630-916A-47 US-08-676-967-5 US-08-676-974-5 US-08-08-487-5 US-08-08-487-5 US-08-08-487-5 US-08-08-487-5 US-08-08-487-5 US-08-08-487-5 US-08-938-2913 US-08-272-882D-1 US-08-232-465-14 US-08-533-669A-5 US-08-614-770A-1 US-08-55-506A-1 US-08-592-874-1 US-08-96-942-2 US-09-96-942-2 US-09-96-942-2 US-08-818-253-1 US-08-818-253-3 US-08-818-253-3 US-08-818-253-3 US-08-576-626A-2 PCT-US92-05532-1 SUMMARIES Query Match Length DB 3472 5020 1910 2261 7218 2040 49272 1312 1312 28804 Score 34.4 34.4 34.4 34.4 33.8 33.8 33.2 33.2 Š. Result

Sequence 5, Appli Sequence 5, Appli Sequence 3, Appli Sequence 3, Appli	Sequence 2, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 1, Appli Sequence 1, Appli	1, 1, 1, 1, 1, 1, 3,
US-08-533-306A-5 US-08-742-923A-5 US-08-533-306A-3 US-08-742-923A-3	US-09-130-114-2 US-07-977-434-7 US-08-458-819-7 PCT-US91-07035-7 US-08-042-747A-7 US-08-042-747A-7 US-09-075-904-1	US-09-335-409-1 US-07-731-157A-1 US-08-541-780-1 US-08-804-227C-13 US-08-804-227C-1 US-09-248-335-65 US-09-248-335-65 US-07-642-734C-3
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2680 2680 2887 2887	2505 2505 2505 2505 2943 50341	68750 2163 2163 13987 43280 971 6386 20235
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32.2.2	31. 31. 31. 31. 31. 44. 44. 44. 44.	31.4 31.2 31.2 31.2 31.3 31.3
27 28 29 30		0 0 0 3 3 8 6 7 8 9 8 8 8 9 8 8 9 8 9 8 9 8 9 9 9 9 9

ALIGNMENTS

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Sequence 24, Application US/08716942
Patent No. 5849491
GENERAL INFORMATION:
APPLICANT: Radomski, Christopher C. A.
APPLICANT: Seow, Kah Tong
APPLICANT: Seow, Kah Tong
APPLICANT: Seow, Kah Tong
APPLICANT: Seow, Kah Hong
TITLE OF INVENTION: METHOD FOR ISOLATING XYLANASE GENE
TITLE OF INVENTION: COMPOSITIONS OBTAINED THEREBY
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
COUNTRY: US98-4412
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
                                                                                                                                                                                                                                                                                                        ADDRESSEE: Oppedahl & Larson
STREET: 1992 Commerce Street, Suite 309
CITY: Yorktown Heights
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Marina T. Larson
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: TERR.P-001
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (914) 245-3252
TELEFAX: (914) 962-4330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60/004,157
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ATTORNEY/AGENT INFORMATION:
NAME: Marina T. Larson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Word Perfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                            X
US-08-716-942-24
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                                                                                                                                                                                                                                                                                                        655 AGTGCCCAGCTGTACATCAAGACTACAAGACACCCAAGAAGACACCCAAGAGCAACGCC 714
                                                                                                                                                                                                                                                                                                                                                                                                                              9.1%; Score 37.4; DB 3; Length 1524; 50.6%; Pred. No. 0.2; tive 0; Mismatches 87; Indels 0
                                                                                          NAME/KEY: sequence of xylanase gene identified by NAME/KEY: amplification of xylanase fragments from soil US-08-716-942-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Summers, R.G.
APPLICANT: Katz, L.
APPLICANT: Donadio, L.
APPLICANT: Donadio, L.
TITLE OF INVENTION: POLYKETIDE-ASSOCIATED SUGAR
TITLE OF INVENTION: BIOSYNTHESIS GENES
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM DOS
OPERATING SYSTEM DOS
SOFTWARE: FAST-SEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/576,626A
FILING DATE: 21-DEC-1995
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Dianne Casuto
REGISTRATION NUMBER: P-40,943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (847) 938-3137
TELEFAX: (847) 938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 8051 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                             Query Match
Best Local Similarity 50.6%
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                  internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
US-08-576-626A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Illinois
              FRAGMENT TYPE: i
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ANTI-SENSE:
                                                         ORGANISM:
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2497 cacccaccidececederredecearcrerredaceacerdacedecerdeacerdeacerdecede 2556
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                                                                                                                        251 ageteaettggageaggaggggaetgeateategatgggggaaegagtggtaegagaaeae 310
                                                                                                                                                                                  131 ccttcccgtctacggcttccatgaccccgcgtcctttgtgaagtccattcagaagccacg 190
                                                                                                                                                                                                                                                                           191 ggtggtgatcatgctcgtcaaggccggcgccagttgaccagaccatcgcgacgctcgc 250
                                                                                     71 gtacaacaggacaacetecaaggtggacgagaccgtgcagcgtgccaaggcagaaggaaa 130
8.7%; Score 35.6; DB 4; Length 8051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/572,951
FILING DATE: 15-DEC-1995
CLASSIFICATION: 800
PRIOR APPLICATION:
                                            0; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08572951
Patent No. 5824790
GENERAL INFORMATION:
APPLICANT: KEELING, PETER L.
APPLICANT: GAN, HANTING
TITLE OF INVENTION: MODIFICATION OF STARCH
TITLE OF INVENTION: SYNTHESIS IN PLANTS
NUMBER OF SEQUENCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: CUSHMAN DARBY & CUSHMAN ADDRESSEE: Intellectual Property Group of ADDRESSEE: Pillsbury Madison & Sutro LLP STREET: 1100 New York Avenue, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Paul N. Kokulis
REGISTRANDIN NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 222957/1.02.15C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   311 ggagaggaggagagaggccatggaggagcgcggc 344
                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DAID: ...
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,602
FILING DATE: 29-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/263,921
FILING DATE: 21-JUN-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202) 861-3000
TELEPAX: (202) 861-3000
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                        45.68;
                                              Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20005-3918
                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
US-08-572-951-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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GENERAL INFORMATION:
APPLICANT: Pirozzi, Gregorio
APPLICANT: KAY, BIJAN K.
APPLICANT: KOALKES, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                721 CGCACCGGCGCGCCACGCGCTGGAGCCTCCGCGGCGCGCCCCGGTCGCCGACGGCGG 662
                                                                                                                                                                                                                                      158 cgcgtcctttgtgaagtccattcagaagccacgggtggtgatcatgctcgtcaaggccgg 217
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                           ;
0
                                                                                                                                                             8.6%; Score 35.2; DB 2; Length 2990;
53.7%; Pred. No. 0.96;
tive 0; Mismatches 63; Indels 0
                                                                                                                                                                                                       63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: MISROCK, S. LESILE
REGISTRATION NUMBER: 19,872
REFENCE/DOCKET NUMBER: 1101-203
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 896-8864/9741
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 3476 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/630,916A FILING DATE: 03-APR-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-630-916A-47; Sequence 47, Application US/08630916A; Patent No. 6011137
LENGTH: 2990 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                            Ouery Match
Best Local Similarity 53.78
                                                                                                                                                                                                                                                                                                                                                                                               278 catcgatggggggaac 293
                                                                                                                                                                                                                                                                                                                                                                                                                                         601 TGCGGAGAGGGAGGC 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                      TYPE: nucleic acid
                                                                              ; MOLECULE TYPE: CDNA US-08-572-951-1
                                                              linear
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STATE: New York
                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-630-916A-47
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/note= "Flagelliform DNA sequence taken from the 5' region. The putative start codon is at position 219"
119 ggcagaaggaaaccttcccgtctacggcttccatgaccccgcgtcctttgtgaagtccat 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   900 GGAGGAAGTGAACCTTTCGGACCAGGAGTGGCTGGAGGACCATACAGCCCAGGTGGAGCT 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 tcagaagccacgggtggtgatcatgctcgtcaaggccggcgcgccagttgaccagtc338
                                                                                                                                                                                                                                                                                      APPLICANT: Lewis, Randolph V
PDLICANT: Hayashi, Cheryl Y
TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
TITLE OF INVENTION: CODING THEREFOR
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8.5%; Score 35; DB 4; Length 2830;
Best Local Similarity 44.9%; Pred. No. 1.1;
Matches 131; Conservative 0; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: VIRGINIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,928B
                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH STREET: 8110 GATEHOUSE RD. SUITE 500E CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JAN-1998
12-JAN-1998
13-JAN-1998
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                                                                                                                                                                                                                              Sequence 1, Application US/09010928B Patent No. 5994099 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGIH: 2830 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 29
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ADDRESSEE: BIRCH, ST
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                        2263 G 2263
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US-09-010-928B-1
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Gaps

Indels

54;

Length 3476;

8.6%; Score 35.2; DB 5; 55.4%; Pred. No. 1; 0; Mismatches

Query Match
Best Local Similarity 55.4¹
Matches 67, Conservative

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CORRESPONDENCE ADDRESS:
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US-08-676-974-5
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                                                                                                                                                                            US-08-676-974-5
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960 GGACCTGGTGGTGCAGGTGGAGCCTATGGACCAGGAGGTGTAGGAACTGGTGGAGCCGGA 1019
                                                                            1020 CCAGGAGGTTACGGACCTGGTGGAGCCGGACCAGGAGGTTATGGACCTGGTGGAGCCGGA 1079
                                                                                                                                                       1080 CCAGGAGGTTACGGACCTGGTGGAGCTGGACCAGGAGGTTACGGACCTGGTGGAGCTGGG 1139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 gtcctttgtgaagtccattcagaagccacgggtggtgatcatgctcgtcaaggccggcgc 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221 gecagttgaccagaccatcgcgacgctcgcagctcacttggagcagggcgactgcatcat 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 cattgcagagaaagggttccccatctctgtgtacaacaggacaacctccaaggtggacga 100
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                                       239 cgcgacgctcgcagctcacttggagcagggcgactgcatcatcgatggggggaacgagtg 298
                                                                                                                    299 gtacgagaacacggaggaggaggagaaggccatggaggagcgcggcctnctgtatcttgg 358
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                                                                                                                                                                                                                                    1140 ccrecagerracegaccrecrecrecagecrecagecrecagerracegaccrecre 1191
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                                                                                                                                                                                                 359 catgggtgtctctggaggaaaggagggtgcccgcaacggcccgtccttgatg 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Science & Technology Law Group
268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: COLLINS, KATHLEEN
TITLE OF INVENTION: Human Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/676,967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08676967
Patent No. 5747317
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REFERENCE/DOCKET NUMBER: UCI
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415)343-4341
TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 47.5
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 268 Busn State CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: CDNAUS-08-676-967-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                    RESULT 6
US-08-676-967-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
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161 gteetttgtgaagteeatteagaageeacgggtggtggtgateatgetegteaaggeeggege 220
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41 cattgcagagaaagggttccccatctctgtgtacaacaggacaacctccaaggtggacga 100
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47.5%; Pred. No. 1.4;
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                                                                                   281 cgatgggggaacgagtggtacgagaacacggagagggggaga 324
                                                                                                                                        741 CGACGACGAGGACGAGGAGGAGAACATCGAGAGCAAGGTGA 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/676,974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Science & Technology Law STREET: 268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCB96-055
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: COLLINS, KATHLEEN
TITLE OF INVENTION: Human Telomerase
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08676974 Patent No. 5770422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415)343-4341
TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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MEDIUM TYPE: Floppy
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41 cattgcagagaaagggttccccatctctgtgtacaacaggacaacctccaaggtggacga 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 gaccgtgcagcgtgccaaggcagaaggaaaccttcccgtctacggcttccatgaccccgc 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

8.4%; Score 34.4; DB 4; Length 2277;
Best Local Similarity 47.5%; Pred. No. 1.4;
Matches 135; Conservative 0; Mismatches 146; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 146; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,487
                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Science & Technology Law Group
STREET: 268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCB96-055
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
                                                                       GENERAL INFORMATION:
APPLICANT: COLLINS, Kathleen
TITLE OF INVENTION: Human Telomerase
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13, Application US/08804439A
Patent No. 6015565
GENERAL INFORMATION:
                                    Sequence 5, Application US/09098487
Patent No. 5917025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rose, Timothy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 2277 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     double
                                                                                                                                                                                   STREET: 268 bur...
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Best Local Similarity
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                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 94104
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                US-09-098-487-5
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RESULT
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1482 CAAGACCACCICCICCATCGAGIICGCCCGGCIGCAGIIIACGIACAACCACAIACAGCG 1541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 8.3%; Score 34; DB 5; Length 2713; Best Local Similarity 47.2%; Pred. No. 2; Matches 103; Conservative 0; Mismatches 115; Indels
                                         GLYCOPROTEIN B OF THE RFHV/KSHV SUBFAMILY OF HERPES VIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Rose, Timothy M.
APPLICANT: Bosch, Marnix L.
APPLICANT: Strand, Kurt
TITLE OF INVENTION: GLYCOPROTEIN B OF THE RFHV/KSHV
TITLE OF INVENTION: SUBFAMILY OF HERPES VIRUSES
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: MOTISON & FOEISTER
                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1662 GGCCGGCGGGTGAGCGCGCGGATGCTCGGCGACGTGA 1699
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                                                                                                                      E: Fish & Richardson P.C.
4225 Executive Square, Ste 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09176/004001
                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,439A
                                                                                                                                                                                                                                                                                        IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: February 21, 1997
CLASSIETCATION: 424
ATTONNEY, AGGNT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/08720229
Patent No. 6022542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 091
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 13:
    Bosch, Marnix L.
                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2713 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                       113
                   Strand, Kurt
                                     TITLE OF INVENTION: GL
TITLE OF INVENTION: SU
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                   STREET: 4220 ....
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US-08-804-439A-13
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APPLICANT:
APPLICANT:
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US-08-720-229-13
                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                       STATE:
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0; Gaps

0; Mismatches 115; Indels

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Matches 103; Conservative
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Best Local 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 ggtgatcatgctcgtcaaggccggcgccagttgaccagaccatcgcgacgctcgcagc 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BURE, RAE L.; PACHL, CAROL; VALENZUELA, PABLO D.T.
TITLE OF INVENTION: EXPRESSION OF RECOMBINANT GLYOPROTEIN
BY FROM HERPES SIMPLEX VIRUS
NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 0S/08/587,179,
FILING DATE: 20-0SP-1990
PRIOR APPLICATION NUMBER: 921,730
FILING DATE: 20-0CT-1986
FILING DATE: 20-0CT-1986
FILING DATE: 20-0CT-1986
FILING DATE: 06-APR-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 8.3%; Score 34; DB 5; Length 2713; Best Local Similarity 47.2%; Pred. No. 2; Matches 103; Conservative 0; Mismatches 115; Indels
                                                                                                                                                                   PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1662 GGGCCGGCGGGTGAGCGCGGGGATGCTCGGCGACGTGA 1699
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                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40.253
REFERENCE/DOCKET NUMBER: 29938-20002.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                        UPEALLY
SOFTWARE: PATCHILL
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,229
FILING DATE: 26-SEP-1996
FILING TATON: 424
                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 2713 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                               Y: USA
94304-1018
        Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
5244792-2
;Patent No. 5244792
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                                                   COUNTRY:
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DB 7; Length 3472;

Score 34; DB 7 Pred. No. 2.1;

Query Match 8.3%; Best Local Similarity 47.2%;

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1913 getgaccetgtggaccgaggcccgcaagctgaaccccaacgccatcgcctcggccaccgt 1972
                                                1793 caagaccacctccatcgagttcgcccggctgcagtttacgtacaaccacatacagcg 1852
                                                                                                                                                  1853 ccatgicaacgataigtigggccgcgtigccatcgcgiggigcgagctgcagaaccacga 1912
                                                                                                 134 tecegictacggeticcatgacecegegicetitgigaagiccatteagaagecaegggi 193
                                                                                                                                                                                                        194 ggtgatcatgctcgtcaaggccggcgccagttgaccagaccatcgcgacgctcgcagc 253
74 caacaggacaacctccaaggtggacgagaccgtgcagcgtgccaaggcagaaggaaacct 133
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46; Conservative 0; Mismatches 165; Indels
                                                                                                                                                                                                                                                                                                                                                               1973 gggccggcgggtgagcgcggatgctcggcgacgtga 2010
                                                                                                                                                                                                                                                                                                               254 tcacttggagcagggcgactgcatcatcgatgggggga 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lev, Sima
APPLICANT: Plowman, Gregory D.
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: RDGB PROTEINS AND RELATED
TITLE OF INVENTION: PRODUCTS AND METHODS
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/938,291A FILING DATE: September 26, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/027,337
FILING DATE: October 11, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-938-291A-3
; Sequence 3, Application US/08938291A
; Patent No. 6117673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,327 REFERENCE/DOCKET NUMBER: 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5020 base pairs
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CURRENT APPLICATION DATA:
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EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Lev, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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276 atcatcgatggggggaacgagtggt 300

216 ggcgcgccagttgaccagaccatcgcgacgctcgcagctcacttggagcagggcgactgc

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NAME/KEY: DNA sequence encoding
NAME/KEY: Streptomyces lividans Protease X
OTHER INFORMATION: bp 12 to 1910 comprises
OTHER INFORMATION: S. lividans DNA sequence, including Protease X.
OTHER INFORMATION: bp 1 to 11 represents cloning vector DNA sequence.
1168 accaagriggagcriccaargaccricarggacaagarcgagagcccagagccggaagacaca 1227
                                                                                                                                                                                                        1228 CAAGATGGTCTGTACCGCCAGGGTGCCCTTGAGGTGGGGTGGCCTCCAGTGTGGAGCAG 1287
                                                                                                                                                                                                                                                                                                                                                                                                1348 GIGCIGCIATIGGIGCIGCACGAGGCACCATCCIGACACAGGCGCGGGGGACCCCAGC 1407
                                                                                                                                                                                                                                                                                         72 tacaacagga---caacctccaaggtggacgagaccgtgcagcgtgccaaggcagaagga 128
                                                                                                                                                               129 aaccttcccgtctacggcttccatgaccccgcgtcctttgtgaagtccattcagaagcca 188
                                                                                                                                                                                                                                                         189 cgggtggtgatcatgctcgtcaaggccggcggccagttgaccagaccatcgcgacgctc 248
                                                                                                                                                                                                                                                                                                                                                         gcagctcacttggagcagggcgactgcatcatcgatggggggaacgagtggtacgagaac 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lichenstein, Henri
TITLE OF INVENTION: Isolation and
TITLE OF INVENTION: Characterization of a Novel Protease
TITLE OF INVENTION: from Streptomyces Lividans
NUMBER OF SQUENES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette, 3.5 inch, DS, 1.4 MB
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh OS 6.0.4
SOFTWARE: Microsoft Word Version 4.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT/US92/05532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application PC/TUS9205532 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Amgen Center
STREET: 1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: NUCLEIC ACID
STRANDEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 19920629
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1910 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: circular
MOLECULE TYPE: Genomic DNA
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FILING DATE: 19920629
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                                                                                                                                                                                                                                                                                                                                                                                                                                               309 acggagagagga 322
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Thousand Oaks
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 cccgcgtcctttgtgaagtccattcagaagccacgggtggtggtgatcatgctcgtcaaggcc 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    491 GTCGAGGGCTGTGCGCTGCACATCCCCGAGGACCTGCGGCTGCGGCGTCCTGGTCGAGCGC 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216 ggcgcccagttgaccagaccatcgcgacgctcgcagctcacttggagcagggcgactgc 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lichenstein, Henri
TITLE OF INVENTION: Isolation and Characterization of No. 5516685el
TITLE OF INVENTION: Protease from Streptomyces Lividans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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8.2%; Score 33.8; DB 1; Length 2261;
Best Local Similarity 47.8%; Pred. No. 2.1;
Matches 98; Conservative 0; Mismatches 107; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/272,882D
FILING DATE:
CLASSIFICATION: 435
371 CTCGCCGACCTCGCCGACGACCGGT 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
                                                                                                                                                                                                                                                STREET: 1840 Dehavilland Drive CITY: Thousand Oaks
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                                                                                                     Sequence 1, Application US/08272882D Patent No. 5516685 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Oleski, Nancy
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2261 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid_STRANDEDNESS: single
                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                          91320-1789
                                                                                    US-08-272-882D-1/c
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RESULT 15

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Gaps 0;

Length 1910;

Query Match 8.2%; Score 33.8; DB 6; Length 1 Best Local Similarity 47.8%; Pred. No. 2; Matches 98; Conservative 0; Mismatches 107; Indels

96 gacgagaccgigcagcgigccaaggcagaaggaaacciicccgictacggciiccaigac 155

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255 cacttggagcaggggggactgcatcatcgatggggggaacgagtggtacgagaacacggag 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 aacaggacaacctccaaggtggacgagaccgtgcagcgtgccaaggcagaaggaaacctt 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 eccgtctacggcttccatgaccccgcgtcctttgtgaagtccattcagaagccacgggtg 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.2%; Score 33.8; DB 1; Length 7218;
                                                                                                                                                 APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 3;
80; Mismatches 138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE.
COMPTEY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
AMDIUM TYPE: Floppy disk
TYPE: TBM PC compatible
TYPE: TBM PC compatible
TYPE: TPM PC COMPAGIBLE
TYPE: TPM PC COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                     Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 2.5%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 30.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFA: ('VC) TELEFA: ('VC) TELEFX: 899149
INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 7218 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , CLONE: pTZgpt-Fls
US-08-232-463-14
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IMMEDIATE SOURCE:
US-08-232-463-14/c
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Search completed: November 4, 2000, 13:33:31 Job time: 16647 sec

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November 4, 2000, 13:43:19; Search time 320.8 Seconds (without alignments) 268.163 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                          480022 segs, 187831343 residues
                                                                        OM nucleic - nucleic search, using sw model
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ARIES			:														
SUMMARIES		OI .	296449	X20248	251822	V74413	X61679	X61677	/ OTO X	A20249	T43709	T70838	0001130	OSCIOI	T72711	222143	
		DB	19	20	21	18	200	200	9 0	9 1	17	18	0	0	18	20	
		Match Length DB	1105	910715	1026	15249	4434	4485	716277	//7011	1435	2580	2500	000	3532	3532	
	Query	Match	14.7	14.1		13,3		13.0								12.9	
		Score	33.6	32.4	30.4	30.4	29.8	29.8	8 60		23.0	29.6	29.6		4.67	29.6	
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Claim 4; Page 291; 640pp; English,

Human HIAP-2 codin EST clone CZ326. Genomic sequence o Human colon cancer EST clone DA505.	Staphylococcus aur Arabidopsis leaf a AF1q cDNA involved	Methanococcus jann DNA encoding a hum R. sphaeroides gen	Human secreted pro H. pylori GHPO 167	BRCA2 cancer susce BRCA2 cancer susce BRCA2 cancer susce	Recombinant papill Human papillomavir	Streptococcus pneu Salmonella enteric Human cancer-relat Human secreted pro	Sequence encoding S. pneumoniae deri Streptococcus pneu Human cancer-relat	Human CtIP cDNA. Human gene signatu Rape abscission/de Soluble human inte Soluble interleuki
V55040 V90010 Z10752 A16054 V89678	V77318 V27310 T44594	721209 730326 746833	804	675 674	834 413	199 751 862 494 267	965 331 382 361	784 729 545 182
V55 V90 Z10 A16 V89		~ ~ ~	x60804 x14581	T/96/6 T/9675 T/9674	T05834 T13413	V52199 X06751 V08862 X20494 V27267	Q05965 Z96331 V37382 V08861	X78784 T22960 Q73729 Q36645 T16482
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3732 388 72604 618 625	360 1530 1579	750 750 759 759	1969	964 1041 1050	599	10/26 22080 416 612 695	1070 1705 1705 3246	3247 251 756 957 1008
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ALIGNMENTS

Treatment; prevention; disease; diagnosis; gene therapy; screening; bacterial; antimicrobial; antibiotic; pathogenesis; infection; ss. Hodgson JE, Knowles DJC, Lonetto MA, Nicholas RO; Streptococcus pneumoniae proteins and related DNA - useful for screening compounds for antibacterial activity S. pneumoniae derived DNA from ORF #277. (SMIK) SMITHKLINE BEECHAM CORP. Z96449 standard; DNA; 1105 BP. 96US-0024022. 97WO-US14436. 10-APR-2000 (first entry) Streptococcus pneumoniae. WPI; 1998-159452/14. P-PSDB; Y86134. WO9806734-A1. 15-AUG-1997; 16-AUG-1996; 19-FEB-1998. Black MT, F Stodola RK; 296449; Z96449/c RESULT

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This invention describes novel isolated Streptococcus pneumoniae polynucleotides (see 296173-296494) and their encoded proteins (see y85792-Y86182). The DNA, vectors and host cells described in the method of the invention are useful for the recombinant expression of the polypeptides. The polypeptides are useful for treatment or prevention of disease, or diagnosis of disease related to expression or activity of such a polypeptide. They can also be useful or screen for compounds which interact with and inhibit or activate such a polypeptide. The polypeptides (or DNA encoding them, via gene thorapy) are also useful for inducing an immunological response in a mammal. The antagonists are useful to inhibit such bacterial polypeptides. The polypeptides are particularly useful to identify antimicrobial compounds and antibiotics. They are also useful to determine their role in pathogenesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224 GTCAAAGATCGAATTTGCAGGCTGAAGTCGCAGCTGTTTCCAAGGATTTGGTATCCGA 165
                                                                                                                                                                                                                                                                                                                                                                                           65 acaagaataggccttgctggattggctgttaatgggcaaaatctggcactcaatattgct 124
                                                                                                                                                                                                                                                                                                                                                                                                                            284 ACTGGTCTGGGCTTGTTTTTGGGCGGATTTTTCCTGCTAAAACCAGCTCCACAAACACT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 tgaaaagggcttcccaattccggttaacaacggaaccatttccaaggttattgggccata 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease; epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis; infection; diagnosis; characterisation; detection; ds.
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Borrelia burgdorfer1 nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention
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0
                                                                                                                                                                                                                                                                                                                           Length 1105;
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                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                       Sequence 1105 BP; 303 A; 244 C; 193 G; 365 T; 0 other;
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                                                                                                                                                                                                                                                                                                                         Score 33.6; DB 19;
Pred. No. 0.17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Borrelia burgdorferi polynucleotide sequence #1.
                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                        infection, dysfunction and disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 agacgaagcaaaccaggaaggaaa 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X20248 standard; DNA; 910715 BP
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                                                                                                                                                                                                                                                                                                                            14.7%;
52.1%;
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                                                                                                                                                                                                                                                                                                                                             Local Similarity 52.1 nes 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MEDI-) MEDIMMUNE INC.
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Staphylococcus aureus glycoprotease; gcp; antibody; vaccine formulation; Helicobacter pylori infection; gastrointestinal carcinoma; gastric ulcer; gastriits; osteomyelitis; septic arthritis; septic thrombophlebitis; acute bacterial endocarditis; Staphylococcal food poisoning; scalded skin syndrome; toxic shock syndrome; antibacterial; cytostatic; antiulcer; antiarthritic; vulnerary; immunosuppressive; ss.
                                                                                                                                                                                                                                                                                                                                                                                                   Db 171315 ATATICITITATAGCATCTTTAAAGGTTGAAAATGAAGATAAACCTGTTCATTTTGATT 171256
                                                     X20248 to X20402 represent polynucleotide sequences isolated from Bornelia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes epidemic and endemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                                                                                                                                                                                                                                                                  57 aaccoacaacaagaataggccttgctggattggctgttaatgggcaaaatctggcactca 116
                                                                                                                                                                                                                                                                                                                                                                                                                                      117 atattgcttgaaaagggcttcccaattccggttaacaacggaaccatttccaaggttatt 176
                                                                                                                                                                                                                                         Sequence 910715 BP; 327171 A; 129646 C; 130753 G; 323091 T; 54 other;
                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                             Length 910715;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 gggccataagacgaagcaaaccaggaaggaaaccttcaatttatggggaa 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus glycoprotease (gcp) polynucleotide.
                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "Glycoprotease polypeptide"
and therapy of infections, particularly Lyme disease
                                                                                                                                                                                                                                                                                                 DB 20;
                                                                                                                                                                                                                                                                                                                                    86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Palmer LM, Kosmatka AL, Traini CM, Warren RL;
                                                                                                                                                                                                                                                                                                 Score 32.4; DE Pred. No. 4.4; 0; Mismatches
                                   Claim 1; Page 157-671; 1128pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
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                                                                                                                                                                                                                                                                                                 ch 14.1%;
1 Similarity 49.4%;
84; Conservative
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p-PSDB; Y70524.
                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                   Lyme disease
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Novel glycoprotease polypeptides and polynucleotides isolated from Staphylococcus aureus, used to screen for antibacterial compounds and
                                                                                           to diagnose diseases -
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Claim 2; Page 2-3; 59pp; English.

The present sequence encodes a novel Staphylococcus aureus glycoprotease
(gcp) polypeptide. This is isolated from a deposited strain
S. aureusWCUH29 containing the full length gcp gene. Gcp polynucleotides
and polypeptides are used as research reagents for the discovery of
treatments and diagnostics for diseases. The polynucleotides may be used
as a source of hybridisation probes, screening genetic mutations, and
as source of hybridisation probes, screening genetic mutations, and
are used to produce antibodies, in vaccine formulations, to identify
are used in the treatment of Helicobacter pylori infections, such as
gastrointestinal carcinoma, gastric ulcers, and gastritis. Other diseases
include osteomyelitis, septic arthritis, septic thrombophlebitis, acute
syndrome, and toxic shock syndrome. The polypeptides can also be used to
reat wounds and toxic shock syndrome. The polypeptides can also be used to treat wounds and body implants to prevent bacterial adhesion and

Sequence 1026 BP; 335 A; 161 C; 224 G; 306 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                         Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                 886 atcccaagtcctaaattatgcacagataatgctgcaatgataggcgttgccggccactat 945
                                                                                                 92 gttaatgggcaaaatctggcactcaatattgcttgaaaagggcttcccaattccggttaa 151
                                 Gaps
                                                32 atttcaggagattaattatgcgctcaacccacaacaagaataggcettgctggattggct 91
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ch 13.3%; Score 30.4; DB 21; Length 1026; 1 Similarity 52.3%; Pred. No. 1.8; 67; Conservative 0; Mismatches 61; Indels 0;
                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus contig SEQ ID #102.
                                                                                                                                                                                                                                        V74413 standard; DNA; 15249 BP.
                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                 toxic shock syndrome; ds.
                                                                                                                                                                           1006 gaagagta 1013
                                                                                                                                                 152 caacggaa 159
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Query Match
            Best Local
Matches 6
                                                                                                                                                                                                                                                                 V74413;
                                                                                                                                                                                                                RESULT
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/note these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence.
                                                                                         the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence.
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
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in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11581..11640
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                                                  THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE S
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Claim 1; Page 600-608; 3271pp; English.

the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"

2581..2640

misc_feature

/*tag= b

/note=

/note "these bases represent a line of missing text in

Location/Qualifiers

Key misc_feature

Staphylococcus aureus.

781..840 /*tag= a

"these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"

of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access the S.aureus DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or D-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The This sequence represents one of 5191 Staphylococcus aureus DNA sequences

8×333333333×8

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This sequence encodes a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members of the Borrelia genus, particularly for the use against Lyme disease in
                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, evelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 gitaaigggcaaaaiciggcacicaaiaitgciigaaaagggciicccaaiiccggiiaa 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          762 ATCCCAAGTCCTAAATTATGCACAGATAATGCTGCAATGATAGGCGTTGCCGGCCACTAT 703
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 atttcaggagattaattatgcgctcaacccacaacaagaataggccttgctggattggct 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antigenic protein; vaccine; Lyme disease; infection; detection; ss.
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                                                                                                                                                                                                                                                                                                                                                                             Length 15249;
                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                Sequence 15249 BP; 4890 A; 2563 C; 2669 G; 4584 T; 543 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B. burgdorferi antigenic protein coding sequence, t502.nt.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        61;
                                                                                                                                                                                                                                                                                                                                                                                      DB 18;
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                                                                                                                                                                                                                                                                                                                                                                                      Score 30.4; DE Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 148-149; 275pp; English.
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97US-0053344.
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1 Similarity 52.3%;
67; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrella genus. The products can also be used for detection of members of the Borrella genus.
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                                                                                                                                                                                                766 ATTITCCCTGTGAATTAATAAACTTAAAGGAGGATAATCATTATATAAACCAACATCAA 707
                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated Borrelia burgdorferi nucleic acids - used to develop products for the diagnosis, prevention and treatment of diseases caused by Borrelia, particularly Lyme disease
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                                                                                                         Length 4434;

 B. burgdorferi antigenic protein coding sequence, f502.nt.

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                                                          Sequence 4434 BP; 1616 A; 416 C; 740 G; 1662 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42;
                                                                                                                                        42;
                                                                                                            DB 20;
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                                                                                                                                                                                                                                                            706 CAAAACTTCCCTTAGCATTGCTATCTAAAAAAAAAA 670
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0; Mismatches
                                                                                                                          No. 4.6;
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                                                                                                          Score 29.8;
Pred. No. 4.6
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                                                                                                            13.0%;
56.7%;
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Best Local Similarity 56.7°
Matches 55; Conservative
                                                                                                                            Best Local Similarity 56.7
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MEDI-) MEDIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Borrelia burgdorferi.
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                                                                                                                Query Match
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X20248 to X20402 represent polynucleotide sequences isolated from Bornelia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of blosynthetic products, e.g. enzymes. Bornelia belongs to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Bornelia causes epidemic and endemic relapsing fever, and Lyme borneliosis, more commonly known as
9 attitticigicatitgcitcaaaiticaggagattaattaigggcicaacccacaacaa 68
                                                                                                                                                                                                                                                                                   Borrelia burgdorferi, spirochete; bacterium; pathogen; Lyme disease; epidemic relapsing fever; Lyme borreliosis; infection; diagnosis; characterisation; detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     products for the detection, diagnosis, characterisation, prevention and therapy of infections, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated Borrelia burgdorferi nucleic acids - used to develop
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith HO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dougherty BA, Fraser C, Lathigra R,
                                                                                                                                                                                                                                                         Borrelia burgdorferi polynucleotide sequence #2.
                                                       69 gaataggccttgctggattggctgttaatgggcaaaa 105
                                                                                    757 CAAAACTTCCCTTAGCATTGCTATCTAAAAAAGAAA 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 672-737; 1128pp; English,
                                                                                                                                                               X20249 standard; DNA; 116277 BP.
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97US-0050359.
97US-0053344.
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                                                                                                                                                                                                                                                                                                                                                 Borrelia burgdorferi.
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1238 tagtatgccaggaatgtgcccttctctaagaaaatgccctatttgcaggggtataatca 1297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotide encoding human inhibitor of apoptosis gene 1 - useful for treating degenerative diseases, as antiviral defence mechanism and preventing cell death during trauma and strokes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell death during stokes of trauma. The cDNA can be isolated from human Jurkat cell lines or human osteoclastoma stromal cell lines and incorporated into bacterial, mammalian or baculovirus expression vectors for use in prodn. of recombinant hIAP-1. It can also be utilised in the diagnosis or gene therapy of diseases related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A cDNA clone (T43709) codes for human inhibitor of apoptosis 1 (hIAP-1) (W04583), a protein useful for treating degenerative diseases, as an antiviral defence mechanism and for preventing cell death during stokes of trauma. The cDNA can be isolated from
                                                                                                                                                    Inhibitor of apoptosis 1; hIAP-1; degenerative disease; rheumatoid arthritis; septic shock; antiviral; trauma; stroke; cell death; oncogenesis; cancer; diagnosis; gene therapy; ss.
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12.9%; Score 29.6; DB 17; Length 1435;
Best Local Similarity 47.8%; Pred. No. 3.6;
Matches 86; Conservative 0; Mismatches 94; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1435 BP; 464 A; 232 C; 317 G; 422 T; 0 other;
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/note= "3' primer binding site"
                                                                                                                                                                                                                                                                                                                                     primer binding site"
                                                                                                                       Human inhibitor of apoptosis gene 1 cDNA.
                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                    complement (10..29)
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                             T43709 standard; cDNA; 1435 BP
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                                                                                         07-FEB-1997 (first entry)
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/note= "5'
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                                                                                                                                                                                                                     Homo sapiens.
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                                                           T43709;
RESULT
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Gaps

Indels

DB 20; Length 116277;

13.0%; Score 29.8; DB 20; 56.7%; Pred. No. 15; tive 0; Mismatches 42;

Best Local Similarity 56.79 Matches 55; Conservative

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Query Match

69 gaataggccttgctggattggctgttaatgggcaaaa 105

9 attitticigicattigeticaaatticaggagattaattaigegeteaaeeeaaaaa 68

Sat Nov

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68

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1358 aaaggtetttaaaatattgttgaacaettgaagecatetaaagtaaaagggaattatga 1417
         Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and hiap-2 genes (170836-41) respectively code for a new class of mammalian proteins (W19581-86) that are inhibitors of apoptosis (IAP). The hiap-1 and hiap-2 genes were cloned by screening a cregion. They were assigned to chromosome 11922-23 by FISH. IAP nucleic acids can be used to express IAP polypeptides in cells and animals to inhibit apoptosis, and as primers and probes to identify animals to inhibit apoptosis, as well as in methods for treating diseases and disorders involving apoptosis (anti-apoptotic gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of susceptibility to apoptotic disease
                                                                                    128 aaagggetteccaatteeggttaacaacggaaccattecaaggttattgggecataaga 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apoptosis inhibitor; HIAP-2; HIV; AIDS; neurodegeneration; myelodysplastic syndrome; ischaemia; myocardial infarction; stroke; reperfusion injury; toxin-induced liver disease; gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human apoptosis inhibitor hiap-2 cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
238..2094
/*tag= a
                                                                                                                                                                                                                                                                                                       T70838 standard; cDNA; 2580 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYOT-) UNIV OTTAWA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-154262/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis; ds
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1963 tagtatgccaggaatgtgccccttctctaagaaaatgccctatttgcaggggtataatca 2022
                                                                                                        2126 aaaggtetttaaaatattgttgaacaettgaagecatetaaagtaaaaagggaattatga 2185
                  2066 agggtactgttcgtacattctctcttaaagaaaaatagtctatattttaacctgcataa 2125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 tattittetgteatitgetteaaatiteaggagattaattatgegeteaacecacaca 67
agaataggccttgctggattggctgttaatgggcaaaatctggcactcaatattgcttga 127
                                                                      128 aaagggetteeceaatteeggttaacaaeggaaceattteeaaggttattgggeeataaga 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The human cellular inhibitor of apoptosis proteins (c-IMP1/2-re1590/T61591) comprise a series of defined structural domain repeats and/or a RING finger domain, in particular, at least two of a first domain repeat (W1354) or W13548), a second domain repeat (W13549 or W13550), and a third domain repeat (W13551 or W13551) and/or a RING finger domain (W13553 or W13554), or a consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequences derived from these human genes.

The nucleic acid is used for recombinant prodn. of human cellular inhibitor of apoptosis protein which modulates apoptosis regulation. The nucleic acids are useful in therapies where increased cell-specific apoptosis is desired, e.g. in restinosis, inflammatory disease states, myocardial infarction, glomerular nephritis, transplant rejection and infectious diseases, e.g. HIV. They can also be used in conditions requiring a reduction in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding cellular inhibitor of apoptosis proteins useful for apoptosis regulation in cells to reduce or increase apoptosis and for pharmacological screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 29.6; DB 18; Length 2589;
Pred. No. 4.5;
0; Mismatches 94; Indels 0;
                                                                                                                                                                                                                                                                                                                                             IAP; inhibitor; apoptosis; RING finger domain; restinosis; myocardial infarction; nephritis; HIV; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 16-18; 35pp; English.
                                                                                                                                                                                                      T61590 standard; cDNA; 2589 BP
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47.8%;
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95US-0512946.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TULA-) TULARIK INC
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                                                                                                                                                                                                                                                                                                                Human c-IAP1
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Gaps

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94; Indels

0; Mismatches

86; Conservative

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Query Match Best Local Similarity

12.9%; Score 29.6; DB 18; Length 2580; 47.8%; Pred. No. 4.5;

tattitititigiteattigetteaaattieaggagattaattatgegeteaaeeeaea 67

2988 agggtactgttcgtacatttctctcttaaagaaaaatagtctatattttaacctgcataa 3047

68 agaataggccttgctggattggctgttaatgggcaaaatctggcactcaatattgcttga 127

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2023 agggtactgttcgtacatttctctcttaaagaaaaatagtctatattttaacctgcataa 2082
                                                                                  68 agaataggccttgctggattggctgttaatgggcaaaatctggcactcaatattgcttga 127
                                                                                                                                                                                                                                                                                                             Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHB; degenerative disease; infectious disease; autoimmune disease; cancer; gene therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homologue B (MIHB) (W19746), a human homologue of baculovirus inhibitor of apoptosis protein (IAP). It was isolated from a human foctal liver CDNA library using primers based on human EST sequences that resemble the BIR domains of Orygia pseudotsuguta polyhedrosis virus IAP. Animal IAP homologue nucleic acids (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated protein homologues of viral inhibitors of apoptosis - used to modulate apoptosis for treatment of degenerative, infectious or autoimmune diseases and cancer
                                                              128 aaagggcttcccaattccggttaacaacggaaccatttccaaggttattgggccataaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              An isolated nucleic acid molecule (T72711) codes for mammalian IAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polyhedrosis virus IAP. Animal IAP homologue nucleic acids (sealso T72710 and T72712-17) can be used to produce polypeptides useful in methods for modulating apoptosis in animal cells, specifically for treatment, by inhibition, of degenerative and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infectious disease or, by promotion, of cancer and autoimmune disease, and can be used for gene therapy of these diseases.
                                                                                                                                                                                                                                                                             Human inhibitor of apoptosis protein homologue MIHB DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3532 BP; 1133 A; 560 C; 711 G; 1128 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 25; Page 50-54; 136pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1160..3016
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                                                                                                                                                                          T72711 standard; DNA; 3532 BP.
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                                                                                                                                                                                                               T72711;
                                                                                                                                                RESULT 11
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inhibit the expression of human Cellular Inhibitor of Apoptosis-1 (c-IAP-1). The antisense compounds may be used for diagnostics, therapeutics (for modulating the expression of c-IAP-1), prophylaxis (e.g. to prevent or delay infection, inflammation, or tumor formation), as research reagents (e.g. to distinguish between members of a biological pathway) and in kits. The present sequence represents the human cellular inhibitor of apoptosis-1 (GenBank accession number: U37547).
                    Cellular Inhibitor of Apoptosis-1; antisense; diagnostic; therapeutic; c-IAP-1; prophylaxis; infection; inflammation; tumor formation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense compounds complementary to Cellular Inhibitor of Apoptosis-1 useful for e.g. diagnostics, therapeutics, and as research reagents -
128 aaagggcttcccaattccggttaacaacggaaccatttccaaggttattgggccataaga 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2988 agggtactgttcgtacattctctttaaagaaaaatagtctatattttaacctgcataa 3047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2928 tagtatgccaggaatgtgcccttctctaagaaaatgccctatttgcaggggtataatca 2987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 agaataggccttgctggattggctgttaatgggcaaaatctggcactcaatattgcttga 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention provides antisense compounds of 8-30 nucleotides that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 tattttttctgtcatttgcttcaaatttcaggagattaattgtgcgctcaacccacaaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 20; Length 3532;
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Pred. No. 5;
0; Mismatches 94; Indels
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                                                                                                                                                                                                          Human cellular inhibitor of apoptosis-1 DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 13; Columns 41-46; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cowsert LM, Ackermann EJ;
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                               Z22143 standard; DNA; 3532 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0205204.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-561047/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-1999
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                                                                                                                                               Z22143;
                                                                               RESULT 12
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Gaps

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94; Indels

Score 29.6; DB 18; Length 3532; Pred. No. 5; 0; Mismatches 94; Indels 0;

ch 12.9%; l Similarity 47.8%; 86; Conservative (

Best Local Similarity

Matches

Query Match

8 tattititctgicatitgcitcaaatticaggagattaattatgcgcicaaccacaaca 67

3148 tagtatgccaggaatgtgcccttctctaagaaaatgccctatttgcaggggtataatca 3207

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This sequence encodes the human HIAP-2 protein, which is a inhibitor of apoptosis protein (IAP), and can be used in the method of the invention. The method is for enhancing apoptosis in cells from a mammal with proliferative disease by treatment with a compound that inhibits biological activity of an IAP or NAIP polypeptide. The inhibitory compounds are used to treat proliferative disease, specially cancers of ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney, liver nasopharnyx, thyroid,central nervous system, prostate, colon, rectum, cervix or endometrium, particularly to increase their sensitivity to chemotherapeutic agents. High levels of the IAP or NAIP proteins are detected in many cancers and are associated with poor prognosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             resistance to chemotherapeutic agents and mutations in p53 (it is suggested that wild-type p53 suppresses transcription of the IAP or NAIP genes). Transgenic animals are used for testing the effects of antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide; proliferative disease; IAP; therapy; cancer; human; HIAP-2 protein; ss.
                                           Inducing apoptosis in proliferative mammalian cells with inhibitor
of IAP or NAIP polypeptide – also methods for prognosis based on
presence of IAP and NAIP, specifically applied to cancers involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Korneluk R, Liston P, Mackenzie AE, Pratt C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3732 BP; 1173 A; 620 C; 760 G; 1179 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= HIAP-2
                                                                                                                                                                                                                                                 V55040 standard; cDNA; 3732 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human HIAP-2 coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; W69296.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baird S,
Tsang B;
                                                                                                                                                                                                                                                                                                                          V55040;
                                                                                                                                                                                      RESULT 13
                                                                                                                                                                                                                       V55040
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Human; secreted protein; expressed sequence tag; EST; haematopoiesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic; receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 gcaaaatctggcactcaatattgcttgaaaagggcttcccaattccggttaacaacggaa 159
                      68 agaataggeettgettggattggetgttaatgggeaaaatetggeacteaatattgettga 127
                                                                       128 aaagggetteecaatteeggttaacaaeggaaceattteeaaggttattgggeeataaga 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a human expressed sequence tag (EST) are polynucleotide, which is a secreted EST, and the encoded protein are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, activin/inhibin activity, chemotractic/chemokinetic activity, activin/inhibin activity, chemotractic/chemokinetic activity, anti-inflammatory activity, cathority activity, anti-inflammatory activity, activity, anti-inflammatory activity, activity, receptor/ilgand activity, anti-inflammatory activity, activity, repeatority suppressor activity, tumour invasion suppressor activity, tumour inhibition activity. The polynucleotide may also be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides encoding human secreted proteins – derived e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.8%; Score 29.4; DB 20; Length 388; 52.0%; Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Merberg D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 388 BP; 134 A; 106 C; 110 G; 38 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MCCOY JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 2.7;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lavallie ER,
Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 402; 618pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-US06955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0838821
                                                                                                                                                                                                        V90010 standard; cDNA; 388
                                                                                                                                                                                                                                                                            15-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GEMY ) GENETICS INST INC.
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Best Local Similarity 52.0'
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Jacobs K, Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-070077/06.
                                                                                                                                                                                                                                                                                                                                                                                                        qene therapy; ss.
                                                                                                                                                                                                                                                                                                                EST clone CZ326.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-0CT-1998.
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                                                                                                                                                                                                                                          V90010;
                                                                                                                                                                      RESULT 14
                                                                                                                                                                                       V90010
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Query Match 12.9%; Score 29.6; DB 19; Length 3732; Best Local Similarity 47.8%; Pred. No. 5.1; Matches 86; Conservative 0; Mismatches 94; Indels 0;

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The present sequence represents HKNG1 (Hong Kong new gene 1). HKNG1
is a gene associated with bipolar affective disorder (BAD). HKCNI
CO polynuclectides are useful to identify compounds modulating HKNG1 gene
expression or HKNG1 polypeptide expression/activity. Compounds inhibiting
co renhancing HKNG1 gene expression or activity; in individuals can then
co pecually neuropsychiatric disorders e.g. BAD, schizophrenia, or
KKNG1-mediated myopia disorders, such as early-onset autosomal
co ferborially neuropsychiatric disorders can be used in gene therapy
techniques to treat such disorders. They are also useful in diagnosis
co identify individuals having, or at risk of developing, HKNG1-mediated
co disorders due to mutations in the HKNG1 gene. Such mutations especially
result in the production of a protein with a different sequence to
the human full-length HKNG1 polypeptide or splice variant sequences,
co the human full-length HKNG1 polypeptide or splice variant sequences,
co resquences from different species) and to produce transgenic
co requences from different species) and to produce transgenic
cor animals.
HKNG1; Hong Kong new gene 1; bipolar affective disorder; BAD; neuropsychiatric disorder; early-onset autosomal dominant myopia; schizophrenia; splice variant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New HKNG1 polynucleotides useful in diagnosis and treatment of neuropsychiatric disorders, e.g. bipolar affective disorders and
                                                                                                                                                                                                                                                               Genomic sequence of the human HKNG1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Fig 3A-R; 205pp; English.
                                                                                                                                                  210752/c
ID 210752 standard; DNA; 72604 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PHARM INC. (REGC ) UNIV CALIFORNIA.
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                                                                                                                                                                                                                                    (first entry)
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                                                            220 tggggaa 226
                                                                                         153 aggagaa 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       schizophrenia
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                                                                                                                                                                                                     210752;
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Sequence 72604 BP; 20579 A; 15146 C; 14859 G; 21900 T; 120 other;

12.7%; Score 29; DB 20; Length 72604;

Query Match

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                                                                     0; Gaps
                                              32 atttcaggagattaattatgcgctcaacccacaacaagaataggccttgctggattggct 91
                     30; Indels
61.0%; Pred. No. 22; tive 0; Mismatches
                                                                                                                                                                                                                   Search completed: November 4, 2000, 13:44:57 Job time: 16424 sec
                                                                                                                                                 62896 CTTCACTGTCTCAATCT 62880
                                                                                                                92 gttaatgggcaaaatct 108
                Conservative
Best Local Similarity
Matches 47; Conserv
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(without alignments)
182.912 Million cell updates/sec
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/cgn2_6/ptodata/2/ina/5B_COMB.seg:*
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/cgn2_6/ptodata/2/ina/5C_COMB.seg:*
/cgn2_6/ptodata/2/ina/B_COMB.seg:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seg:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seg:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                          262060 segs, 75620727 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                             OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	;	-ì c	:	H	'n	Sequence 7, Appli	'n	,		, ,		, ,	<u>,</u> c	, ,	, ,	Sequence 1, Appli	'n	1,	ì ,-	,	Sequence 1. Appli		* ~	,	0	ce 4	. 518	Patent No. 5183745	
SUMMARIES	. dı	PCT-IIS95-059222-1	US-08-511-485.7	DOMESTIC CONTRACTOR	FC1 -0390*12860*1	US-US-ZUS-ZU4-I	/-T/6-7T7-60-S0	US-08-589-080-3	US-08-589-080-2	US-08-755-587-23	US-08-755-587-22	US-08-755-587-21	US-08-737-336-5	PCT-US95-11859-2	US-08-530-165-1	115-07-004-073-1	T-5/0-#06 /0 50	US-U/-904-U/I-I	US-08-381-603-1	PCT-US94-02414-1	PCT-US96-08899-1	US-07-821-716-1	US-08-643-704A-44	US-08-643-704A-47	US-08-643-7042-46	TIC-08-643-7048-40	_	T-07/50TC	5183/45-5	US-08-277-231A-1
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Sequence 4, Appli Sequence 1, Appli Sequence 3, Appli Sequence 8, Appli Sequence 8, Appli Sequence 19, Appli Sequence 19, Appli Sequence 5, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli	Gene 1	
26.6 11.6 9432 3 US-08-473-750-4 26.6 11.6 9432 4 US-08-477-326-4 26.5 11.4 17041 1 US-08-929-329-3 26 11.4 2095 2 US-08-910-990-8 26 11.4 2095 3 US-08-910-990-8 27 11.4 2095 3 US-08-276-8 28 11.3 6973 2 US-08-76-910-990-8 29.4 11.1 722 3 US-08-649-341A-5 29.4 11.1 722 3 US-08-649-341A-5 29.4 11.1 722 3 US-08-839-032A-5 29.4 11.1 722 4 US-08-839-032A-5 29.4 11.1 722 4 US-08-839-032A-5 29.4 11.1 722 5 US-08-839-032A-5 29.4 11.1 722 6 US-08-839-032A-5 29.4 11.1 722 6 US-08-839-032A-5 29.4 11.1 1018 1 US-08-181-271A-30	ALIGNMENTS 1. Lication PC/TUS950592A HE, ET AL. ENTION: Human Inhibitor of Apoptosis GUEADDRES: GCALLA BYRNE, BAIN, GILFILLAN, CECCHI, STEWART & OLSTEIN BECKER FARM ROAD BECKER FARM ROAD BECKER FARM ROAD BECKER FARM ROAD BECKER FARM ROAD BECKER FARM ROAD BECKER FARM ROAD BECKER FARM ROAD BEREET S. INCH DISKETTE IBM PS/2 SYSTEM: MS-DOS WORD PERFECT 5.1 ICATION DATA: N NUMBER: PCT/US95/05922A E: 11 MAY 1995 E: 11 MAY 1995 E: 11 MAY 1995 E: 11 MAY 1995 FION: NUMBER: 35.34 NON NUMBER: 35.34 NON NUMBER: 35.34 NON NUMBER: 35.34 NON NUMBER: 35.34 NON NUMBER: 35.34 NON NUMBER: 35.34 NON NUMBER: 35.34 NON NUMBER: 35.34 NON NUMBER: 35.34	*EDECOMMUNICATION INFORMATION: TELEFONE: 201-994-1700 TELEFAX: 201-994-1744 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LEWITH: 1435 RASE DATES
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 PCT-US95-05922A-1 Sequence 1, App GENERAL INFORM APPLICANT: TILLE OF INV NUMBER OF SE CORRESPONDEN ADDRESSEE: STREET: 6 CITY: ROS STATE: NE COUNTRY: 1 ZIP: 0706 COMPUTER REAM MEDIUM TYPI COMPUTER: 0 PREATING SOFTWARE: CURRENT APPL: CLASSIFICATION FILING DATIC FILING	TELEPHONE: TELEFAX: TELEFAX: TELEFAX: SEQUENCE CHA: TENGTH: 1.

Query Match
12.9%; Score 29.6; DB 6; Length 1435;
Best Local Similarity 47.8%; Pred. No. 0.64;
Matches 86; Conservative 0; Mismatches 94; Indels 0; Gaps

LENGTH: 1435 BASE PAIRS TYPE: NUCLEIC ACID STRANDEDNESS: SINGLE

TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
PCT-US95-05922A-1

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                                                                                                                                                                                            1358 AAAGGTCTTTAAAATATTGTTGAACACTTGAAGCCATCTAAAGTAAAAGGGAATTATGA 1417
1238 TAGTATGCCAGGAATGTGCCCTTCTCTAAGAAAATGCCCTATTTGCAGGGGTATAATCA 1297
                                                                                                                      1298 AGGGTACTGTTCGTACATTTCTCTTTAAAGAAAAATAGTCTATATTTTAACCTGCATAA 1357
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                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONTEST ADDRESS:
ADDRESSE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/08511485
Patent No. 5919912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFRAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic) US-08-511-485-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2580 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 02110-2804
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STREET: ...
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TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-1 EXPR
FILE REFERENCE: RIS-0020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1963 TAGTATGCCAGGAATGTGCCCCTTCTCTAAGAAAATGCCCTATTTGCAGGGGTATAATCA 2022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2023 AGGCTACTCTCCTCTCTCTTAAAGAAAAATAGTCTATATTTTAACCTGCATAA 2082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2083 AAAGGTCTTTAAAATATTGTTGAACACTTGAAGCCATCTAAAGTAAAAAGGGAATTATGA 2142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 agaataggccttgctggattggctgttaatgggcaaaatctggcactcaatattgcttga 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 06 AUG 1996
CIASSPETCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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                                                                                                                                                                             ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12860
                                                                                                           INHIBITORS OF APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/205,204 CURRENT FILING DATE: 1998-12-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER: PCT/US96/12860
06 AUG 1996
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                       Sequence 1, Application PC/TUS9612860 GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REPRENCE/DOCKET NUMBER: A-624
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09205204 Patent No. 5958772
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APPLICANT: Elizabeth J. Ackermann
APPLICANT: Lex M. Cowsert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 12.9%;
Best Local Similarity 47.8%;
                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2589 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                           TITLE OF INVENTION: INF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                          CITY: San Francisco
STATE: Californi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US96-12860-1
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US-09-205-204-1
RESULT 3
PCT-US96-12860-1
                                                                                                                                                                                                                                                                               COUNTRY:
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146 ggttaacaacggaaccatttccaaggttattgggccataagacgaagcaaaccaggaagg 205
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12.4%; Score 28.4; DB 2; Length 270;
Best Local Similarity 62.9%; Pred. No. 0.76;
Matches 44; Conservative 0; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/589,080
FILING DATE: U3-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9501386.8
FILING DATE: 23-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         E: BURNS, DOANE, SWECKER & MATHIS P.O. Box 1404
                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: COHEN, AMOS
APPLICANT: TSE, William
APPLICANT: ZHU, Weimin
APPLICANT: ZHU, Weimin
TITLE OF INVENTION: SEQUENCE OF AFIG CDNA
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: COHEN, Amos
APPLICANT: TSE, William
APPLICANT: ZHU, Weimin
TITLE OF INVENTION: SEQUENCE OF AF1q CDNA
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  024916-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PC-DOS/MS-DOS
                                                                                                                                                     ; Sequence 3, Application US/08589080; Patent No. 5808026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 2, Application US/08589080
; Patent No. 5808026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Rea, Teresa Stanek
REGISTRATION NUMBER: 30,427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 02.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 270 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDNA
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                                                                                                             RESULT 6
US-08-589-080-3
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APPLICANT: Liston, Peter
APPLICANT: Liston, Peter
APPLICANT: Liston, Peter
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: DETECTION WIDER: US/09/212,971B
TITLE OF INVENTION: DISEASE
FILE REPERBENCE: 07891/009002
CURRENT APPLICATION NUMBER: US/09/212,971B
CURRENT FILING DATE: 1996-12-16
EARLIER APPLICATION NUMBER: 60/017,354
EARLIER FILING DATE: 1996-11-14
EARLIER FILING DATE: 1996-11-14
EARLIER FILING DATE: 1996-11-14
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3208 agggtactgttcgtacatttctctcttaaagaaaaatagtctatattttaacctgcataa 3267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 3532;
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                                                                                                                                                                                                                                             Query Match 12.9%; Score 29.6; DB 4; Length 3 Best Local Similarity 47.8%; Pred. No. 0.97; Matches .86; Conservative 0; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09212971B Patent No. 6107041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86; Conservative
                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: (1160)..(3016)
US-09-205-204-1
NUMBER OF SEQ ID NOS: 47
                                                                   TYPE: DNA
ORGANISM: HOMO sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-09-212-971-7
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Best Local Similarity
                                              LENGTH: 3532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3732
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                         SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                               FEATURE
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us-09-300-482-27.rni

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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Materials and methods relating to the TITLE OF INVENTION: identification and sequencing of the BRCA2 cancer TITLE OF INVENTION: susceptibility gene and uses thereof. NUMBER OF SEQUENCES: 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 ggttaacaacggaaccatttccaaggttattgggccataagacgaagcaaaccaggaagg 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Bell Seltzer Park & Gibson
310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 12.4%; Score 28.4; DB 2; Length 1629; Best Local Similarity 62.9%; Pred. No. 1.7; Matches 44; Conservative 0; Mismatches 26; Indels 0
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                                                                                                                                                           CEPTE 12213-1404

COMPUTER ENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: TEMP PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/589,080
FILING DATE: 23-JAN-1996
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9501386.8
FILING DATE: 23-JAN-1995
ATTORNEY/AGNET INFORMATION:
NAME: REA: TERES Stanck
REGISTRATION NUMBER: 30,427
REFERENCE/POCKET UNMBER: 30,427
REFERENCE/POCKET UNMBER: 30,427
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEO ID NO: 2:
SEQUENCE CHRARACTERISTICS:
INFORMATION FOR SEO ID NO: 2:
LEMTH: 1629 base pairs
                    ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: P.O. Box 1404 CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23, Application US/08755587 Patent No. 6045997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Futreal, Phillip A
APPLICANT: Wooster, Richard F
ASPLICANT: Ashworth, Alan
APPLICANT: Stratton, Michael R
                                                                                              STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Selt:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
US-08-589-080-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 310
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APPLICANT: Ashworth, Alan
APPLICANT: Stratton, Michael R
TITLE OF INVENTION: Materials and methods relating to the
TITLE OF INVENTION: identification and sequencing of the BRCA2 cancer
TITLE OF INVENTION: susceptibility gene and uses thereof.
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Bell Seltzer Park & Gibson
STREET: 310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
CITY: Raleigh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
12.0%; Score 27.4; DB 5; Length 964;
Best Local Similarity 53.2%; Pred. No. 3;
Matches 58; Conservative 0; Mismatches 51; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DAFA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/755,587
FILING DATE: 25-NOV-1996
PRIOR APPLICATION NUMBER: GB 9523959.6
APPLICATION NUMBER: GB 952555.0
FILING DATE: 23-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9617961.9
FILING DATE: 14-DEC-1995
PRIOR APPLICATION NUMBER: GB 9617961.9
FILING DATE: 28-NUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kenneth D 51bley
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 3405-135
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 964 base pairs
TYPE: nucleic acid
STRATIONDENES: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/755,587 FILING DATE: 25-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22, Application US/08755587; Patent No. 6045997
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Futreal, Phillip A APPLICANT: Wooster, Richard F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ), NAME/KEY: exon
; LOCATION: 501..615
US-08-755-587-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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LOCATION: 501.
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NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Seltzer Park & Gibson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Bell Seltzer Park & Gibson
310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
12.0%; Score 27.4; DB 5; Length 1041;
Best Local Similarity 53.2%; Pred. No. 3.1;
Matches 58; Conservative 0; Mismatches 51; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/755,587
FILING DATE: 25-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9523959.6
FILING DATE: 23-NOV-1995
PRIOR APPLICATION DATA:
                                       PRIOR APPLICATION DATA:
APPLICATION UNDRER:
GP 52555.0
FILING DATE: 14-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9617961.9
FILING DATE: 28-dG-1996
ATTORNEY AGENT INFORMATION:
NAME: Kenneth D 51bley
REGISTRATION NUMBER: 31.665
REFERENCE/DOCKET NUMBER: 5405-135
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1041 base pairs
  GB 9523959.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21, Application US/08755587
Sequence 10, Application US/08755587
GENERAL INFORMATION:
APPLICANT: Putreal, Phillip A
APPLICANT: Ashworth, Alan
APPLICANT: Ashworth, Alan
Stratton, Michael R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: GB 9525555.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                   FILING DATE: 23-NOV-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                    LENGTH: 1041 base pair
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
COMPUTER READABLE FORM:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon
501..541
                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 503..541
FEATURE:
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US-08-755-587-21/c
                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
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US-08-755-587-22
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12.0%; Score 27.4; DB 5; Length 1050;
53.2%; Pred. No. 3.1;
tive 0; Mismatches 51; Indels 0; Gaps
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ZIP: 2007-5109

COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,336
FILING DATE: 16-740-1997
CLASSIFICATION NUMBER: WO PCT/AU95/00292
FILING APPLICATION DATA:
APPLICATION NUMBER: MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PM 5667
FITTENC APPLICATION DATA:
APPLICATION NUMBER: AU PM 5667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: FRAZER, Ian
APPLICANT: ZHOU, Jian
TITLE OF INVENTION: RECOMBINANT PAPILLOMA VIRUS L1
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                             5405-135
             PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9617961.9
FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: AU PM 5667
FILING DATE: 17-MAY-1994
ATTORNEY AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 65064/1:
TELECOMMUNICATION INFORMATION:
                                                                                           NAME: Kenneth D Sibley
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405-
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1050 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08737336
Patent No. 6013262
                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
14-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           exon
501..550
                                                                                                                                                                                                                                                                                                                            CDS
502..550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 3000 K Št
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                linear
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; LOCATION:
US-08-755-587-21
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                                                                                                                                                                                                                                                                                                                            NAME/KEY:
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                          68 agaataggccttgctggattggctgttaatgggcaaaatctggcactcaatattgcttga 127
                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application PC/TUS9511859
GENERAL INFORMATION:
APPLICANT: JANSEN, KATHRIN U.
APPLICANT: HOFMANN, KATHRIN U.
TITLE OF INVENTION: DNA ENCODING HUMAN PAPILLOMA VIRUS TYPE
TITLE OF INVENTION: 6A
UNGBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                Query Match 12.0%; Score 27.4; DB 5; Length 1599; Best Local Similarity 53.2%; Pred. No. 3.8; Matches 58; Conservative 0; Mismatches 51; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 E. LINCOLN AVENUE - P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19307 PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHRISTINE E. CARTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (908) 594-6734
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                TELEX: 904136
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1599 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 8010 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
(202)672-5300
                  (202)672-5399
                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: CDNA
PCT-US95-11859-2
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  TELEPHONE:
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LOCATION:

US-08-737-336-5
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                    TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
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                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Isaac, Peter G.
APPLICANT: Roberts, Jeremy A.
APPLICANT: COUPE, Simon A.
TITLE OF INVENTION: Control of Plant Abscission and Pod Dehiscence
Score 27.4; DB 6; Length 8010;
Pred. No. 8;
0; Mismatches 51; Indels 0;
                                                                                                                                                                                          7076 AAAGGAAAAGCCATATAAGAACCTTAGTTTTGGGAGGTTAAT 7124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.8%; Score 27; DB 3; Length 756; 62.7%; Pred. No. 3.7;
                                                                                                                                                                    128 aaagggcttcccaattccggttaacaacggaaccatttccaaggttatt 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/00689
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATE: GB9306726.2
FILING DATE: 31-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/530,165
FILING DATE: 29-SEP-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                  US-08-530-165-1/c
; Sequence 1, Application US/08530165
; Patent No. 5907081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 31-MAR-1993
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
        12.0%;
53.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 756 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 11.85
Best Local Similarity 62.75
Matches 42; Conservative
        Query Match
Best Local Similarity 53.28
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20002
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; LOCATION: 15..
US-08-530-165-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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181 cataagacgaa 191

Db Qy

226 CAACACAAAGAGAAACTTTGGTTTGTTCCTGCTAAGGTGGAGGATTCAGGACATTACTAT 285

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APPLICANT: Dower, Steven K.
APPLICANT: March, Carl J.
APPLICANT: March, Carl J.
APPLICANT: Sims, John
APPLICANT: Urdal, David L.
TITLE OF INVENTION: Method of Using Soluble Human
TITLE OF INVENTION: Interleukin-1 Receptors to Suppress Inflammation
                                                                                                                                                                                                                                                                                                                                                                                       COMPOUTER READABLE FORM:

COMPOUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CSOFTWARE: PatentIn Release #1.0, Version #1.25
CNORENT APPLICATION NATA:
APPLICATION NUMBER: US/07/904,073
FILING DATE: 19920617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 455488
FILING DATE: 21-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 258756
FILING DATE: 13-CCT-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160550
FILING DATE: 25-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 125627
FILING DATE: 25-NOV-1987
ATTORNEY/AGENT INFORMATION:
NAME: WIGHT, CLISTOPHER: 2002-A
TELEPHONE: (206) 587-0430
TELEPHONE: (206) 587-0606
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                             ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                    Sequence 1, Application US/07904073
Patent No. 5488032
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1008 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
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ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: HULL-1R
                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                 STREET: 51 Univers
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: CDS
; LOCATION: 1..1008
US-07-904-073-1
                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
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JS-07-904-073-1
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GENERAL INFORMATION:
APPLICANT: Dower, Steven K.
APPLICANT: March, Carl J.
APPLICANT: Sins, John
APPLICANT: Sins, John
APPLICANT: Sins, John
APPLICANT: Urdal, David L.
TITLE OF INVENTION: Method of Using Soluble Human
TITLE OF INVENTION: Interleukin-1 Receptors to Suppress Immune Responses
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/07/904,071
FILING DATE: 19920617
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION 1914
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 455488
FILING DATE: 21-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 258756
PRIOR APPLICATION DATA:
APPLICATION DATE: US 160550
FILING DATE: 25-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 12567
FILING DATE: 25-NOV-1987
PRIOR APPLICATION NUMBER: US 1257
FILING DATE: 25-NOV-1987
APPLICATION NUMBER: US 12567
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SR: 2002-B
                                                                                                                                                                                                                                                                                                                                                                       E: Immunex Corporation
51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Wight, Christopher L.
REGIETRATION NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2002.
TELECOMMUNICATION INFORMATION:
TELEPAN: (206) 587-0430
TELEPAN: (206) 587-0606
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                Sequence 1, Application US/07904071 Patent No. 5492888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: CDNA to MRNA HYPOTHETICAL: NO
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                       ADDALL STREET: 51 C. CITY: Seattle
346 AATGAGCCTAA 356
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CLONE: HUIL-IR
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ORIGINAL SOURCE:
ORGANISM: HOMC
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                                                                       RESULT 15
US-07-904-071-1
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61 cacaacaagaataggccttgctggattggctgttaatgggcaaaatctggcactcaatat 120

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11.8%; Score 27; DB 1; Length 1008; 50.4%; Pred. No. 4.2; tive 0; Mismatches 65; Indels

Best_Local Similarity 50.43 Matches 66; Conservative

Query Match

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; LOCATION: 1..1008
US-07-904-071-1
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ó 0; Gaps Query Match
11.8%; Score 27; DB 1; Length 1008;
Best Local Similarity 50.4%; Pred. No. 4.2;
Matches 66; Conservative 0; Mismatches 65; Indels

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181 cataagacgaa 191 || || || || 346 AATGAGCCTAA 356

Search completed: November 4, 2000, 13:33:34 Job time: 16650 sec

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November 4, 2000, 11:52:05; Search time 4352.3 Seconds (without alignments) 325.314 Million cell updates/sec
                                                                           ___cagaccttattttttttgtc......ttcaatttatggggaacaa 229
                                                                                                                            14379728
 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                           7189864 seqs, 3091403243 residues
                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                        OM nucleic - nucleic search, using sw model
                                                                                         IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                               US-09-300-482-27
229
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Maximum DB seq length: 200000000
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em_esthum1:*
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Perfect score:
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em_gss6:* em_gss7:* em_gss8:*

em_gss4:*
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gb_gss6:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	22117 sm67f12	0.1152N[L 1016	95821 NF099E09	20243 sm42d	09 EST31803	58071 MtBA22A0	32847 MtBC10C1	57204 MtBA12HU	45 MTBAUZBI	05/43 MTBAUZBU	SECTA NEOUSFUE	200	10923 AV41037	97 EST3060	58600 MTBA25E0	5038 coau0002	BE204727 EST39740	50814 EST4017	50460 sl50f03	590 737 Lambda	6953 AV52695	52543 AV55254	SUUDS AVSSUUUS	05063 MLL358	11175 FCT34527	54720 ML1006	43110 EST39595	50451 EST31549	03238 WHE04	E406322 WHEU413_	28880 MTD011.H	//090 DGI_4_BI	358 LG1_222_	86839 LGI_222_	6879 LG1_222_	9/862 WHEU95/_	725 DG1_9_A1	303048 LG1_243_	TOU //C	EDITOR WIEDGOS	E493944 WREIZ39	E43/080 WHEO33/-
Ð	BE02	AW/19/8	AV40668 AW69582	BE02024	AW58640	AL36807	AL38284	AL36720	AL36574	AL36574	AW68861	AV41020	AV4 LUYD	AV425/8	AT.36860	AT055038	BE20472	BE4508	AW76046	T04690	AV52695	AV55254	AV55000	AW25506	AV54003	AW25472	BE34	3 AW56045	5 BE40323	5 BE40632	5 BE42888	3 AW67709	1 AW28685	1 AW28683	1 AW28687	5 BE49786	5 BE36302	3 AW56364	5 BE36307	18/1038	5 BE49594	DE49/88
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ALIGNMENTS

/lab.host="Wholubur of the property of the protector paluescript II XR; Site_1: EcoRI; Site_2: XhOI; The mRNA was isolated from roots of Glycine max 'Supernod' plants generously donated by Dr. Gary Stacey. The seedlings were innoculated with Bradyrhizobium paponicus, strain USDAIIO priot to harvest. Stratagene's cDNA synthesis Kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dcrp, hence the ligated cDNA was hemimerthylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V=A,C, or G) was added to the 3' end of the primer (GAGAGAGAGAGAGAGAGAGAGACACTGCTCGGG(T)8V) to anchor the primer at the 5' end of the poly(A) tract. After second strand synthesis, the cDNA ends were filled in with close for DNA polymersase, lighted to EcoRI adapters and subsequently phosphorylated. The XhOI site within the first-strand synthesis primer was then restricted by digestion with XhOI; all XhOI sites in the cDNA constructs were size-fractionated with a 500bp cutoff, using dibcoRL Life Technologies' cDNA size Fractionation column. The column eluent was then ligated into stratagene's pBluescript II XR Predigested vector (PBLuescript II SK(+) that has been digested with EcoRI And phosporylated by Stratagene's Both the and XhoI, and phosporylated by Strategene). Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=25). This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell." A. Bolla, B., Marra, M., Hillier, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, P., Waterston, R. and Wilson, R. Eukaryota, Viridiplantae; Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine. Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3322 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@enomesystems.com or
info@enomesystems.com web site: www.genomesystems.com
High quality sequence stop: 398.
Location/Qualifiers NE ID: BE022117 561 bp mRNA EST (06-JUN-2000 sm67f12.yl Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE Gm-c1028-9000 5' similar to TR:022111 022111 6-PHOSPHOGLUCONATE Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1810 Fax: 314 286 1810 /db_xref="taxon:3847" /clone="GENOME SYSTEMS CLONE ID: Gm-c1028-9000" /clone_lib="Gm-c1028" /tissue_type="roots of 'Supernod' plants"
/lab_host="DH108" Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project 158 t /organism="Glycine max" DEHYDROGENASE ;, mRNA sequence. 130 g BE022117.1 GI:8284549 115 c Unpublished (1999) Glycine max 158 a soybean. source BASE COUNT ORIGIN SOURCE ORGANISM DEFINITION ACCESSION VERSION REFERENCE AUTHORS FEATURES KEYWORDS TITLE COMMENT

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Lotus japonicus.
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Lotus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="5 and 7 week-old plants"
/note="Organ: Nodule; Vector: pSPORT1; Site_1: Sall;
Site_2: Not1; The library was prepared using mRNA
extracted from nodules of 5 and 7 week-old Lotus plants.
Nodules were induced by, and contained Mesorhizoblum
strain R7A."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 532)
Colebatch, G., Freund, S., Trevaskis, B and Udvardi, M.
Lotus japonicus root nodule ESTs: tools for functional genomics
Unpublished (2000)
Contact: Udvardi MK
                                                                                                                              121 tgcttgaaaagggcttcccaattccggttaacaacggaaccatttccaaggttattgggc 180
                                                                                                                                                                                                         2; Gaps
                                                                       1 cagaccttatttttttttgttcatttgcttcaaatttcaggagattaattgcgctcaacc 60
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                 60.9%; Score 139.4; DB 32; Length 561; 81.2%; Pred. No. 7.6e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

49.5%; Score 113.4; DB 24; Length 532;
Best Local Similarity 74.2%; Pred. No. 8.5e-25;
Matches 170; Conservative 0; Mismatches 56; Indels 3;
                                                                                                                                                                                                                                                 181 cataagacgaagcaaaccaggaaggaaaccttcaatttatggggaacaa 229
                                                                                                                                                                                                                                                                    41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Max Planck Institute of Molecular Plant Physiology
Am Muehlenberg 1, 14476 Golm, Germany
Fax: 49 331 567 8250
Email: udvardi@mpimp-golm.mpg.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 others
                                               0; Mismatches
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/cultivar="Gifu (B-129)"
/db_xref="taxon:34305"
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Location/Qualifiers
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Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
Magnoliophyta, eudicotyledons, core eudicots, Rosídae, eurosids I,
Fabales, Fabaceae, Papilionoideae, Lotus.
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: yanakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:34305"
/db_xref="taxon:34305"
/clone="MWL008a02_r"
/clone="lb="Lotus" japonicus young plants (two-week old)"
/dev_zetage="yung plants (two-week old)"
/note="Vector: pBluescriptII SK; Site_1: EcoRI; Site_2:
XhoI; isolate=Miyakojima MG-20"
a 87 c 102 g 114 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 430).
Asamizur, E., Makanura, Y., Sato, S. and Tabata, S.
Generation of 7137 non-redundant expressed sequence tags from a legume, Lotus japonicus
63 c--aacaagaataggccttgctggattggctgttaatgggcaaaaatctggcactcaatat 120
                         121 tgcttgaaaagggcttcccaattccggttaacaacggaaccatttccaaggttattgggc 180
                                                                                                              64 aacaagaataggccttgctggattggctgttaatgggcaaaatctggcactcaatattgc 123
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                                                                                                                                                                     48.2%; Score 110.4; DB 18; Length 73.9%; Pred. No. 6.8e-24; tive 0; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 aagacgaagcaaaccaggaaggaaaccttcaatttatggggaacaa 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Res. 7 (2), 127-130 (2000) 20277479
                                                                                                                                                                                                                                                                                                                                    mRNA
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Matches 167; Conservative
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3

AW695821

RESULT

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76.8%;
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    Glycine max
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                                                                                                                                              Medicago truncatula belantae; Embryophyta; Tracheophyta; Spermatophyta; Bukaryota; Viridiantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Pabaceae; Papilionoideae; Medicago.

I (basea: 1 to 653)

He, X.—Z., Shadle, G., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and Dixon
                                                                                                                                                                                                                                                                                                       Expressed Sequence Tags from the Samuel Roberts Noble Foundation
NF099E09ST1F1070 Developing stem Medicago truncatula cDNA clone NF099E09ST 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 gggcttcccaattccggttaacaacggaaccatttccaaggttattgggccataagacga 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 AGGATTCCCAATTTCTGTTTATAACAGAACAACATCAAAGGTTGACGAAACTGTGGAACG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 24; Length 653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7302 Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 108.6; DB 2,
Pred. No. 2.7e-23;
0; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Medicago truncatula"
/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Developing stem"
/tissue_type="stem"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: radixon@noble.org
Insert Length: 653 Std Error: 0.00
Plate: 099 row: E column: 09
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     internodal stem segments'
126 c 158 g 182
                                                                                                                                                                                                                                                                                                                                Medicago truncatula stem library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 AGCAAAACAGGAGGAAATCTTCCACT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191 agcaaaccaggaaggaaaccttcaatt 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="NF099E09ST"
                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Dixon RA
Plant Biology Division
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                                                                                        AW695821.1 GI:7570583
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Best Local Similarity 73.4%;
Matches 152; Conservative (
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                                                                                                                             barrel medic.
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/lab.host="Notes" Data Bulasscript II XR; Site_I: ECORI; Site_2: Xhoi; The mana was solated from roots of Glycine max xhoi; The mana was solated from roots of Glycine max supernod' plants generously donated by Dr. Gary Stacey. The seedlings were innoculated with Bradyrhizoblum japonicus, strain GDAAll priot to harvest. Stratagene's cDNA synthesis Kit (catalog number 200401) was used to synthesize the CDNA. First-strand synthesis was performed with 5-methyl dorp, hence the ligated CDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An "anchor' nuclectide (V=A,C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAACTAGTCTCGAG[T]18V] to anchor the primer at the 5' end of the Poly(A) tract. After second-strand synthesis, the CDNA ends were filled in with cloned Pfu DNA Polymerase, ligated to EcoRI adapters and subsequently phosphorylated. The XDNI site within the subsequently phosphorylated. The XDNI site within the first-strand synthesis primer was then restricted by digestion with XDOI; all XDOI sites the CDNA would be protected by their hemimethylated status. The CDNA constructs were size-fractionated with a 500bp cutoff, constructs were size-fractionated with a 500bp cutoff, using GlbcoBRL Life Technologies' CDNA Size Fractionation column. The column eluent was then ligated with EcoRI (PBluescript II SK(+) that has been digested with EcoRI (PBluescript II SK(+) that has been digested with plasmids with cDNA inserts, based on size (n=25). This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell."
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Bukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; Rosidae; eurosids I; Fabalee; Fabaceae; Papilionoideae; Glycine.

[Abases I to 499)

[Bonemaker, R., Kelm, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Matter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
This clone is available through: Genome Systems, Inc. 4633 World
This clone is available through: Galla Francher information
call: (800) 430-0030 or (314) 427-3322 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
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/clone="GENOME SYSTEMS CLONE ID: Gm-c1028-6560"
/clone_lib="Gm-c1028"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      info@genomesystems.com web site: www.genomesystems.com
High quality sequence stop: 382.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="roots of 'Supernod' plants"
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125 ATTICIGITIATAACAGAACAACAACAAGGITGACGAAACTGIGGAACGAGCAAAACA 184
                                                                                                                              141 attocogttaacaacggaaccatttocaaggttattgggccataagacgaagcaaaccag
                                                                                                                                                                                                                          201 gaaggaaaccttcaatt 217
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/dev.stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host="E. coli strain SOLR"
/lab_host="E. coli strain SOLR"
/note="Vector: pBluescript SR-; Site_1: EcoRI; Site_2:
Xhoi: cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The cDNA was
directionally ligated into the Unizap XR vector from
Stratagene and packaged using Glomacy versiforme. The containing cDNA inserts were excised
from the recombinant lambda-zap phage using Ex-assist
helper phage and propagated in SOLR cells."

64 a 115 c 139 g 154 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Medicago truncatula/Glomus versiforme mixed EST
                                                                                                                                                                                                                                                                                                                                                                                                                                           Medicago truncatula/Glomus versiforme mixed EST library.
Medicago truncatula/Glomus versiforme mixed EST library
Eukaryots; mixed EST libraries.

1 (bases 1 to 573)
Harrison,M.J., Liu,J., Peng,H., Gonzales,M., Ellis,L., Town,C.D.,
Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M.
ESTS from roots of Medicago truncatula after colonization with
                                              113 ctcaatattgcttgaaaagggcttcccaattccggttaacaacggaaccatttccaaggt 172
                                                                           EST318032 MHAM Medicago truncatula/Glomus versiforme mixed EST library cDNA clone pMHAM-5403, mRNA sequence.
14 GCTCAACCCTCAACAAGAATACGCCTTGCTGGACTGGCTGTTATGGGCCAAAATCTAGCA 73
                                                                                                                                                                                                                                                                                                               20-MAR-2000
                                                                                                                                     173 tattgggccataagacgaagcaaaccaggaaggaaaccttcaatttatggggaacaa 229
                                                                                                                                                                /cultivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
/clone="pMHAM-5403"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2510 Sam Noble Parkway, Ardmore, OK 73401, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'http://chrysie.tamu.edu/medicago'
Seg primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      More information is available at. .
                                                                                                                                                                                                                                                                                                             mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mjharrison@noble.org
Noble EST name:N253596e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glomus versiforme
Unpublished (2000)
Contact: Maria J. Harrison
Plant Biology Division
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                                                                                                                                                                                                                                                                                                      573 bp
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Fax: 580-221-7380
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papillionoldeae; Medicago.
                                                                                                                                                                                                                                                           AL368071 430 bp mRNA EST 03-AUG-2000
MtBA22A07F1 MtBA Medicago truncatula cDNA clone MtBA22A07 T3, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Pascal Gamas and Etienne-Pascal Journet, Laboratoire de Balologie Moleculaire des Relations Plantes Microorganismes, CNRS-INRA, BP 27 31336 Castanet-Tolosan Cedex, France (Email: Mt-est@toulouse.inra.fr Website:
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
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Location/Qualifiers
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0; Mismatches
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185 GAGGGAAATCTTCCACT 201
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21 atttgcttcaaatttcaggagattaattatgcgctcaaccacaacaagaataggccttg 80

Score 96.2; DB 23; Length 573; Pred. No. 1.8e-19; 0; Mismatches 48; Indels 2;

42.0%; 74.6%;

Matches 147; Conservative

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Best Local Similarity

Query Match

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XhoI; M. truncatula sterilised seeds were germinated for
72h at 25 C, before transplanting into a 1/3 Epoisses soil
2/3 calcined Terragreen mix in the presence of onion
root fragments colonized by the arbuscular mycorrhizal
fungus Glomus intraradices (Schenck & Smith, isolate LPAR)
). The plants were watered every day and twice a week with
a modified nutrient Long Ashton solution without phosphate
but with a high level of nitrate. After 3 weeks RNA was
extracted from whole root systems. CDNA was prepared from
polyA+ enriched RNA. The CDNA was directionally ligated
into Uni-zap XR vector from Stratagene and packaged using
Glapack Gold packaging extracts. Plasmids containing cDNA
inserts were mass-excised from phage stocks using ExAssit
helper phage and propagated in Solre cells. Clone ordering
and sequencing was performed by the Centre National de
Sequencing experienced by the Centre National de
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Medicago.
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BP 191 91006 EVRY cedex - France
BRail: seqreféqenoscope.cns.fr, Web: www.genoscope.cns.fr
Contact : Pascal Gamas and Etlenne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
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Location/Qualifiers
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2 CTTCAATTTTCAGGAAATACATTATG-GCTCAACCACTTACAAGAATAGGCCTTGCCGGA 60
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Unpublished (2000)
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FEATURES

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Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
Magnoliophyta; eudicotyledons, core eudicots, Rosidae; eurosids I;
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MtBA12H03F1 MtBA Medicago truncatula cDNA clone MtBA12H03 T3, mRNA
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Genoscope - Centre National de Sequencage
Genoscope - Centre Centre France
BP 191 91006 ERVIX cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email:
Mt-est@toulouse.inra.fr Website:
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Journet, E. P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O., Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Gianinazzi-Pearson, V. and Gamas, P.
                                                                                                                                                                                                                                                                                                                             93 ttaatgggcaaaatctggcactcaatattgcttgaaaagggcttcccaattccggttaac 152
                                                                                                                                                                                                                                                                                                                                                                        60 ITATGGGCCAAAATCTCGCACTCAATATTGC-CGACNAAGGATTCCCAATTTCTGTTAT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TITCAGGAAATACATTATG-GCTCAACCACTTACAAGAATAGGCCTTGCCGGACTGGCTG 59
                                                                                                                                                                                  33 tttcaggagattaattatgcgctcaacccacaacaagaataggccttgctggattggctg 92
                              Score 89.6; DB 14; Length 420; Pred. No. 1.9e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Medicaqo truncatula ESTs from nitrogen-starved roots
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Location/Qualifiers
                                                                                                            Indels
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39.1%; Scor. 74.6%; Pred. No. 1...
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/db_xref="taxon:3880"
/clone="MtBA12H03"
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ORIGIN

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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL365745 479 bp mRNA EST 03-AUG-2000
MtBA02B10F3 MtBA Medicago truncatula cDNA clone MtBA02B10 T3, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anote—Vector: pBluescript pSK; Site_1: EcoRI; Site_2: XhoI; Plants were grown in an aeroponic chamber for 14 days on nitrogen-rich medium followed by 3 days on N-free medium. RNA was extracted from root tips (1-3 cm). cDNA was prepared from poly4+ enriched RNA. The cDNA was directionally ligated into Uni-zapxR vector from Stratagene and packaged using Gigapack Gold packaging extracts. Plasmids containing cDNA inserts were
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Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O.,
Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Gianinazzi-Pearson
, V. and Gamas, P.
Medicago truncatula ESTs from nitrogen-starved roots
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BP 191 91006 EWRX cedex - France
Email: segref@genoscope.cns.fr. Web : www.genoscope.cns.fr
Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Blologie woleculaire des Relations Plantes Microorganismes,
CNRS-INRA, BP 27 31326 Castenet-Tolosan Cedex, France (Email :
Mt-est@toulouse.inra.fr Website :
                                                                                                                                                                                                                          53 gctcaacccacaacaagaataggccttgctggattggctgttaatgggcaaaatctggca 112
                                                                                                                                                                                                   ctcaatattgcttgaaaagggcttcccaattccggttaacaacggaaccatttccaaggt 172
                                                                                                                                            16 GCTCAACCACTTACAAGAATAGGCCTTGCCGGACTGGCTGTTATGGGCCAAAATCTCGCA 75
                                                      1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Medicago truncatula"
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/clone="MtBabOsh"
/clone=lib="MtBA"
/tissue_type="root tips"
/dev_stage="harvested after 3 days of N-starvation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://sequence.toulouse.inra.fr/Mtruncatula.html).
Location/Qualifiers
                                                      41; Indels
                                                                                                                                                                                                                                                                                                                        135 TGACGAAACTGTGGAACGAGCAAAAACAGGAGGAAATCTTCCACT 179
                                                                                                                                                                                                                                                                                                tattgggccataagacgaagcaaaccaggaaggaaaccttcaatt 217
  Score 87.4; DB 14;
Pred. No. 8.6e-17;
                                              0; Mismatches
38.2%;
74.5%;
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                                            Matches 123; Conservative
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AL365745
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Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids I,
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MtBA02B09F3 MtBA Medicago truncatula cDNA clone MtBA02B09 T3, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Genoscope
Genoscope
Genoscope
Genoscope
Genoscope
BP 191 91006 EVRY cedex - France
Bmall: Seqref@genoscope.cns.fr
Contact: Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email:
Mt-est@toulouse.inra.fr Website:
http://sequence.toulouse.inra.fr/Mtruncatula.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 481)
Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O.,
Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Gianinazzi-Pearson
, V. and Gamas, P.
Medicago truncatula ESTs from nitrogen-starved roots
                                                                                         53 geteaacceacaacaagaataggeettgetggattggetgttaatgggeaaaatetggea 112
                                                                                                                                                                                  113 ctcaatattgcttgaaaagggcttcccaattccggttaacaacggaaccatttccaaggt 172
                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="MtBA"
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/dev_stage="harvested after 3 days of N-starvation"
                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
       Length 479;
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                                                   41; Indels
                                                                                                                                                                                                                                                                                                               132 TGACGAAACTGTGGAACGAGCAAAACAGGAGGAAATCTTCCACT 176
                                                                                                                                                                                                                                                                     Fabales; Fabaceae; Papilionoideae; Medicago.
  Score 87.4; DB 14;
Pred. No. 9.4e-17;
0; Mismatches 41;

    .481
    /organism="Medicago truncatula"
/cultivar="Jemalong"
/db_xref="taxon:3880"
/clone="MtbA02B09"

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AL365743.1 GI:9665496
    38.2%;
74.5%;
                                        Matches 123; Conservative
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Best Local Similarity 74.5'
Matches 123; Conservative
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                        11
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula stem library Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 630)
He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bel
,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
                                                                                                                                                                                                                                                                                                                                          NF009F08SI1F1000 Developing stem Medicago truncatula cDNA clone NF009F08SI 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152 CTCAATATTGC-CGACAAAGGATTCCCAATTTCTGTTTATAACAGAACAACATCAAAGGT 210
                                                                                                            113 ctcaatattgcttgaaaagggcttcccaattccggttaacaacggaaccatttccaaggt 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="stem"
//dev.stage="Pooled developmental"
//dev.stage="Pooled developmental"
//note="vector: Lambda Zap; Contains a mixture of
internodal stem segments"
// 124 c 150 g 172 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 87.4; DB 23; Length 630;
Pred. No. 1e-16;
0; Mismatches 41; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 tattgggccataagacgaagcaaaccaggaaggaaaccttcaatt 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 TGACGAAACTGTGGAACGAGCAAAACAGGAGGGAAATCTTCCACT 255
                                                                                                                                                                                               132 TGACGAAACTGTGGAACGAGGAAAACAGGAGGAAATCTTCCACT 176
                                                                                                                                                                         173 tattgggccataagacgaagcaaaccaggaaggaaaccttcaatt 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Dixon RA,
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Fax: 580 221 7382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fabales; Fabaceae; Papilionoideae; Medicago.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: radixon@noble.org
Insert Length: 630 Std Error: 0.00
Plate: 009 row: F column: 08
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:3880"
/clone="NF009F08ST"
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Best Local Similarity 74.5%;
Matches 123; Conservative
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AW688619
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1 (bases 1 to 379)

Sasmizu, E., Nakamura, Y., Sato, S. and Tabata, S.; Generation of 7137 non-redundant expressed sequence tags from a legume, Lotus japonicus
                                                                                                                                                                                                      Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Pabales; Fabaceae; Papilionoideae; Lotus.

1 (bases 1 to 321)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
Generation of 7137 non-redundant expressed sequence tags from a legume, Lotus japonicus

20277479
                                                                                                                                                                                                                                                                                                                                                                                                                                        The First Laboratory for Plant Gene Research
Assusa DNA Research Institute
Yana 1532-3, Kisarazu Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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XhoI; isolate=Hiyakojima MG-20"
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                                           AV410206 Lotus japonicus young plants (two-week old) Lotus japonicus cDNA clone MWL068h09\_r 5', mRNA sequence.
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    /organism="Lotus japonicus"

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1 (bases 1 to 394)
Asamizu.E., Nakamura,Y., Sato,S. and Tabata,S.
Generation of 7137 non-redundant expressed sequence tags from a
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Razusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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/dev_stage="young plants (two-week old)"
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XhoI; isolate=Myakojima MG-20"
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AV425788 Lotus japonicus young plants (two-week old) Lotus
japonicus cDNA clone WWM059a03_r 5', mRNA sequence.
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 DNA Res. 7 (2), 127-130 (2000)
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DNA Res. 7 (2), 127-130 (2000)
20277479
                                  Contact: Yasukazu Nakamura
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                                                                                                                                                                                                                                    Length 394;
                                        Indels
   DB 18;
Query Match
37.4%; Score 85.6; DB 18
Best Local Similarity 71.6%; Pred. No. 3.2e-16;
Matches 126; Conservative 0; Mismatches 49
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AC003970 Arabidops X83923 S.tuberosum AJ000184 Spinacia AJ00182 Spinacia AJ00172 Nicotiana U32737 Haemophilus X84229 A.thaliana AJ001359 Arabidops X84230 A.thaliana AJ158811 Homosapi AJ006246 Cyanidium
DB ID	7 AC003970 45 STGEPDHPI 45 STG001184 45 NTTPG18 65 U32737 8 ATGEPDHE5 45 NTTPG16 8 ATGGEPDH15 64 ALLS8831 8 CCA6246
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Score	76.2 68.6 66.6 66.7 61.2 61.2 61.2 60.6 60.6 60.6 8.8 8.9 8.9 8.9 8.9 8.9 8.9 8.9 8.9 8.9
Result No.	C C C C C C C C C C C C C C C C C C C

Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA 4 (bases 1 to 95865) Federspiel, N.A., Palm, C.J., Conway, A.B., Kurtz, D.B., Conway, A.R., Aau, M., Araujo, R., Buehler, E., Dewar, K., Feng, J., Kim, C., Li, Y., Oji, O., Osborne, B.I., Shinn, P., Sun, H., Toriumi, M., Vyotskaia, V., Yu, G., Ecker, J., Theologis, A. and Davis, R.W. Direct Submission Submitted (28-AUG-1998) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA (bases 1 to 95865) Federspiel. N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Nguyen, M., Lam, B., Southwick, A., Ecker, J., Theologis, A. Direct Submission Submitted (26-JUL-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA-94304,	Or Jun 3, 1998 this sequence version replaced gi:2829860. On Jun 3, 1998 this sequence version replaced gi:2829860. Bases 94718-95865 of clone F14J9 overlap with bases 1-1148 of 'IGF' clone F2IM12, gb AC000132 e-mail for correspondence: arab&sequence.stanford.edu Genes with similarity to proteins in the databases are described as 'putative', '-like' or 'similar to'. Genes that have EST similarity but no significant protein similarity are described as 'unknown proteins'. Genes that are annotated based only on gene prediction software are described as 'hypothetical proteins' The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.orni.gov/section/index.html), GENSCAN (Chris Burge, http://gnomic.stanford.edu/-chris/GENSCANW.html), Fexa (V.Solovyev & A.Salmow, Sanger Centre, http://genomic.sanger.ac.uk/), and NATPIANTGANE.	Denmark, http://www.oualifiers Location/Qualifiers Location/Qualifiers 1. 95865 rorganism="Arabidopsis thaliana"	9403. 9405. 3971 3405. 3971 /gene="Ft409.2" /gote="Ft409.2" /gote="Ft409.2" /codo_start=1 /codo_start=1 /do_xref=[61:3482911" /tbarslation="MUVLVLYIFTPHIEGVEADCPTEALINSICIENEDYGFCNKIIH /translation="MUVLVLYIFTPHIEGVEADCPTEALINSICIENEDYGFCNKIIH /translation="MUVLVLYIFTPHIEGVEADCPTEALINSICIENEDYGFCNKIIH /krprprIKELFSKGEYELMDEALISTAKKILEECRODFLIPPYKEPLLEKKRVMRILIT MSAVSGHWYNERASLISSVVTAQFFNI" 6504. 7028 /gene="F14J9.3"
REFERENCE AUTHORS TITLE JOURNAL TITLE JOURNAL	COMMENT	FEATURES SOURCE GONE GENE	gene gene
U09032 Anastrepha AF269359 Staphyloc AF269560 Staphyloc AB021914 Anastreph AL121764 S. Dombe Cr 295395 S. pombe chr S67872 Zw-glucose- D90906 Synechocyst U83195 Chlamydia t AE00129 Chlamydia t AE00129 Chlamydia t AE002314 Chlamydia t AE00129 Chlamydia t AE00129 Chlamydia t AE00129 Chlamydia t AE00129 Chlamydia t AE00129 Chlamydia t AE00129 Chlamydia t AE001291 Chlamydia t AE001291 Chlamydia t AF012861 Petroseli AJ010970 Arabidops AE004417 Vibrio ch AJ010971 Arabidops	X99405 N. tabacum m AJ010712 Solanum t D88189 Actinobacil U09033 Ctenolepism AF246307 Acidithio AE01175 Thermotog AJ001769 Nicotiana Z71517 S. cerevisia X77346 S. cerevisia X37796 Nostoc sp. Z69381 S. cerevisia L32796 Nostoc sp. Z69381 S. cerevisia Z1911 M. musculus U09040 Rhagoletis AJ001770 Nicotiana	PLN 26-JUL-2000 F14J9 genomic sequence e.e. Tracheophyta; Spermatophyta; adicots; Rosidae; eurosids II; s. A. Kurtz,D.B., Conway,A.R., Toriumi,M., Kim,C., Li,Y., Joriumi,M., and Davis,R.W. S., Kurtz,D.B., Conway,A.R.,	Feng, J., Kim, C., Li, Y., ', Toriumi, M., Vyotskaia, V., Stanford University/DNA California Avenue, Palo Alto, B., Kurtz, D.B., Conway, A.R., ', Toriumi, M., Vyotskaia, V., is, R.W. g and Technology Center,
2002 2002 2003 2003 2003 2003 2003 2003	9 1953 45 9 10903 2 7 460 54 6 11895 1 16 11895 45 11 2399 45 11 3782 45 11 6672 2 11 6672 4 11 38855 45 11 3885	ALIGNMENTS AC003970 95865 bp DNA PLN 26-JUL-2000 Arabidopsis thaliana chromosome I BAC F14J9 genomic sequence contains phya marker, complete sequence. AC003970. G1:3176695 HTG. Arabidopsis thaliana Arabidopsis thaliana Busaryota; viridiplantae; Embryophyta; Tracheophyta; Spermatophy Magnollophyta; eudioctyledons; core eudicots; Rosidae; eurosids Brassicales; Brassicaceae; Arabidopsis. I (bases I to 95865) Federspiel, N.A., Palm, C.J., Conway, A.B., Kurtz, D.B., Conway, A.R. Au, M., Araujo, R., Buehler, E., Dewar, K., Feng, J., Kim, C., Li, Y., Oji, O., Osborne, B.I., Shinn, P., Sun, H., Toriumi, M., Vysotskaia, V.S., Yu, G., Ecker, J., Theologis, A. and Davis, R.W. Unpublished 2 (bases I to 95865) Federspiel, N.A., Palm, C.J., Conway, A.B., Kurtz, D.B., Conway, A.R. Federspiel, N.A., Palm, C.J., Conway, A.B., Kurtz, D.B., Conway, A.R.	Au, M., Araujo, R., Buehler, E., Dewar K., Feng, J., Kim, C., Li, Y., Au, M., Osborne, B. I., Shinn, P., Sun, H., Toriumi, M., Vyotskaia, V., Yu, G., Ecker, J., Theologis, A. and Davis, R.W. Direct Submission Submitted (31-DEC-1997) Biochemistry, Stanford University/DNA Sequencing and Technology Center, 855 California Avenue, Palo Altc CA 94304, USA 3 (bases 1 to 95865) 3 (bases 1 to 95865) 4 (bases 1 to 95865) A Araujo, R., Buehler, E., Dewar K., Feng, J., Kim, C., Li, Y., Au, M., Araujo, R., Buehler, E., Dewar K., Feng, J., Kim, C., Li, Y., Oji, O., Osborne, B. I., Shinn, P., Sun, H., Toriumi, M., Vyotskaia, V., Yu, G., Ecker, J., Theologis, A. and Davis, R.W. Direct Submission Submitted (03-JUN-1998) DNA Sequencing and Technology Center,

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

JOURNAL REFERENCE AUTHORS

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JOURNAL

TITLE JOURNAL

REFERENCE AUTHORS

RESULT 1 AC003970/c LOCUS DEFINITION

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CKLYEMIPDKDNIARTSWILGKKEGRYDEAREIFDEMSERSUTWITHMYGYGGUNR
DDARK FEDVWERTEVSWISMLMGYVONGRIEDAEELFEWPVKPVIACNAMISGLG
OKGE IARARRYEDSMKERNDASWQTVYKIHERNGEELEALDEFILMGYGYGREPFPFIL
ISILSVCASLASLHHGKOVAGLURCOFDVDVYVASVLMTMYIRGGELVKSKLIFDRF
PSKDIIMWNSIISGYASHGLGEEALKVFCEMPLSGSTKPNEVTFVATLSAGSYAGWYE
BCLKIYEBEMSYRGYRPTAHYACWDMLGRAGRRHREAMENIDSMTYEPEDAAVWGSLL
GACRTHSGLDVARFCAKKLIFIEPENSGTYILLSNWYASGRWADVAELRKLMKTRLY
RKSPGCSWTEVENKYHAFTGGINSHPEQESILKILDELDGILREAGYNPDCSYALHD
VDEEKNNSLKYHSERLAVATALKLSEGIPIRWMKNLRVCSDCHTAIKIISKVKERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(20243. .20480,20574. .20774,20850. .21052,21153. .21310,21508. .21635,21716. .21921,22053. .22167,22228. .22346,22444. .22691,22778. .22982,23217. .23318))/gene="Fi4J99,8" / Complement(joint to Glucose-6-phosphate dehydrogenases,gi12276344, gi12829880, gi12352919 and others; Location of
                           /translation="MKSQILLRRTYSTTIPPPTANVRITHLSRIGKIHEARKLFDSCD
                                                                                 DLMPERNVVSWTALVKGYVHNGKVDVAESLFWKMPEKNKVSWTVMLIGFLQDGRIDDA
                                                               SKSISSWNSMVAGYFANLMPRDARKLFDEMPDRNIISWNGLVSGYMKNGEIDEARKVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; Asteridae; Solananae; Solanales; Solanaceae; Solanum; Potatoe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (13-JAN-1995) A. Von Schaewen, Universitäet Osnabrueck, FB5 Biologie/Chemie, Pflanzenphysiologie, Barbarastrasse 11, 49076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 21876 GAAGCTCTGGTGGATGTGGCATGCACCATTGGAGATAACGCTCAGGCACCACGAGGCTGG 21817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 21816 ACTCGAATAATAGTTGAGAAACCTTTTGGTTTAACTCACATTCGTCTCATCAGTTAACA 21757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecular characterization of the plastidic glucose-6-phosphate dehydrogenase from potato in comparison to its cytosolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 aatogoataatatttgagaagcoatttggctttgatgcactttctcccataggctgaca 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 gaagcactitiggaigtigcgicaigteitgcaagcagigcicagacccagaagggaigg 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 76.2; DB 7; Length 95865; Pred. No. 1.1e-09;
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tuberosum mRNA for glucose-6-phosphate dehydrogenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g6pdh gene; glucose-6-phosphate dehydrogenase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 caatatcttctttcaaactttcaggaaaagcaaatatag 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="vegetative stage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     complement(20243. .23318)
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/haplotype="diploid (2n)"
                                                                                                                                                                                                                                                                                                                                                                          Illrdanrfhhfrngecsckdyw"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene-"F14J9.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 67.1%;
Matches 108; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.0%;
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JOURNAL
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14786. .15018)
                                                                                                                                                                                                                                                                                                                         complement(join(7954. .8155,8251. .8402,8490. .8648,
8762. .9014,9101. .9217,9294. .9356,9577. .9606,9895. .9938,
10404. .10444.10829. .10925))
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GLONSSPLIACALTNILDPAVFFLLAIFROGTVGIKKASGQAKVIGTLVCVIGAMVLS
FYHGHIGIGESKIHWAYARNITKHGSSGHSNFFIGSPLIMAAAVSWAARFIIOTKM
SETFAAPTTSTLLMGARSIOCGAIALISDHIISDNSLSSPLRFISALYAGVVASALA
FCLMSWAMQRKGPLYVSVFSPLLLVVVAIFSWALLEEKLYTGTFNGSALVVIGLYGV
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IVNSAFTKAVTFFKOAYTSKIVNIEKKVSMAVDICKTDFNVLGYQINPLIEKNROTKI
LLSMEQIVSHMVSS"
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NSDTGGLVAGLGYSIGLPNGRSFFQRETGRLSDGRLVJDFLCQSLNTSLLNPYLDSLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSKFQNGANFAIVGSSTLPRYPFALNIQLAMPELHFKSRALELASISDLKEWILDSLV
GFRNALYMIDIGONDIADSFSKGLSYSRVKLIPNVISEIKASISDPLKEWMIGES
GFRNALYMIDIGONDIADSFSKGLSYSRVKLIPNVISEIKSAIKILYDEGGSKFWPH
WIGPLGCLPQKLSWYBSKGFDKHGCLATYNAAAKLIPNEGLDHKCRDIRTELKEANIYY
VDIYALKYDLIANSNNYGFERPLMACCGYGGPPYNYNNVITCGNGGSKSCDEGSRFIS
WAGIHYTETANAIVANAKYLSMQHRTPFTPFFHFFCGG"
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WGESPVSTTRVFRADDPSNETPPRRLKTDEIPTIINDFRLAARNATEAGFDGVEIH
GAHGYLIDQFRKDSVNDRTHOSYGGSLENRCRPALOVIEAVSKRIGDPRKGIRLSPFAD
YMESGDTDPRRLGSTNARSLARFEILYCHMIBPRMKTVSEIFECRESLTPMRNAFNGT
FIVAGGYTREDGNKAVAEGRTDLVAYGRLFLANPDLPKRFELNAPLNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAC33200.1"
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16328. .16468,16571. .16596))
/gene="P14J9.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Similar to MtN21, gi|2598575, Megicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"Hypotherical protein; Similar to Arabidopsis selenium-binding protein, gi|2244760 and Arabidopsis hypothetical proteins gi|3033399, gi|2464864, gi|2244839 and several others"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Similar to nodulins and lipase; location of EST E6C2T7, gb|AAO42309. similar to nodulins gl|3328240, gi|2129854 and others and lipase, gi|2129636"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gi|2765083 and old-yellow-enzyme homolog, gi|2232254" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Similar to 12-oxophytodienoate reductase,
                                                         /note="Hypothetical protein"
                                                                                                               /protein_id="AAC33197.1"
                                                                                                                                                                                                                                                                                        complement(7954. .10925)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAC33198.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAC33199.1"
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                                                                                                                                             /db_xref="GI:3482912"
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                              /gene="F14J9.3"
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/gene="F14J9.5"
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LDAIEGERRLFIRSDELDAAWALFTPLLKELEEKKIAPELYPYGSRGPVGAHYLAAKH
                                                                                                                                                                                                                         /translation="MCVQLRLNPCSSSSAATSPSTFHNGTPYFCKKFNFLPFRTQPLN
WVSGIYSRIQPRKHFEVFSSNGFPLNAVSVQDVQVPLTELGSGDTTVSITVIGASGDL
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                                                                                                                                                                                                                                                                                                                                             LRFSNLVFEPLWSRNYIRNVQFIFSEDFGTEGRGGYFDHYGIIRDIMQNHLLQILALF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [ (bases 1 to 1396) Ferroud, P.F., Crespi, P. and Greppin, H. Nucleotide sequences of glucose-6-phosphate dehydrogenase from Spinacia oleracea cloned by RT-PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 teneaginaaaateetneaggittaagggitteaaannnagniittgageeaceitngag 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 cataatatttgagaagccatttggctttgatgcacttcttcccataggctgacacaata 125
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Spinacia oleracea mRNA for glucose-6-phosphate dehydrogenase,
partial, clone O28FA38.
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                                                                                                                                    /product-"glucose-6-phosphate dehydrogenase"
/protein_id="CAA8775.1"
/db_xref="G1:1197385"
/db_xref="SWISS-PROT:Q43839"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGPD gene; glucose-6-phosphate dehydrogenase spinach.
                     /cell_type="mesophyll"
/clone_lib="lambda_ZAPII"
/clone="pBSK-plafull #3,#4"
    tissue_type="green leaves"
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Spinacia oleracea mRNA for glucose-6-phosphate dehydrogenase,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="Glucose-6-phosphate dehydrogenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 117; Indels
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Pred. No. 3.1e-07;
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252 c 329 d 397 t
                                                                                   /organism="Spinacia oleracea"
/plasmid="pZb1"
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/db_xref="G1:2276348"
                                                                                                                                                                                                                                                                                     /dev_stage="vegetative"
/tissue_type="leaves"
1. .1396
                                                                                                                                                                       /cultivar="Matador"
/db_xref="taxon:3562"
/clone="028FA38"
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                          Location/Qualifiers
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AJ000182.1 GI:2276343
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943 IGGIGGAGAATTIATCIGITCIACGCTITITCAAAICIAGTITITIGAACCTCTAIGGICAA 1002

1003 GGAACT 1008

248 gnacnt 253

188 ncaginaaaaiccincaggiitaagggiitcaaannnagniitigagccacciingagnn 247

94 Oy Oy

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/LTAISLATION-MEELVSCHHIPLICIQSSVPPNGCLTFFQDSACORCSHSEFSNG
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SYSLDAEDIRNEVKVLRSMFPIKLQDVVGGYKRGHSKGNESYSGYTDDPYPUNNST
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TMELVLRVQPDBAIYLKINNKVPGLGMRLDRTDLLCYSTRYRGETPDAYBRLLCAI
                                                            Direct Submission
Submitted (21-JUL-1997) Fink A., Laboratoire de Biochimie et de
Physiologie Vegetale, University of Geneva, 3, Place de
1, Universite, CH-1211 Geneve 4, SWITZERLAND
                                                                                                                                                                       Diogon,T., Perroud,P.F., Crespi,P. and Greppin,H. de sequences of glucose-6-phosphate dehydrogenase from
Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia
1 (bases 1 to 2049)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="Glucose-6-phosphate dehydrogenase"
/protein_id="CAA03939.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="G6PD catalytic site'
                                                                                                                                                                                                                                                                                                          /organism="Spinacia oleracea"
/db_xref="taxon:3562"
                                                                                                                                                                                                                                                                                                                                                                              /organism="Spinacia oleracea"
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                                                                                                                                                                                               Nucleotide sequences of glucose-6-p
Spinacia oleracea cloned by RT-PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="vegetative"
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/clone="028FA14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="leaves"
147. .2049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /EC_number="1.1.1.49"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="GI:2276344"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:3562"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="leaves"
2028. .2036
                                                                                                                                                                                                                                                                  tocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                            /cultivar="Matador"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cultivar="Matador"
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                                                                                                                                                                                                                                                                                                                                                                                                     /plasmid="pZL1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="030A4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="G6PD"
147. .1871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /plasmid="pZL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147. .1871
/gene="G6PD"
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/gene="G6PD"
                                                                                                                                                       2 (bases 1 to 2049)
Fink, A., Diogon, T.,
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                                                                                                                                                                                                                                           Unpublished
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                                       Fink, A.
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/translation="MGGQLQLMPCSSSSVATTFHNGAHKFCRNFNILPFKAHSLESSV
ASTFHWGIYSRIQPRHIFEIMSSNGFHLNAVSLLDGSASKSMPEQVPLTELENAETTV
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RIDQREWCEAKMDFHEERCFYHSGQYHSEDDFAELDYKLKAKEGSRVSNRLFYLSIPP
NIFVDVVRCASLKASSTSGWTRVIVEKPFGRDLESSSELTRCLKKYTTEBQIFRIDH
LGKELVENLSVLRFSNLVFEPLWSRNYIRNVQFIFSEDSGTEGRGYFDNYGIIRDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ONHELOTLALPAMETPYSMDAEDTRNEKVYVLRSMRPLOLEDYVLGGYKGHSKGGKLY
PATUDPTVPNGSVTPTFSAAALFINNARWDGVPFLMKAGKALHTRRAEIRVOFRHUP
GNLYKRNFGTDLJKATNRELVLRLQPDEAIYLKINNKVPGLGHRLDRSDLNLLYKAKYR
GEIPDAYERLLJDALEGGERTLFIRSDELDAAWALFTPLLKELEEKKIAPELYPYGSRG
PVGAHYLAAKHNVRMGDLSGDP
1 342 C 433 g 538 t
                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, euphyllophytes, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Asteridae, euasterids I; Solanales, Solanaceae,
                                                                                                                                                                                                                                                                                                                                                                                                    Wendt,U.K., Hauschild,R., Lange,C., Pietersma,M., Wenderoth,I. and von Schaewen,A.
Von Schaewen,A.
Evidence for functional convergence of redox regulation in G6PDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (18-5EP-1997) von Schaewen A., Plant Physiology,
University Osnabrueck, Barbarastr. 11, D-49069 Osnabrueck, GERMANY
Location/Qualifiers
                                                                17-AUG-1999
                                                  NTTPG18 1869 bp mRNA PLN 17-AUG-
Nicotiana tabacum mRNA for plastidic glucose-6-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="glucose-6-phosphate dehydrogenase"
22. .1788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="glucose-6-phosphate dehydrogenase"
/protein_id="CAA04994.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isoforms of cyanobacteria and higher plants
Plant Mol. Biol. 40 (3), 487-494 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="young sink leaves"
22. .219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="G1:3021532"
/db_xref="SPTREMBL:065856"
                                                                                                                                                                                    glucose-6-phosphate dehydrogenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="mesophyll"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cultivar="Samsun NN"
/db_xref="taxon:4097"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                             AJ001772.1 GI:3021531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="TCG18"
                                                                                                           dehydrogenase TPG18.
AJ001772
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                                                                                                                                                                                                                      common tobacco.
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                                                                                                                                                                                                                                                                                                                                                          Nicotiana.
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                         NTTPG18
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RESULT
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0; Mismatches 117; Indels

25.3%; Score 66.6; DB 45; 52.4%; Pred. No. 3.1e-07;

Best Local Similarity 52.49 Matches 129; Conservative

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Query Match

Length 2049;

8 tittggatgttgcgtcatgtcttgcaagcagtgctcagacccagaagggatggaatcgca 67

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Kirkness, E.F., Adams, M.D., White, O., Clayton, R.A.,

Kirkness, E.F., Kerlavage, A.R., Bult, C.J., Tomb, J., Dougherty, B.A.,

Merrick, J.M., McKenney, K., Sutton, G.G., FitzHugh, W., Fields, C.A.,

Gocayne, J.D., Scott, J.D., Shirley, R., Liu, L.I., Glodek, A.,

Kelley, J.M., Weidman, J.F., Phillips, C.A., Spriggs, T., Hedblom, E.,

Cotton, M.D., Utterback, T., Hanna, M.C., Nguyen, D.T., Saudek, D.M.,

Groghagen, N.S., Gnehm, C.L., McDonald, L.A., Small, K.V., Fraser, C.M.,

Smith, H.O. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (27-SEP-1997) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA The H. influenzae sequence has been updated by R. Fleischmann. New database matches have been assigned, product names have been improved, and a number of frame shifts have been corrected. We gratefully acknowledge the work of Tatusov et. al. We have incorporated their annotation into the /notes fields of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    032737 10195 bp DNA BCT 29-MAX-1998
Haemophilus influenzae Rd section 52 of 163 of the complete genome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (25-JUL-1995) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA
                                                                                                                                                         126 tettettteaaaettteaggaaaageaaatatatagaattganeatetaetaggaaggaa 185
                                                                                                                                                                                                                                                                                                                                                               801 CCTAAAGAAGTATCTAACTGAGGAGGAAATTTCCGAATTGACCATTACTTGGGAAAGGA 860
                                                                                                                                                                                                                                                                                                                                                                                                                         186 toncaginaaaaiccincaggittaagggittcaaannnagniittgagccacciingag 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 cataatatttgagaagccatttggctttgatgcactttcttcccataggctgacacaata 125
                                                                                                                                                                                                                                                                  741 AGTCATTGTTGAGAAACCGTTTGGTCGTGACTTAGAATCATCTAGTGAGCTGACCAGATG 800
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Haemophilus.
                                                            Gaps
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White,O., Clayton,R.A., Kerlavage,A.R. and Fleischmann,R.D.
Direct Submission
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White,O., Clayton,R.A., Kerlavage,A.R. and Fleischmann,R.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Whole-genome random sequencing and assembly of Haemophilus
                                                                                                             6 acttttggatgttgcgtcatgtcttgcaagcagtgctcagacccagaagggatggaatcg
                                                         ;
0
        Length 1869;
                                                         Indels
     Score 62.2; DB 45;
Pred. No. 4.2e-06;
0; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 269 (5223), 496-512 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus influenzae Rd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemophilus influenzae
        23.78; 51.28;
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                                                         Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 influenzae Rd
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                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      921 CAGAAACT 928
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                Query Match
                                           Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U32737/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
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VERSION SOURCE

RESULT LOCUS

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/translation="MSYKGDIGVIGIAVMGQNLILNMNDHGFKVVAYNRTTSKVDEFL
QGAAKGTNIIGAYSLEDLAAKLEKPRKVMLMYRAGDVVDGTEALLPHLEEGDIIIDG
GGAAKGTNIIGAYSLEDLAAKLEKPRKVMLMYRAGDVVDGTEALLPHLEEGDIIIDG
GNANYPDTNRRYKALARKGIRFIGSCOVSGEEGRARGPSIMPGGNOEAMQYVRFIFQA
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AIFAEWKNTELDSYLLDITTDILGYKDASGEPLVBKILDFAQGKGTGKWTGINADFG
AIFAEWKNTELDSYLLDITTDILGYKDASGEPLVBKILDFAQGKGTGKWTGINALDFG
TPLILITERSPSEQFGOWDINYGATALLMREGGIIRSRFLGNHIBDAYRALLASKIIS
YAGGFWLIRBASEQFGWDINYGATALLMREGGIIRSRFLGNHIBDAYBANDRUFGKST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MISITAESCELENIPFYOFAQMKKECPEDIPAIKADYKLHWDNW KAIIOSVSAQLGTPPAKPHIESWTNOWQVRAHFFAYFKYEFNONSAAIFSVLLHRRRL KAIIOSVSAQLGTPFALPROINWOOVRQWLDOFPETHWREDESEXDDFRQVKVISEK NLILESDEDFWGIGKSIEKAELMQIDPVLFITHTIOQLOPLYDRCHQ" complement (1676. 3130)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MATYFVGDLQGCYDELQLLLERVDFNPTQDKLYLVGDLVARGDK
SLECLRFVKSLGNAAQTVLGNHDLHLIATALDIKKVRPRDYVDAIFNBADFDELHWL
RHQPLLVHNEKLNFLMSHAGISPDWDLKTAKSCAAGVEQILQHGDFHYLIENWYSEQP
RHWSPDLOGLARHRY INAFTRANFCYLDHRFDFACKSPLKOAPAGELTPWFNDNPLY
KQIPIVFGHWASLVDEPTPKGIYALDTGCVWNNRMTMLRWEDKQFFTQSAVKNYSDF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to GB:D10483 SP:P05637 GB:X04711 PID:216474 PID:40919 percent identity: 52.77; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to SP:P70718 PID:1651212 percent identity: 91.53; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="H. influenzae predicted coding region H10552"
/protein_id="AAC22216.1"
/db_xref="GI:1573538"
                                                                                                                  Submitted (28-MXY-1998) The Institute for Genomic Research, 9715 Medical Center Dr. Rockville, MD 20850, USA The whole genome was shifted by 588 nucleotides for a new start on Sep 30, 1996 this sequence version replaced gi:1221227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="hypothetical protein; identified by GeneMark; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="hypothetical protein; identified by GeneMark;
                White,O., Clayton,R.A., Kerlavage,A.R., Fleischmann,R.D., Peterson,J., Hickey,E., Dodson,R. and Gwinn,M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
/product="diadenosine-tetraphosphatase (apaH)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/transl_table=11
/product="6-phosphogluconate dehydrogenase,
                                                                                                                                                                                                                                                                                                          /organism="Haemophilus influenzae Rd"
/db_xref="taxon:71421"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAHTYERTDKPRGEFFHTNWTGRGGNTASTTYDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             decarboxylating (gnd)"
/protein_id="AAC22210.1"
/db_xref="G1:1573539"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAC22209.1"
/db_xref="GI:1573537"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(1676. .3130)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity; putative" /codon_start=1
                                                                                                                                                                                                                                                        Location/Qualifiers
1. .10195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="HI0553"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="H10552"
927. .1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="HI0554"
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                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="HI0551"
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(bases 1 to 10195)
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/transl_table=11

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INQOMQLNDLGNYVRQCWENIPMFFFQVRIDEFVIMPNHLHGIIEIIEQVKGKCNLPL
QLRATQLPQKGTSQTIGSIVRRFKAGVTSWARKNSEIFDVWQRNYYEHIIRDEKSYLQ
IYEYIQNNPILWEQDQLYVD"
                                                    /db_xref="G1:1573540"
/translation="MTTKYNAGIHHRRSIRLKHYNYRSEGFYFITICCKNKECLFGHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MEILAYILTALVTLEHFYILXLEMFTIESKSGVRGSRVIQRLFG
SRDYFWLCHOPNFGDLFLFRLCDYRRSFWGSYDED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MYPSDPESNYGEVQKLLFDHIOIPAENIHRIRGENEPHFELKR
FEBELSAVIPNGVFDWIILGMGIDGHTASLFPHQTNFDDENLAVIAKHPESGQIRISK
TAKLIEQAKRITYLVTGESKADILKEIQTTPAENLPYPAAKIKAKNGVTEWYLDKAAV
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LIDKYQTCGWTFYYMSTPFSLYGYTBECLAAHGLWEETGWRRIIVERFGYDEKTAO
LIDVOQHRFFEEDHQIYRIDHYLGKETVONLLVLRFSNGWFEDHWRNRIDDYBLTGAE
SIGVERGGYTDGSGAARDMRONHLLQYLAAVAMEPPAIIANNSMDEVARVHSLRE
PITSEDMENNLVLGGYTPAEINGKMENGYLERGGYPANSRTFTYIALRCEIENWRWAGV
PETYVRTGKRLPARVFEIVIHRYTFPHPVFSQNAPENKLIIRIQPDEAISMRRGLKRG
AGFEAKEVSMOFRYADLAGAQVLTAYERLLLDAMKGDATLEARTDAVHAAWKFVQDIL
DYKANGGRIHPYEAGTWGPVAADKLIAKQGKVWRKPSGLMKKV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(5264. .6748)
/gene="HI0558"
/note="similar to SP:P77809 PID:1651208 percent identity: 85.22; identified by sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to SP:P46016 PID:556607 percent identity: 35.82; identified by sequence similarity; putative"
/product="H. influenzae predicted coding region HI0554"
/protein_id="AAC22217.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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complement[5264. 6748)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(5059. .5181)
/gene="H10557"
/note="hypothetical protein; identified by GeneMark;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="glucose-6-phosphate 1-dehydrogenase (zwf)"
/protein_id="AAC22213.1"
/db_xref="GI:1573543"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="oxidoreductase, putative (devB)"
                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
/product="conserved hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAC22211_1"
/db_xref="G1:1573541"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAC22212.1"
/db_xref="G1:1573542"
                                                                                                                                                                                        complement(4243. .4482)
                                                                                                                                                                                                                                                complement(4243. .4482)
/gene="H10555"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(4482. .4973)
/gene="H10556"
complement(4482. .4973)
/gene="H10556"
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/gene="HI0557"
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/transl_table=11
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                                                                                                                                                                                                                        /gene="HI0555"
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PID:145690 percent identity: 36.07; identified by sequence
                                                                                                                              /translation="MTEADLFVSQFLTEKLTALFPNVPVLSEENCHISFEERKNWKEY
                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; Rosidae; Capparales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1630)
Firk,A., Greppin,H. and Tacchini,P.
Nucleotide sequence of a cDNA encoding the glucose-6-phosphate dehydrogenase from Arabidopsis thallana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.thaliana mRNA for glucose-6-phosphate dehydrogenase (clone E5).
                                                                                                                                                                                                                                                              53 agggatggaatcgcataatatttgagaagccatttggctttgatgcactttctcccata 112
                                                                                                                                                                                                                                                                                                             113 ggctgacacaatatcttctttcaaactttcaggaaaagcaaatatatagaattgancatc 172
                                                                                                                                                                                                                                                                                                                                                                                         173 tactaggaaggaatcncagtnaaaatcctncaggtttaagggtttcaaannnagnttttg 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="leaves, stems, some flowers and roots"
/cell_line="A.thalian Co"
/clone_lib="lambda ZAP"
                                                                           /product="sulfite synthesis pathway protein (cysQ)"
                                                                                                                                                                                                            ö
                                                                                                                                                                         Length 10195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (23-7AN-1995) A.F.A. Fink, Lab de 31C ir
Physiologie, Vigitales, Universiti de Geneve, 3 placs on
1'Universiti, 1211 Geneva, SWITZERLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="glucose-6-phosphate 1-dehydrogenase"
/protein_id="CAA59011.1"
                                                                                                                                                                     Score 61.4; DB 65; Length
Pred. No. 6.7e-06;
0; Mismatches 101; Indels
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                                                                                             /protein_id="AAC22214.1"
/db_xref="GI:1573544"
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/dev_stage="adult"
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/codon_start=2
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FGTEGRGGYFDNYG ITRDIMONHLLQILALEAMETPWSLDAEDIRNRVWLRSMRPI
RVEDVVIGQYKSHTKGGYTYPAYTDDKTVPKGSLIPPTFAAAALFIDNARWDGVPFLMK
AGKALHTRASBIRVQFRHYPORLYNRWTGSDLOGATNBLLVHRVQPDEALYFKINNKVP
GLGMRLDRSNINLLYSARYSKEIPDAYFRLLLDAIEGERRLFIRSDELDAAWSLFTPL
IKEIEBKKRIPPYFYGSRGPVGAHYLAAKHKVQWGDVSIDQ"
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Submitted (23-58P-1998) vonSchaewen A., Plant Physiology,
University Osnabrueck, Barbarastr. 11, D-49069 Osnabrueck, GERMANY
On Sep 25, 1998 this sequence version replaced 91:3021530.
                                        /translation="QSQSTVSITVVGASGDLAKKKIFPALFALYYEGCLPEHFTVFGY
SRSKMTDVELRNMVSKTLTCRIDKRANCGEKMEEFLKRCFYISGQYDSQEHFIELDKK
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Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Asteridae; euasterids I; Solanales; Solanaceae;
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University Osnabrueck, Barbarastr. 11, D-49069 Osnabrueck, GERWANY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        von Schaewen, A. Evidence for functional convergence of redox regulation in G6PDH isoforms of cyanobacteria and higher plants Plant Mol. Biol. 40 (3), 487-494 (1999)
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Nicotiana tabacum mRNA for plastidic glucose-6-phosphate
Aehydrogenase TPG16.
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                      /db_xref="SPTREMBL:Q43728"
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glucose-6-phosphate dehydrogenase.
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Wendt,U.K., Hauschild,R., Lange,C., Pietersma,M., Wenderoth,I. and
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta: Tracheophyta;
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Plant Mol. Biol. 40 (3), 487-494 (1999)
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                                         /organism="Nicotiana tabacum"
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glucose-6-phosphate dehydrogenase.
                                                                                                           /cell_type="mesophyll"
                                                              /cultivar="Samsun NN"/db_xref="taxon:4097"
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von Schaewen, A.
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL158831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polyA_signal
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                                                                                gene
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                                                                                                                                                                                                   LRFSNLVFEPIWSRNYIRNVQLIFSEDFGTEGRGGFEDOYGIIRDIMONHLLQILALF
AMETPVSLDAEDIRSEKVKVLRSMKPLRLEDVVVGQYKGHNKGGKTYPGYTDDPTVPN
HSLTPTFAAAAMFINNARWDGVPFLMKAGKALHTRGAEIRVQFRHVPGNLYKKSFATN
                                                                                                                                                          MEQFIKRCFYHSGOYNSEEDFAELNKKIKEKEAGKISNRLYYLSSTPKILIVDEVRCAS
LRASSENGWTRVIVEKPFGRDSESSGELTRCLKQYLTEEQIFRIDHYLGKELVERLSY
                                                                                                                                                                                                                                                                  LDNATNELVIRVQPDEGIYLRINNKVPGLGMRLDPRDLNLLYRSRYPREIPDAYERLL
LDAIEAERRLFIRSDELDAAWELFTPALKEREEKKIIPELYPYGSRGPVGAHYLASKY
                                                                                               /translation="mathsmitdspsssssslataaspeketlplesrsltpprsle
SQVRLRFFAEKHSQLDTSNGCATNFASLQDSGDQLTEEHVTKGESTLSITVVGASGDL
                                                                                                                                         AKKKIFPALFALFYEGCLPQDFSVFGYARTKLTHEELRDMISSTLTCRIDQREKCGDK
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
euphyllophytes, Spermatophyta, Magnoliophyta, eudicotyledons;
Rosidae, Capparales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.thaliana mRNA for glucose-6-phosphate dehydrogenase (clone E15).
                 /product="plastidic glucose-6-phosphate dehydrogenase"
/protein_id="CAA04696.1"
/db_xreff="GI:3021305"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 gcactttcttcccataggctgacacaatatcttctttcaaactttcaggaaaagcaaata 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 tatagaattgancatctactaggaaggaatcncagtnaaaatcctncaggtttaagggtt 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            728 AGAGCCTCCTCAGAGAATGGCTGGACAAGGGTCATTGTGGAAAAGCCATTTGGCCGTGAC 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               788 TCTGAATCATCCGGAGAGTTAACTAGATGTCTGAAACAGTATCTTACAGAGGAGCAAATC 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             848 TTCAGGATTGATCACTATTTGGGAAAGGAGCTTGTTGAGAACCTTTCAGTGCTCCGATTC 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fink, A., Greepin, H., and Tacchini, P.
Nucleotide sequence of a CDNA encoding the glucose-6-phosphate dehydrogenase (GenBank X84230) from Arabidopsis thaliana
Plant Physiol. 108, 1343-1343 (1995)
Ref [3]: Plant Gene Register PGR95-021 (1995).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 agtgctcagacccagaagggatggaatcgcataatatttgagaagccatttggctttgat 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (23-JAN-1995) A.F.A. Fink, Lab de Biochimie et Physiologie, Vigitales, Universiti de Geneve, 3 Place de l'Universiti, 1211 Geneva, SWITZERLAND
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1975;
                                                                                                                                                                                                                                                                                                                                                                                                           22.8%; Score 60; DB 8; Length 1975
52.5%; Pred. No. 1.5e-05;
tive 0; Mismatches 103; Indels
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thale cress.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               563 t
                                                                              /db_xref="SPTREMBL:065577"
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                                                                                                                                                                                                                                                                                                                               447 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /haplotype="diploid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="adult"
/codon_start=1
                                                                                                                                                                                                                                                                                                              NVRWGDLGEA"
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NLVFEPLWSRNY IRNVELIFSEDFGTEGRGGFPDQYGIIRDIHQNHLLQILALFAMET
VSLDAEDIRGEKVKVLRSMKPLRLEDVVVGQYKGHNKGGKTYPAYTDDPTVPNHSLT
PTFAAAAMFINNARMDGVPFLMKAGKALHTRGAEIRVQFRHYFGKLKKKSFAVNLDNA
TNELVIRVQPDGGIILLAINNKVPGLGMRLDRSDLMLLYRSKYPREIPDAYBRLLLDAI
EGERRLFIRSDELDAAWDLFTPALKELEEKKIIPELYPYGSRGPVGAHYLASKYNVRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (21-MXY-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           581 ATTCGTTGATGTGGTTAGGTGTGCAAGTCTTAGAGCCTCCTCAGAGAATGGCTGGACAAG 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 cataatatttgagaagccatttggctttgatgcactttctcccataggctgacacaata 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               641 GGICATIGIGGAAAAGCCATIIGGICGIGACICIGAAICAICGGAGAGTIAACIAGAIG 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 tettettteaaaettteaggaaaageaaatatatagaattganeatetaetaggaaggaa 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 teneaginaaaateeineaggittaagggitteaaannnagnittigageeaeeiingag 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      761 GCTTGTTGAGAACCTTTCAGTGCTCCGATTCTCAAATCTTGTTTTCGAGCCTCTGTGGTC 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 acttttggatgttgcgtcatgtcttgcaagcagtgctcagacccagaagggatggaatcg 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens chromosome 9 clone RP11-564A4, *** SEQUENCING IN PROGRESS ***, 33 unordered pieces.
/tissue_type="leaves, stems, flowers and roots"
/cell_line="A.thaliana Co"
/clone_lib="lambda ZAP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1772;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 59; DB 8;
Pred. No. 2.8e-05;
                                                                                                                                                                      /EC_number="1.1.1.49"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  419 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
                                                                                                                                                                                               /codon_start=1
                                                                                                      /gene="G6pDH"
141. .1685
                                                                                                                                                    /dene="G6PDH"
                                                             /clone="E15"
141. .1685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.4%;
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AL158831.5 GI:9212620
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1756. .1761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.4%
Matches 125; Conservative
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us-09-300-482-4.rge

COMMENT

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103148 103247: gap of 100 bp 104758 104757: contig of 1510 bp in length 104758 104857: gap of 100 bp 104858 106680: contig of 1823 bp in length 106681 106788: gap of 100 bp 106781 108222: contig of 1442 bp in length 10823 108322: gap of 100 bp 108323 109526: contig of 1204 bp in length 109527 109628: gap of 100 bp 109527 109628: gap of 100 bp 109527 109628: gap of 100 bp 109527 109627 155013: contig of 46387 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211582: contig of 12522 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199061 211582: ccm--, 211583 211682: gap of 100 bp 210583 220373: contig of 8691 bp in length.
                                                                                                                                                                                                                                                                                                                                                             ap of 100 bp
contig of 27096 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                           189786 189885: gap of 100 bp
189886 198960: contig of 9075 bp in length
198961 199060: gap of 100 bp
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/note="assembly_fragment:00723

fragment_chain:2"

34827...36278

7.0nte="assembly_fragment:00747

fragment_chain:3"

63799...57138
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/note="assembly_fragment:00108
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57239. 6130
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/note-"assembly_fragment:01455
fragment_chain:3"
61496. .63183
/note-"assembly_fragment:01321
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73190. .81026
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68976. .71548
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/note="assembly_fragment:00187"
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/note="assembly_fragment:01175
fragment_chain:4"
64447. .66218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20674. .22382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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                                                                                                                                                                                                                                                   Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08755; 100% of reads Sequencing vector: plasmid; L08755; 100% of reads Consensus quality: 200906 bases at least Q40 Consensus quality: 213166 bases at least Q30 Consensus quality: 213166 bases at least Q30 Insert size: 217173; sum-of-contigs Insert size: 317787; agarose-fp Quality coverage: 3.42x in Q20 bases; sum-of-contigs Quality coverage: 3.42x in Q20 bases; sum-of-contigs Quality coverage: 4.71x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is
                        On Jul 15, 2000 this sequence version replaced gi:7939701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  p of 100 bp contig of 20760 bp in length
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100313 103147: contig of 2835 bp in length
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contig of 1850 bp in length
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88550: contig of 5474 bp in length
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89972; contig of 1322 bp in length
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100212: contig of 3046 bp in length
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73089: contig of 1441 bp in length
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36278: contig of 1452 bp in length
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contig of 4157 bp in length
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68875: contig of 1191 bp in length
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71548; contig of 2573 bp in length
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81026: contig of 7837 bp in length
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19505 20573: contig of 1069 bp in length
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22382: contig of 1709 bp in length
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63183: contig of 1688 bp in length
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                                                                                                                                                                                 Contact: humquery@sanger.ac.uk
------ Project Information
Center project name: bA564A4
                                                                                                                                                     Web site: http://www.sanger.ac.uk
                                                              Center: Sanger Centre
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FPONTRUPELYYLAVPSQVPEMVYHHYBESGRTORGMNRIYMERPEPTYKLIDGELUNFEDS
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                                                                                                                                        Direct Submission
Submitted (27-MAY-1998) von Schaewen A., Pflanzenphysiologie,
Universitaet Osnabrueck, Barbarastr. 11, 49076 Osnabrueck, GERMANY
Location/Qualiflers
                 von Schaewen,A.
Evidence for functional convergence of redox regulation in G6PDH isoforms of cyanobacteria and higher plants
Plant Mol. Biol. 40 (3), 487-494 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     749 AAGTATTIGAAAATGIGGIACATCATGITCATGAAAGCGGAAGACGCAACGAGGTIGGA 808
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321 c 404 q 628 t
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    1976
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259. .1845
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von Schaewen, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCA6546 1976 bp mRNA PLN 17-AUG-1999 Cyanidium caldarium mRNA for glucose-6-phosphate 1-dehydrogenase. AJ006246 G:5734371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91164 TGCAGAAAATTAAATAATCAAATAAGAAAGTCTTTTAAAGAAGAAGAATATTTAGAAT 91105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 gacccagaagggatggaatcgcataatatttgagaagccatttggctttgatgcactttc 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 ttcccataggctgacacaatatcttctttcaaactttcaggaaaagcaaatatatagaat 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 58.4; DB 64; Length 220373;
Pred. No. 4e-05;
0; Mismatches 99; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales;
Porphyridiaceae; Cyanidium.
1 (bases 1 to 1976)
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103248...104757
/note="assembly_fragment:01234"
104858..106680
/note="assembly_fragment:01312"
106781..108222
/note="assembly_fragment:01421"
106781..108222
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/note-"assembly_fragment:00180
fragment_chain:5"
199061. .211582
/note-"assembly_fragment:00696
fragment_chain:5"
33077. .88550
/note="assembly_fragment:00825"
                                                        /note="assembly_fragment:00990"
90073. .94252
                                                                                             'note="assembly_fragment:01020"
                                                                                                         /note="assembly_fragment:01173"
100313. .103147
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fragment_chain:5"
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/note="assembly_fragment:01298
fragment_chain:5
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52.6%;
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                  Unpublished
2 (bases 1 to 3015)
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Muscomorpha; Tephilitidae; Anastrepha.

I (bases 1 to 463)
Soto-Adames,F.N., Robertson,H.W. and Berlocher,S.H.

Phylogenetic utility of partial DNA sequences of G6PDH at different taxonomic levels in Hexapoda with emphasis on Diptera
Ann. Entomol. Soc. Amer. 87, 723-736 (1994)
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Anastrepha suspensa glucose-6-phosphate dehydrogenase mRNA, partial
                                                                                                                                                                                                                                                                                                                                    Direct Submission Submission (19-APR-1994) Felipe N. Soto-Adames, Entomology, Submitted (19-APR-1994) Felipe S. Goodwin Ave., Urbana, IL 61801, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus/Staphylococcus group; Staphylococcus.

(bases 1 to 3015)

Kimmerly,W.J., Taylor,J.David, Nelsen,A.J., Godlevski,M.M.,
Rubino,M.A., Nelson,F.J., Rivers,P.R., Torruella-Miller,I.,
Listenbee,S., Ashanti,C., Altshuller,G., Mamo,L., Shepherd,N.S.,
Fuchs,R., Fleming,T., Guan,X., Du,L., Cain,D.H., Miller,G.S. and
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                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.5%; Score 56.6; DB 30; Length 463; 61.8%; Pred. No. 0.00011;
Live 0; Mismatches 55; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"glucose-6-phosphate dehydrogenase"
/protein_id-"AAB02776.1"
/db_xref="G1:606622"
                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Anastrepha suspensa"
/db_xref="taxon:28587"
/note="partial sequence from PCR product"
<1. .>463
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Staphylococcus epidermidis
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Best Local Similarity
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Submitted (22-MAY-2000) Departments of Genomic Sciences and Bioinformatics, Genetics Directorate, Glaxo Wellcome, Inc., 5 Moore
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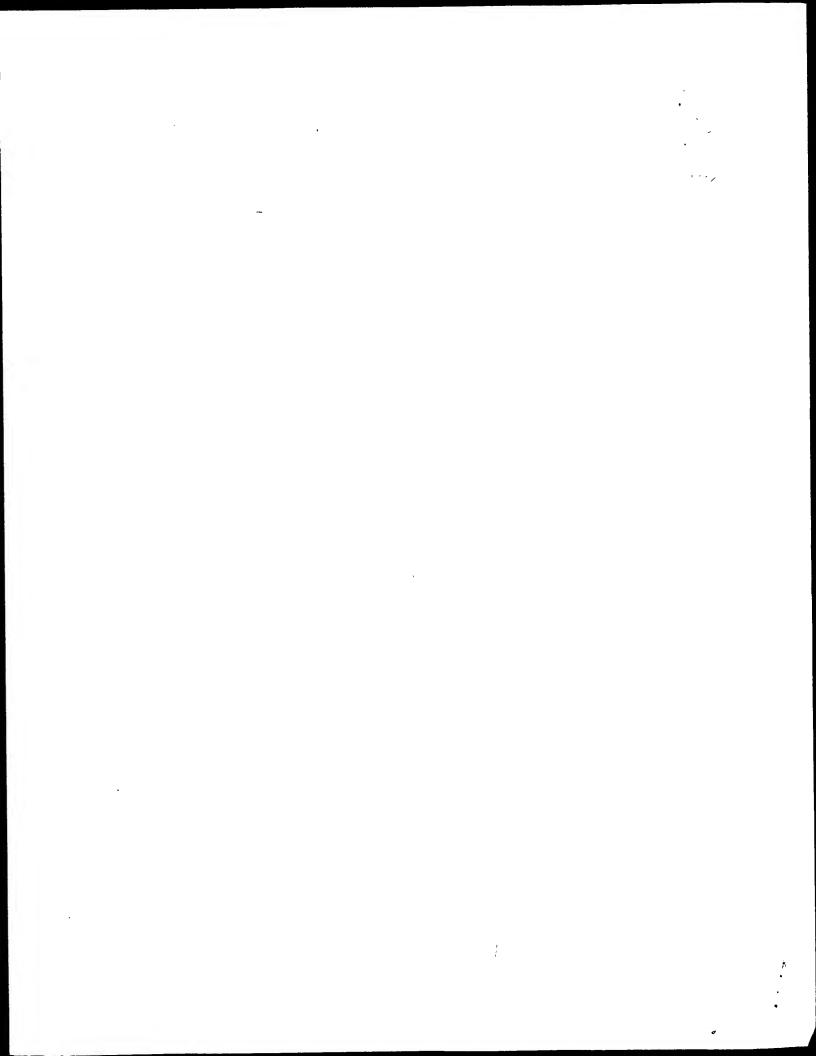
1 (bases 1 to 3081)

Kimmerly, W.J., Taylor, J. David, Nelsen, A.J., Godlevski, M.M.,
Rubino, M.A., Nelson, F.J., Rivers, P.R., Torruella-Miller, I.,
Listenbee, S., Ashanti, C., Altshuller, G., Mamo, L., Shepherd, N.S.,
Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D.H., Miller, G.S. and
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Rubino,M.A., Nelson,F.J., Rivers,P.R., Torruella-Miller,I.,
Listenbee,S., Ashanti,C., Altshuller,G., Mamo,L., Shepherd,N.S.,
Fuchs,R., Fleming,T., Guan,X., Du,L., Cain,D.H., Miller,G.S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF269560 3081 bp DNA BCT 01-AUG-2000 Staphylococcus epidermidis strain SR1 clone step.1010e05 genomic
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Taylor, J. David, Kimmerly, W.J., Nelsen, A.J., Godlevski, M.M., Rubino, M.A., Nelson, F.J., Rivers, P.R., Torruella-Miller, I., Listenbee, S., Ashanti, C., Altshuller, G., Mamo, L., Shepherd, N.S., Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D.H., Miller, G.S. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1315 GAACGTAAAAGGGGTGATGCGAATAATTATAGAAAAACCATTTGGTGATGATTTAAAATC 1374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 tgancatctactaggaaggaatcncagtnaaaatcctncaggtttaagggtttcaaannn 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 gacccagaagggatggaatcgcataatatttgagaagccatttggctttgatgcactttc 104
                                                                                                                                                                                                        Submitted (19-MAY-2000) Departments of Genomic Sciences and Bioinformatics, Genetics Directorate, Glaxo Wellcome, Inc., 5 Drive, Research Triangle Park, North Carolina 27709-3398, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 3015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                 /organism="Staphylococcus epidermidis"/strain="SR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 54; DB 1;
Pred. No. 0.00053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  978 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 20.5%; Score 54; DB Best Local Similarity 54.5%; Pred. No. 0.00 Matches 114; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1493 TATATTGAACCACTTTGGAATAATAAGT 1521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225 agnttttgagccaccttngagnngnacnt 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:1282"
/clone="step:1002e12"
1 384 c 515 g
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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Drive, Research Triangle Park, North Carolina 27709-3398, USA
Location/Qualifiers
1. 3081
/organism="Staphylococcus epidermidis"
/strain="SR1"
/db_xref="taxon:1282"
/db_xref="taxon:1282"
/clone="step.1010e05"
963 a 528 c 419 g 1171 t
                                                                                                                                                        BASE COUNT
                           FEATURES
                                                                                                                                                                            ORIGIN
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2286 T--GCAAAAATTAAATAATCAAATAAGAAAGTCTTTTAAGAAGAAAAAAATTTGGAAT 2229 105 ttcccataggctgacacaatatcttctttcaaactttcaggaaaagcaaatatatagaat 164 Query Match 20.5%; Score 54; DB 1; Length 3081; Best Local Similarity 54.5%; Pred. No. 0.00053; Matches 114; Conservative 0; Mismatches 93; Indels QQ δ

Search completed: November 4, 2000, 13:30:39 Job time: 16888 sec



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November 4, 2000, 13:40:19; Search time 320.8 Seconds (without alignments) 307.978 Million cell updates/sec
                                                                                                                                                                                                                           1 gaagcacttttggatgttgc.....agnngnacntnnnnganna 263
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                    OM nucleic - nucleic search, using sw model
                                                                                                                                                                                         US-09-300-482-4
263
                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                         Sequence:
                                                                                                            Run on:
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IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

480022 segs, 187831343 residues Searched:

960044 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Databas

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Enterococcus faeca Staphylococcus aur G6PD coding sequen Essential Staphylo Streptococcus pneu DNA encoding a S. Streptococcus pneu Thermostable gluco Polynucleotide seq Glucose-6-phosphat Polynucleotide seg Brevibacterium fla
SUMMARIES	X13065 V74364 V38808 A28852 V32895 V65241 V56039 V56039 V56039 V56039 V56030 V5
	20 118 119 119 110 110 110
Query Amatch Length DB	32768 16592 2750 2494 1488 2764 13121 1488 10820 1482 254
% Query Match	22.1 19.4 19.2 18.9 18.3 17.0 17.0 15.1 15.1
Score	58.2 511.4 50.6 49.6 488 444.8 44.8 44.8 39.8
Result No.	C C C C C C C C C C C C C C C C C C C

H. Pylori cytoplas Leuconostoc lactis Leuconostoc dextra Leuconostoc citreu L.dextranicus gluc Stealth virus nucl Scarface 3 gene co Human growth facto	Human Stealt Human EST cl Human Malari Nucle	Hereditary haemoch Human nibrin DNA. Human growth facto Leuconostoc mesent GlC6PD genome. Le Human IL-Ira BAC c Probe sequence for BPV1 LI ORP. Bovi	om ce Sin in
T68126 T30576 T30577 T30575 T30575 X84323 X34730 X33972	245852 X654322 X65255 V86185 X83003 N90223 X91990 Z52939	V5/903 289046 234650 T30574 Q24526 X02998 X89755 Q47166	047167 V23923 V24099 V25817 V25818 V09855 V12162
1368 X333 X333	X83 X83 X83 X83 X83 X83	X X X X X X X X X X X X X X X X X X X	047 V23 V25 V25 V09 V09
18 110 110 110 110 110 110 110 110 110 1	1200118	12 21 13 13 20 20 14	110 110 110 110
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44444444444444444444444444444444444444			11.3 11.3 11.3 11.3 11.3 11.3
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113 115 117 118 119 20 21	22 22 23 23 30	332 332 34 37 37 37 37	00044444 00012645
υ	0 00	U	

ALIGNMENTS

X13065	
13065	standard; DNA; 32768 BP.
x13065;	
19-MAR-1999	(first entry)
Enterococcus	faecalis genome contig SEQ ID NO:128.
Enterococcus vaccine; atte	Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.
Enterococcus	faecalis.
WO9850555-A2.	
12-NOV-1998.	
04-MAY-1998;	98WO-US08985.
14-NOV-1997; 06-MAY-1997;	97US-0066009. 97US-0044031.
16-MAY-1997;	97US-0046655.
(HUMA-) HUMAN GENOME SCI	GENOME SCI INC.
Barash SC, D	Dillon PJ, Kunsch CA;
WPI; 1999-045171/04.	171/04.
New isolated - used to dev- use in vaccin- infection.	. New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus infection.

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"these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
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given in the specification for this DNA sequence"
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are included to maintain the nucleotide numberin
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                                                             A computed retaining that the first the form the Enterococcus facealist genome. X12938 to X13919 represent these nucleotide sequences isolated from the Enterococcus facealist genome. X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as configs. The computer-based system can identify fragments of the Enterococcus facealist genome with commercial importance. The products can be used to detect the presence of Enterococcus facealis in samples. They can also be used for diagnosing Enterococcual infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus facealis, or modulate related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus facealis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19353 aattaaatgaagaaattcgtgctgcatttcctgaacaagatattttccgaattgaccatt 19412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19413 acttaggcaaagaaatgatccaaaatatttcagccattcgttttgccaataatatttttg 19472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19293 aaggetttgategtetaattategaaaageeatttggttetgattatgaatetgeetaeg 19352
                                                computer readable medium has been developed which has recorded on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 agggatggaatcgcataatatttgagaagccatttggctttgatgcactttctcccata 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 ggctgacacaatatcttctttcaaactttcaggaaaagcaaatatatagaattgancatc 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 tactaggaaggaatcncagtnaaaatcctncaggtttaagggtttcaaannnagnttttg 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 32768;
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 32768 BP; 9529 A; 6883 C; 5611 G; 10720 T; 25 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 58.2; DB 20;
Pred. No. 9.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 19473 aatcacaatggaacaatcgttacattgataa 19503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 agccacctingagnngnacninnnnnganna 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus contig SEQ ID #53.
Claim 1; Page 767-783; 2084pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
121..180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.1%;
51.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       toxic shock syndrome; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification tor this DNA sequence"
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                                                                                                                                                                                                                                                                                                                                                                                       these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
     "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
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the sequence listing in the specification. They
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kunsch CA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 403-413; 3271pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-374922/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
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the S.aureus DNA sequences allows putative functions to be assigned so industrial importance can be obtained. Specifically, sequences which are likely to encode antiqens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The S.aureus in a sample. S.aureus is implicated in numerous human diseases, skin and surgical wound infections, food poisoning, osteomypalitis, syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences homologues of any of the S.aureus is implicated in numerous toxic shock for recombinant production of the polypeptides. The new DNA sequences homologues of any of the S.aureus bDNA sequences for isolating
                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                 52 aagggatggaatcgcataatattgagaagccatttggctttgatgcactttcttcccat 111
                                                                                                                                                                                                                                                                                                                                                                                                                814 aaaggatttaaaacgccttgttatcgaaaaaccattcggtagtgatttaaaatcagccgaa 873
                                                                                                                                                                                                                                                                                                                                                                                          112 aggotgacacaatatotttctttcaaactttcaggaaaagcaaatatatagaattgancat 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 ctactaggaaggaatcncaginaaaatccincaggiitaagggiitcaaannnagniiit 231
                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polymerase chain reaction; glucose-6-phosphate dehydrogenase; PCR;
                                                                                                                                                                                                                                                                                Length 16592;
                                                                                                                                                                                                                            Sequence 16592 BP; 5028 A; 3005 C; 2294 G; 5653 T; 612 other;
                                                                                                                                                                                                                                                                                                              99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E. coli; G6PD; drug; transformation; primer; amplify; ss.
                                                                                                                                                                                                                                                                        19.5%; Score 51.4; DB 18;
51.0%; Pred. No. 7.9e-06;
tive 0; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            994 gaaccattatggaataacaaat 1015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q38808 standard; DNA; 2750 BP
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                                                                                                                                                                                                                                                                                                   Matches 103; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaslow DC, Shahabuddin M;
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/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum.
                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G6PD coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1993-117467/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; R33424.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9306125-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1993
                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   038808;
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The present sequence represents an essential Staphylococcus aureus gene. The invention relates to a method for screening for an antibacterial agent. The method comprises determining if a test compound is active against the essential bacterial genes (A26850-A26956). The invention also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Essential gene; Staphylococcus aureus infection; screening; prevention; antibacterial agent; bacterial infection; ss.
                                                                                                                                                                                                                                                                                                                                        52 aagggatggaatcgcataatatttgagaagccatttggctttgatgcactttctcccat 111
                                                                                                                                                                                                                                                                                                                                                                                  112 aggotgacacaatatottcotttcaaactttcaggaaaagcaaatatatagaattgancat 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                172 ctactaggaaggaatcncaginaaaatccincaggiitaagggiitcaaannnagniit 230
                                                                                          This sequence encodes Plasmodium falciparum glucose-6-phosphate dehydrogenase (GGPD). This sequence was isolated using the primers given in 038806-07. This sequence was used in the production of transformed E. coli which produce a recombinant P. falciparum G6PD. These transformed cells can be used in a method of screening drugs for activity against P. falciparum G6PD.
DNA segments encoding Plasmodium falciparum G6PD obtd. by PCR used to express proteins and raise antibodies for diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel methods for screening for antibacterial agents, useful for treatment or prevention of Staphylococcus infection, by testing compounds against, essential bacterial genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Malouin F;
                                                                                                                                                                                                                                                              Length 2750;
                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                        Sequence 2750 BP; 1164 A; 260 C; 323 G; 1003 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sun D,
                                                                                                                                                                                                                                                                                            83;
                                                                                                                                                                                                                                                       Query Match 19.4%; Score 51; DB 14; Best Local Similarity 53.6%; Pred. No. 5.9e-06; Matches 96; Conservative 0; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schmid MB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Column 35-38; 256pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Essential Staphylococcus aureus gene #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Benton B, Lee VJ, Martin PK,
                                                               Claim 1; Fig 1; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A26852 standard; DNA; 2494 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0714918.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MICR-) MICROCIDE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-0003798
95US-0009102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JUN-2000 (first entry)
                                 treatment of malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-282222/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-SEP-1995;
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                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae glucose 6-phosphate dehydrogenase encoding DNA.
includes a method for evaluating an agent for activity on the essential genes. Also included in the invention is the production of an antibacterial agent. The antibacterial agents of the invention are used to treat or prevent bacterial infections, particularly where caused by stabhylococcus aureus. The antibacterial agents are unlikely to be affected by known resistance mechanisms.
                                                                                                                                                                                                                                                                                                                                                                                                                       1425 AAAGGATTTAAAACGCCTTGTTATCGAAAACCATTCGGTAGTGATTTAAAATCAGCCGAA 1366
                                                                                                                                                                                                                                                                                                                                                               1365 GCATTAAACAATCAAATTCGTAAATCATTTAAAGAAGAAGAAATTTAYCGTATKGACCAC 1306
                                                                                                                                                                                                                                                                                                                           112 aggetgacacaatatettettteaaaettteaggaaaagcaaatatatagaattgancat 171
                                                                                                                                                                                                                                                                                                                                                                                                 172 ctactaggaaggaatcncagtnaaaatcctncaggtttaagggtttcaaannnagntttt 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents the Streptococcus pneumoniae glucose 6-phosphate dehydrogenase (G6PD) encoding DNA sequence. The
                                                                                                                                                                                                                                                    52 aagggatggaatcgcataatatttgagaagccatttggctttgatgcactttcttcccat 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding glucose-6-phosphate dehydrogenase - isolated from Streptococcus pneumoniae, used to treat, prevent and diagnose infections, especially meningitis
                                                                                                                                                                                                                    ;
                                                                                                                                                                                Length 2494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/product= "Streptococcus pneumoniae G6PD"
                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glucose 6-phosphate dehydrogenase; G6PD; meningitis; ds
                                                                                                                             Sequence 2494 BP; 809 A; 396 C; 389 G; 880 T; 20 other;
                                                                                                                                                                              Score 50.6; DB 21;
Pred. No. 7.5e-06;
2; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Fig 1-1B; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1245 GAACCATTATGGAATAACAAAT 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 gagccacctingagnngnacnt 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                    19.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V32895 standard; DNA; 1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-OCT-1998 (first entry)
                                                                                                                                                                                                       Best Local Similarity 50.09
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-379058/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; W49070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JAN-1997;
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                                                                                                                                                                                        Query Match
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V32895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding a S. pneumoniae protein having function in cell division.
                                                                                                                                                                                                                                                                                                                                                                           172 ctactaggaaggaatcncagtnaaaatccincaggittaagggittcaaannnagniitt 231
                                                                                                                                                                                                                                                                                                                                                                                               52 aagggatggaatcgcataatatttgagaagccatttggctttgatgcactttcttcccat 111
                                                                                                                                                                                                                                                                        412 aaaggttttgagcgcttgatcgttgaaaaaccatttggtacagattacgcaactgcaagc 471
                                                                                                                                                                                                                                                                                                        S. pneumoniae G6PD DNA and protein are claimed to be useful for treating, preventing and diagnosing S. pneumoniae infections such as meningitis. Primers (V32896-V32897) and probes based on the G6PD DNA sequence are claimed to be useful for determining the stage and type of infection, and also for identifying and isolating related
                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae nucleic acid sequences - used in DNA chips for evaluating gene expression, and identification of virulence
                                                                                                                                                                                                                                                                                                                                          472 aagttgaatgacgaactectageaacatttgacgaagaacaaatttteegtattgaecat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae protein; recombinant; gene expression; DNA chip; virulence; antibody; infection; detection; treatment;
                                                                                                                                                                        DB 19; Length 1488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dehoff BS, Hoskins JA, Jaskunas
Peery RB, Rockey PK, Rosteck PR;
Solenberg PJ, Treadway PJ;
                                                                                                                                                                      Score 49.6; DB 19; Length 1
Pred. No. 1.3e-05;
0; Mismatches 109; Indels
                                                                                                                      Sequence 1488 BP; 449 A; 328 C; 293 G; 418 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                232 gagccaccttngagnngnacntnnnnnganna 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               592 gaaaacgtttggaacaaggattttatcgacaa 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 94; 333pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V65241 standard; DNA; 2764 BP
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                                                                                                                                                                          Query Match
Best Local Similarity 48.6%;
Matches 103; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baltz RH, Burgett SG,
Mills BJ, Norris FH,
Skatrud PL, Smith MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ELIL ) LILLY & CO ELI
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                                                                                              sednences
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the protein sequences. The invention also provides a DNA chip having arrayed on it at least 15 base pair fragment of any one or more of these DNA sequences. The DNA chip can be used methods for evaluating gene expression in S. pneumoniae and for identifying virulence genes in S. pneumoniae. Antibodies that selectively bind to the above proteins or peptide fragments can be used to treat S. pneumoniae infection. The antibodies can also be used to detect S. pneumoniae cells.
the above nucleic acids can be used for the recombinant expression of
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Sequence 2764 BP; 829 A; 515 C; 646 G; 774 T; 0 other;

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                                                                                                         2743 AAAGGTTTTGAGGGGTTGATCGTTGAAAAACCATTTGGTACAGATTACGCAACTGCAAAC 2684
                                                                                                                                                                2623 TATCTTGGTAAGGAAATGATCCAAAGCATCTTGCAGTTCGCTTTGCAAACTTGATTTTT 2564
                                                                         52 aagggatggaatcgcataatatttgagaagccatttggctttgatgcactttctcccat 111
                                                                                                                                             112 aggotgacacaatatottcttcaaactttcaggaaaagcaaatatatagaattgancat 171
                                                                                                                                                                                                                   172 ctactaggaaggaatcncagtnaaaatcctncaggtttaagggtttcaaannnagnttt 231
                                                 0; Gaps
     18.3%; Score 48; DB 19; Length 2764; 51.3%; Pred. No. 4.6e-05; tive 0; Mismatches 94; Indels (
                                     99; Conservative
                                                                                                                                                                                                                                                                                                                             2563 GAAAACGTTTGGA 2551
                                                                                                                                                                                                                                                                                           232 gagccaccttnga 244
Query Match
Best Local Similarity
                                       Matches
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Streptococcus pneumoniae genome fragment SEQ ID NO:126. V52259 standard; DNA; 13121 BP. 23-OCT-1998 (first entry) RESULT 7 V52259 V52259;

Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay; computer readable medium; vaccine; pharmaceutical composition; ds. 97WO-US19588 Streptococcus pneumoniae 30-OCT-1997; WO9818931-A2 07-MAY-1998.

Dillon PJ, Dougherty BA, Fannon M; (HUMA-) HUMAN GENOME SCI INC. Choi GH, Barash SC, Kunsch CA,

Rosen CA;

960S-0029960.

31-OCT-1996;

WPI; 1998-272225/24.

Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus pneumoniae

Claim 1; Page 869-876; 1409pp; English.

The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (V52134 to V55524) recorded on it, or a representative fragment or a sequence at least 95% identical

(KIKK) KIKKOMAN CORP.

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to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:11 to 391 (V52134 to V52524) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced
                                                                                                 by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the
                                                                                                                                                                                                                                                                                                    S. pneumoniae genome of commercial importance, or expression modulating fragments of the S. pneumoniae genome. Products from the present
                                                                                                                                                                                                                                                                                                                                               invention can be used in diagnosis kits and assays, and pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3612 tatottggtaaggaaatgatocaaagcatotttgcagttcgctttgcaaacttgattttt 3671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3492 aaaggttttgagcgcttgatcgttgaaaaaccatttggtacagattacgcaactgcaagc 3551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 aagggatggaatcgcataatatttgagaagccatttggctttgatgcactttcttcccat 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 ctactaggaaggaatcncagtnaaaatcctncaggtttaagggtttcaaannnagntttt 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glucose-6-phosphate dehydrogenase; thermostable; heat-resistant; enzyme; recombinant; high stability; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 13121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "glucose-6-phosphate dehydrogenase"
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13121 BP; 3698 A; 3021 C; 2439 G; 3963 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermostable glucose-6-phosphate dehydrogenase encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 18.3%; Score 48; DB 19; Best Local Similarity 48.1%; Pred. no. 7.5e-05; Matches 102; Conservative 0; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                  compositions and vaccines for S. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3672 gaaaacgtttggaacaaggattttatcgacaa 3703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 gagccacctingagnngnacntnnnnnganna 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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transformant or a transductant containing a recombinant DNA in which the heat-resistant (thermostable) glucose-6-phosphate dehydrogenase gene is inserted to a vector DNA, can be cultured to produce the enzyme recombinantly. The method can prepare heat resistant glucose-6-phosphate dehydrogenase of high stability efficiently.
                                                                                                                                                                This DNA encodes a heat-resistant glucose-6-phosphate dehydrogenase. A
                                                                                                                                                                                                                                                                                                                                                                                                                             52 aagggatggaatcgcataatatttgagaagccatttggctttgatgcactttcttcccat 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  430 aatggttttaaccgattaattatcgaaaaacccttcggacgtgattatcccagcgctaaa 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 aggotgacacaatatottctttcaaacotttcaggaaaagcaaatatatagaattgancat 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         490 gaattgaattctaatttcgggttcctttaaagaagaacagatttttagaattgatcat 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 ctactaggaaggaatcncagtnaaaatcctncaggtttaagggtttcaaannnagntttt 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              550 tatttaggtaaggaaccgatccagtcaattgctggattacggtttggggaacgcattgttc 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treponema pallidum infection; syphilis; Borrelia infection; animal;
                                                                 Heat-resistant glucose-6-phosphate dehydrogenase gene - useful for
                                                                                                                                                                                                                                                                                                                                                       Match 17.0%; Score 44.8; DB 19; Length 1488; Local Similarity 47.2%; Pred. No. 0.00033; Local 100; Conservative 0; Mismatches 112; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polynucleotide sequence from the genome of Treponema pallidum.
                                                                              efficiently preparing hear-resistant glucose-6-phosphate dehydrogenase of high stability
                                                                                                                                                                                                                                                                                                   Sequence 1488 BP; 496 A; 249 C; 308 G; 435 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232 gagccacctingagnngnacntnnnnnganna 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        610 aactcgctttggaataaggaacatattgataa 641
                                                                                                                                         Claim 1; Pages 5-6; 7pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X20527 standard; DNA; 10820 BP
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                                                                                                                                                                                                                                                                                                                                                                                                 Matches 100; Conservative
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               WPI; 1998-513903/44.
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                                P-PSDB; W80567.
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6607 IGCGIGCCCACTITCAGGAAAACCAAACCIATCGCATCGATCACTATCTGGGTAAGGAAA 6548
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                                                                                detecting
                                                                                                                                                                                                                                                                                                          128 ttettteaaaettteaggaaaageaaatatatagaattganeatetaetaggaaggaate 187
                                                                                                                                                                                                                                                                                                                                                                    188 ncaginaaaatccincaggittaagggittcaaannnagnittigagccacciingagnn 247
                                                                                                                                                                                                                                               68 taatatitgagaagccatttggctttgatgcactttcttcccataggctgacacaatatc 127
                                  X20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detections diseases related to Borrella infections in animals, and for the production of biosynthetic products such as enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New glucose-6-phosphate dehydrogenase gene from Bacillus species used for expressing stable, very pure enzyme, useful in assay of creatine kinase.
                                                                                                                                                                                      Length 10820;
                                                                                                                                           Sequence 10820 BP; 2418 A; 2982 C; 2962 G; 2450 T; 8 other;
                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glucose-6-phosphate dehydrogenase; creatine kinase; ss.
                                                                                                                                                                                    Score 44.8; DB 20;
Pred. No. 0.00062;
0; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glucose-6-phosphate dehydrogenase gene.
         Claim 1; Page 343-349; 1150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         005236 standard; DNA; 1482 BP
                                                                                                                                                                                         17.0%;
48.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                6487 GGACCCATATCGATTA 6472
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                                                                                                                                                                                                                                                                                                                                                                                                                                    248 gnacntnnnnnganna 263
                                                                                                                                                                                                         Best Local Similarity 48.0
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; ; p; German
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TOXN ) TOYO JOZO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1990-211190/28
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V Match 15.1%; Score 39.8; DB 20; Length 554; Local Similarity 49.5%; Pred. No. 0.0074; hes 97; Conservative 0; Mismatches 98; Indels 1,

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Matches

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105 ttcccataggctgacacaatatcttttcaaactttcaggaaaagcaaatatatagaat 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         471 Cgcaaaaaaactaaatgaagaaatacgccaatcgttttcagaggagcaaattttccgtat 530
                                                                                                                                                                                                                                                                                                                                                                                           45 gacccagaagggatggaatcgcataatatttgagaagccatttggctttgatgcacttc 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 tgancatctactaggaaggaatcncagtnaaaatcctncaggtttaagggtttcaaannn 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     531 tgaccattatctcggcaaagaaatggtgcaaaacatcgaggtcattcgctttgcgaacgc 590
                                                                                                                                                                                                                                                                                                                                                        Gaps
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The protein produced, on culturing host cells transformed with a Vector contg. this sequence, is useful as a reagent for assaying creatine kinase. It has improved long term and thermal stability over known forms of the enzyme.
                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                           Ouery Match 16.0%; Score 42.2; DB 11; Length 1482; Best Local Similarity 46.1%; Pred. No. 0.002; Matches 101; Conservative 0; Mismatches 118; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotide sequence from the genome of Treponema pallidum.
                                                                                                                                                           Sequence 1482 BP; 473 A; 313 C; 328 G; 368 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225 agnttttgagccaccttngagnngnacntnnnnganna 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     591 cattitogaacogototoggaataacogotitatigocaa 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X21060 standard; DNA; 554 BP
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                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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T88030 standard; DNA; 2260 BP

RESULT 12

T88030;

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The present sequence encodes the Brevibacterium flavum JM-233 glucose-6-phosphate dehydrogenase (G-6-PD). The G-6-PD can be recombinantly produced by transforming coryneform bacteria with the DNA molecule encoding it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glucose-6-phosphate dehydrogenase - which can be recombinantly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          produced by transforming coryneform bacteria with DNA molecule encoding it
                                                                     Brevibacterium flavum glucose-6-phosphate dehydrogenase DNA.
                                                                                                         Brevibacterium flavum; glucose-6-phosphate dehydrogenase; recombinant production; coryneform; bacteria; bacterium; ds.
                                                                                                                                                                                                                                                    /product glucose-6-phosphate_dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2260 BP; 512 A; 659 C; 592 G; 497 T; 0 other;
                                                                                                                                                                                                 Location/Qualifiers 629..2083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Pages 6-8; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                  (MITU ) MITSUBISHI CHEM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                 96JP-0036345.
                                                                                                                                                                                                                                                                                                                                                                 96JP-0036345.
                                   22-DEC-1997 (first entry)
                                                                                                                                                               Brevibacterium flavum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-484096/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; W27612
                                                                                                                                                                                                                                                                                       JP09224661-A.
                                                                                                                                                                                                                                                                                                                                                                                             23-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                             23-FEB-1996;
                                                                                                                                                                                                                                                                                                                         02-SEP-1997
X20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrelia infections in animals, and for the production of blosynthetic products such as enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis
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Gaps

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Ouery Match 15.1%; Score 39.6; DB 18; Length 2260; Best Local Similarity 45.4%; Pred. No. 0.013; Matches 99; Conservative 0; Mismatches 119; Indels 0;

Sequence 554 BP; 141 A; 159 C; 126 G; 127 T; 1 other;

Claim 1; Page 1045; 1150pp; English.

(HUMA-) HUMAN GENOME SCI INC

WPI; 1999-081273/07.

Fraser CM;

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carbohydrate metabolism.

The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify H. Pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified
                                                                                                                                                            1091 gcacacgagetcaaccagetggtcaacgcagtetteccagaatettetgtgtteegcate 1150
                                1031 accgaagaagcatggcgccgcgtgatcatcgagaagcctttcggccacaacctcgaatcc 1090
                                                                   106 toccataggotgacacaatatottctttcaaactttcaggaaaagcaaatatatagaatt 165
                                                                                                                                      gancatctactaggaaggaatcncagtnaaaatcctncaggtttaagggtttcaaannna 225
46 acccagaaggatggaatcgcataatatttgagaagccatttggctttgatgcactttct 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence encodes a H. pylori cytoplasmic protein involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                    H. pylori cytoplasmic protein ORF 13ee10216orf43.
                                                                                                                                                                                                                                            1211 ctgtttgagccactgtggaactccaactacgttgacca 1248
                                                                                                                                                                                                           226 gnttttgagccaccttngagnngnacntnnnnnganna 263
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/note= "no stop codon given"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page 914; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                   T68126 standard; DNA; 780 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96WO-US09122
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                                                                                                                                                                                                                                                                                                                                                                                                       17-JUL-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Berglindh OT, Smith D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-052306/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter pylori.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-1995;
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                                                                                                                                                                                                                                                                                                     RESULT 13
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and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                                                                                         61 aatcgcataatatttgagaagccatttggctttgatgcactttcttcccataggctgaca 120
                                                                                                                                                                                            121 caatatottotttoaaaotttoaggaaaagcaaatatatagaattgancatotactagga 180
                                                                                                                                                                                                       412 actcgtttgattctagaaaagcctttagggcatgatttaaagacttgtaaagagttttc 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New mutant glucose-6-phosphate dehydrogenase enzymes - used partic.
to form conjugates for use in homogeneous immunoassays for analytes
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/note= "bases n at positions 1171-1185 are not
identified in the specification"
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/note= "bases n at positions 187-213 are not
identified in the specification"
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                                                                                       14.8%; Score 39; DB 18; Length 780; 54.3%; Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                Leuconostoc lactis glucose-6-phosphate dehydrogenase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Glucose-6-phosphate dehydrogenase; G6PDH; immunoassay; ss.
                                                                                                                  63; Indels
                                                   Sequence 780 BP; 244 A; 135 C; 154 G; 247 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caldwell RM,
Ullman EF;
                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key Location/Qualifiers misc_difference 187..213 /*tag= a
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Silen JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leuconostoc lactis strain NCDO 546.
                                                                                                                                                                                                                                                                                                                                         T30576 standard; DNA; 1461 BP
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                                                                                                                                                                                                                                                                misc_difference 1051..1089
                                                                                                                                                                                                                                                 181 aggaatcncagtnaaaat 198
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                                                                                   Ouery Match
Best Local Similarity 54.50

Local Similarity 54.50

Local Similarity 54.50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BEHRINGWERKE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYNT ) SYNTEX USA INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; R95963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09424559-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-APR-1994;
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Leuconostoc dextranicum ATCC 19255. The enzymes may be mutated to increase stability, or to improve or modulate activity, pref. by deletion or substn. of 1 or more lyshe residues, or introduction of 1 or more cysteine residues. The mutant enzymes are prepd. by mutating the G6PDH gene and expression in host cells. They are used partic, to form conjugates for use in homogeneous immunoassays for analytes.
                                 G6PDH genes (T30574-77) respectively code for the glucose-6-phosphate dehydrogenases (R95961-64) of Leuconostoc mesenteroides ATCC 12291, Leuconostoc citreum NCIMB 3351, Leuconostoc lactis NCDO 546 and
                                                                                                                                                                                                                                                                                                                            gacccagaagggatggaatcgcataatatttgagaagccatttggctttgatgcactttc 104
                                                                                                                                                                                                                                                                                                                                                        411 ggccacaactggttacaaccgtttgatgatcgaaaagccatttgggacatcatacgaaac 470
                                                                                                                                                                                                                                                                                                                                                                                                                            471 agctgaaaagttgcaaaacgaattggaaaacgcctttgatgatgaccaattgttccgtat 530
                                                                                                                                                                                                                                                                                                                                                                                          105 ttcccataggctgacacaatatcttttcaaactttcaggaaaagcaaatatatagaat 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                           165 tgancatctactaggaaggaatcncagtnaaaatcctncaggtttaagggtttcaaannn 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        531 tgaccactaccttggtaaggaaatggtccaaaatattgcggctttgcgttttggtaaccc 590
                                                                                                                                                                                                                                                                                                     0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leuconostoc dextranicum glucose-6-phosphate dehydrogenase gene.
                                                                                                                                                                                                                                                          14.2%; Score 37.4; DB 16; Length 1461;
44.7%; Pred. No. 0.052;
tive 0; Mismatches 121; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glucose-6-phosphate dehydrogenase; G6PDH; immunoassay; ss.
                                                                                                                                                                                                      Sequence 1461 BP; 395 A; 284 C; 324 G; 377 T; 81 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225 agnttttgagccaccttngagnngnacntnnnnnganna 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             591 aatctttgatgcagcctggaacaaggactacatcaagaa 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caldwell RM,
Ullman EF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leuconostoc dextranicum strain ATCC 19255
Disclosure; Page 60; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bott RR,
Silen JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T30577 standard; DNA; 1455 BP
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                                                                                                                                                                                                                                                                                          98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barnett CC, Becker MJ,
Jakobovits EB, Levy MJ,
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Best Local Similarity
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Disclosure; Page 62-63; 122pp; English.

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G6PDH genes (T30574-77) respectively code for the glucose-6-phosphate dehydrogenases (R95961-64) of Leuconostoc mesenteroides ATCC 12291. Leuconostoc citreum NCIMB 3351. Leuconostoc lactis NCDO 546 and Leuconostoc dextranicum ATCC 19255. The enzymes may be mutated to increase stability, or to improve or modulate activity, pref. by deletion or substn. of 1 or more lysine residues, or introduction of 1 or more cysteine residues. The mutant enzymes are prepd. by mutating the G6PDH gene and expression in host cells. They are used partic. to form conjugates for use in homogeneous immunoassays for analytes.
                                                                                                                                                                                                                                                                                                                                                                                                                   50 agaagggatggaatcgcataatatttgagaagccatttggctttgatgcactttcttccc 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                413 agactggctacaatcgtttgatgattgaaaagccttttggtacatcatacgccaccgcag 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              473 aagaattgcaaagtgatttggaaaatgcatttgatgatgaccaactgttccgtattgacc 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 atctactaggaaggaatcncagtnaaaatcctncaggtttaagggtttcaaannnagntt 229
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                          Sequence 1455 BP; 452 A; 275 C; 318 G; 410 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230 ttgagccaccttngagnngnacntnnnnnganna 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        593 ttgatgccgcttggaataaggactatatcaaaaa 626
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                                                                                                                                                      1 gaagcacttttggatgttgc.....agnngnacntnnnnganna 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, A Sequence 5, A Sequence 5, A Sequence 7, A Sequence 3, A Sequence 3, A Sequence 1, A Sequence 1, A Sequence 1, A Sequence 1, A Sequence 1, A Sequence 1, A Sequence 16, A Sequence 16, A Sequence 5, A
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Sequence 5,
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Sequence 10
Sequence 1,
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgr2_6/ptodata/2/ina/5C_COMB.seq:*
4: /cgr2_6/ptodata/2/ina/5C_COMB.seq:*
5: /cgr2_6/ptodata/2/ina/6_COMB.seq:*
6: /cgr2_6/ptodata/2/ina/PCTUS_COMB.seq:*
7: /cgr2_6/ptodata/2/ina/pcTuS_COMB.seq:*
7: /cgr2_6/ptodata/2/ina/pcTuS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-445-46438-3

US-08-445-4646-3

US-08-022-096-1

US-08-045-4638-7

US-08-33-821-16

US-08-93-821-16

US-08-93-821-16

US-08-91-16-16

US-09-143-068-5

US-09-143-068-5

US-08-181-19

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US-08-445-463B-5
US-08-445-464C-5
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PCT-US94-03437-7
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                                              OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Sequence 5,
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APPLICANT: Lee, Ving
APPLICANT: Malouin, Francois
APPLICANT: Malouin, Francois
APPLICANT: Sanid, Molly B.
APPLICANT: Schnid, Molly B.
APPLICANT: Schnid, Molly B.
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Salte 4700
US-08-472-673-7

US-08-475-782-1

US-08-475-782-2

US-08-472-678-1

US-08-484-503-1

US-08-484-503-2

US-08-316-239B-1

US-08-316-239B-1

US-08-316-239B-1

US-08-316-239B-1

US-08-229-140-1

US-08-229-140-1

US-08-229-140-1

US-08-24-1344-22

US-08-724-3344-22

US-08-66-386-5

US-08-66-386-5

US-08-66-386-5

US-08-66-386-5

US-08-966-386-5
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ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM COMPALIABLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714, 918
FILING DATE: September 13, 1996
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: 60/009,102
RILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: SEPTEMBER 15, 1995
APPLICATION NUMBER: 60/003,798
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REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 322/005
TELECOMMUNICATION INFORMATION:
TELEFROME: (213) 955-0440
TELERX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2494 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08714918; Patent No. 6037123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 2494 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Benton, Bret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-714-918-3/c
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Appli

Sequence Seguence Sequence Sequence Sequence

US-08-445-463B-1 US-08-445-464C-1 PCT-US91-07715A-1 US-07-596-867C-1

US-08-032-869A-2

US-08-032-869A-1

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14.2%; Score 37.4;
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TELEPHONE: (847) 267-5364
TELEPHONE: (847) 267-5376
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEE: Dade Behring Inc.: 1717 Deerfield Road Deerfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: RUSZAIA, LOIS K.
REGISTRATION NUMBER: 39,074
REFERENCE/DOCKET NUMBER: BEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                     2563 GAAAACGTTTGGA 2551
                                                                                                                                                                                                                             232 gagccacctinga 244
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MOLECULE TYPE: DN
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                1425 AAAGGATTTAAAACGCCTTGTTATCGAAAAACCATTCGGTAGTGATTTAAAATCAGCCGAA 1366
                                                                                                                                                                                                                                                                                             1365 GCATTAAACAATCCAAAATCCTAAAATCATTTAAAGAAGAAGAAATTTAYCGTATKGACCAC 1306
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                                                                                                                                                                                                                                                                                                                                             172 ctactaggaaggaatcncagtnaaaatcctncaggtttaagggtttcaaannnagnttt 231
                                                                                                                                                                        52 aagggatggaatcgcataatatttgagaagccatttggctttgatgcactttctcccat 111
                                                                                                                                                                                                                                                          112 aggotgacacaatatottctttcaaactttcaggaaaagcaaatatatagaattgancat 171
                                                                                                                                   Gaps
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                                                                                                                                   0;
                                                                                     Query Match
19.2%; Score 50.6; DB 5; Length 2494;
Best Local Similarity 50.0%; Pred. No. 4.6e-07;
Matches 101; Conservative 2; Mismatches 99; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.3%; Score 48; DB 4; Length 2764; 51.3%; Pred. No. 3.2e-06; tive 0; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08986963
; Sequence 5558730
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF SEQUENCES:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Blillly and Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC COMPATIBLE
COMPOTER: IBM PC COMPATIBLE
COMPOTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,963
FILING DATE: December 8, 1997
CLASSIFICATION: 435
ATONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Webster, Thomas D. REGIGTRATION NUMBER: 39,872 REFERENCE/DOCKET NUMBER: x-11763 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1245 GAACCATTATGGAATAACAAAT 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                     232 gagccacctingagnngnacnt 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 317/276-3334 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2764 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 51.39
Matches 99; Conservative
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single
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                 TOPOLOGY: linear
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STRANDEDNESS:
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US-08-986-963-4/C
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                                       US-08-714-918-3
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2623 TATCTTGGTAAGGAATGATCCAAAGCATCTTTGCAGTTGGCTTTGCAAACTTGATTTT 2564
                   172 ctactaggaaggaatoncagtnaaaatcctncaggtttaagggtttcaaannnagntttt 231
APPLICANT: Caldwell, Robert M.
APPLICANT: Caldwell, Robert M.
APPLICANT: Bort, Richard R.
APPLICANT: Barnett, Christopher C.
TITLE OF INVENTION: Homogenous Immunoassays Using Mutant TITLE OF INVENTION: Glucose-6-Phosphate Dehydrogenases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/445 1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BEH-7261 DIV 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JMBER: US/08/445,463B
22-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/044,857
FILING DATE: 08-ARR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           ; Sequence 5, Application US/08445463B
; Patent No. 6033890
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jakobovits, Edward B. APPLICANT: Jakobovits, Edward B. APPLICANT: Silen, Joy L. APPLICANT: Levy, Mark J. APPLICANT: Goodman, Thomas C.
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Length 1461;

DB 5;

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                                                                                      105 ttcccataggctgacacaatatcttttcaaactttcaggaaaagcaaatatatagaat 164
                                                                                                                                                                        471 AGCTGAAAAGTTGCAAAAAGGAATTGGAAAACGCCTTTGATGATGACCAATTGTTCGTAT 530
                                                            45 gacccagaagggatggaatcgcataatatttgagaagccatttggctttgatgcactttc 104
                                                                                                                                                                                                                        165 tgancatctactaggaaggaatcncagtnaaaatcctncaggtttaagggtttcaaannn 224
                                                                                                                                                                                                                                               APPLICANT: Jakoboits, Edward B.
APPLICANT: Silen, Joy L.
APPLICANT: Levy, Mark J.
APPLICANT: Goodman, Thomas C.
APPLICANT: Becker, Martin
APPLICANT: Caldwell, Robert M.
APPLICANT: Bott, Richard R.
APPLICANT: Barnett, Christopher C.
TITLE OF INVENTION: Homogenous Immunoassays Using Mutant
TITLE OF INVENTION: Glucose-6-Phosphate Dehydrogenases
      44.7%; Pred. No. 0.0059;
tive 0; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                      225 agnttttgagccaccttngagnngnacntnnnnganna 263
                                                                                                                                                                                                                                                                                                                                          591 AATCTTTGATGCAGCCTGGAACAAGGACTACATCAAGAA 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: RUSZALA, LOIS K.
REGISTRATION NUMBER: 39,074
REFERENCE/DOCKET NUMBER: BEH-7261 DIV 1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/445,464C
FILING DATE: 22-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/044,857
FILING DATE: 08-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 5, Application US/08445464C
; Patent No. 6090567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Dade Behring Inc.
1717 Deerfield Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (genomic)
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                         98; Conservative
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1461 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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MOLECULE TYPE:
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                                                                                                                                                                                                                              471 AGCIGAAAAGTIGCAAAACGAAIIGGAAAACGCCIIIGAIGAIGACCAAIIGTICCGIAI 530
                                                                                                                                 411 GGCCACAACTGGTTACAACCGTTTGATGATCGAAAAGCCATTTGGGACATCATACGAAAC 470
                                                                                                                                                                                105 ttcccataggctgacacaatatcttctttcaaactttcaggaaaagcaaatatatagaat 164
                                                                                                                                                                                                                                                                          165 tgancatctactaggaaggaatcncagtnaaaatcctncaggtttaagggtttcaaannn 224
                                                                                                                                                                                                                                                                                                                    531 TGACCACTACCTTGGTAAGGAAATGGTCCAAAATATTGCGGCTTTGCGTATTGGTAACCC 590
                                                          Gaps
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14.2%; Score 37.4; DB 5; Length 1461; 44.7%; Pred. No. 0.0059; tive 0; Mismatches 121; Indels 0
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44.7%; Pred. No. 0.0059;
tive 0; Mismatches 121; Indels 0;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                  225 agnttttgagccaccttngagnngnacntnnnnnganna 263
                                                                                                                                                                                                                                                                                                                                                                                                                 591 AATCITIGAIGCAGCCIGGAACAAGGACIACAICAAGAA 629
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APPLICATION NUMBER: PCT/US94/03437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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NCDO 546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1461 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                      Best Local Similarity 44.79
Matches 98; Conservative
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Best Local Similarity 44.78
Matches 98; Conservative
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PCT-US94-03437-5
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PCT-US94-03437-5
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Query Match
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INFORMATION FOR SEQ ID NO: 3:
                SEQUENCE CHARACTERISTICS:
LENGTH: 1467 base pairs
TYPE: nucleic acid
                                                                             single
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TITLE OF INVENTION:
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                                                                                                                                                      ANTI-SENSE: NO ORIGINAL SOURCE:
                                                             TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Illi
COUNTRY: US
ZIP: 60015
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US-08-445-463B-3
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                                                                                               TOPOLOGY:
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PCT-US94-03437-3
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Best Local Similarity 44.9%; Pred. No. 0.0068;
Matches 96; Conservative 0; Mismatches 118; Indels 0;
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                                                                                                                                                                               TITLE OF INVENTION: HOMOGENEOUS IMMUNOASSAYS USING MUTANT TITLE OF INVENTION: GLUCOSE-6-PHOSPHATE DEHYDROGENASES
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                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
        591 AATCTTTGATGCAGCCTGGAACAAGGACTACATCAAGAA 629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN: ATC 19255
PCI-US94-03437-7
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                   Sequence 7, Application PC/TUS9403437 GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1455 base pairs
                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 124
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA genomic HYPOTHETICAL: NO
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
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PCT-US94-03437-3
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                                                                                         PCT-US94-03437-7
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50 agaagggatggaatcgcataatatttgagaagccatttggctttgatgcactttcttccc 109
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                                                                                                                                                                                    Score 37.2; DB 6; Length 1467; Pred. No. 0.0068;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445.463R
                                                                                                                                                                                                                                      0; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 ttgagccaccttngagnngnacntnnnnganna 263
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22-MAY-1995
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APPLICATION NUMBER: US 08/044,857
FILING DATE: 08-ARR-1993
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Jacobovits, Edward B. APPLICANT: Silen, Joy L. APPLICANT: Silen, Joy L. APPLICANT: Goodman, Phomas C. APPLICANT: Becker, Martin APPLICANT: Ulnan, Edwin F. APPLICANT: Caldwell, Robert M. APPLICANT: Bott, Richard R.
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; Patent No. 6033890
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                                                                                    Leuconostoc citreum
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                                                                                                                                                                                           14.18;
MOLECULE TYPE: DNA genomic
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Best Local Similarity 44.99
Matches 96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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Bott, Richard R.
Barnett, Christopher C.
[INVENTION: Homogenous Immunoassays Using Mutant INVENTION: Glucose-6-Phosphate Dehydrogenases SPONTRICES: 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
NAME: Ruszala, Lois K.
REGISTRATION NUMBER: 39,074
REFBERCE, POCKET NUMBER: BEH-7261 DIV 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 267-5364
TELEFAX: (847) 267-5376
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 1571 base pairs
TYPE: nucleic acid
STRAE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              230 ttgagccaccttngagnngnacntnnnnnganna 263
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FILING DATE: 22-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jakobovits, Edward B. APPLICANT: Silen, Joy L. APPLICANT: Levy, Mark J. APPLICANT: Becker, Martin APPLICANT: Ullman, Edwin F.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6090567
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                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 44.9%
Matches 96; Conservative
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STATE: Illinois
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                                                                                                                                                                                                                                                                      ; ANTI-SENSE: NO
US-08-445-463B-3
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US-08-445-464C-3
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APPLICANT:
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RESULT 10
US-07-737-071A-1
Sequence 1, Application US/07737071A
Patent No. 5229286
GENERAL INFORMATION:
APPLICANT: JARSCH, Michael
TITLE OF INVENTION: CLONING AND OVEREXPRESSION OF
TITLE OF INVENTION: GLUCOSE-6-PHOSPHATE DEHYDROGENASE FROM LEUCONOSTOC
TITLE OF INVENTION: DEXTRANICUS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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14.1%; Score 37.2; DB 5; Length 1571;
Best Local Similarity 44.9%; Pred. No. 0.007;
Matches 96; Conservative 0; Mismatches 118; Indels 0.
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O7/737,071A
FILING DATE: 19910730
                                                              NAME: KUSZAJA, LOJSK
REGISTRATION NUMBER: 39,074
REFERENCE/DOCKET NUMBER: 39,074
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 267-5364
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1571 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 4024158.9
FILING DATE: 30-JUL-1990
APPLICATION NUMBER: US 08/044,857 FILING DATE: 08-APR-1993
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                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                       FILING DATE: 08-APR-1993
ATTORNEY/AGENT INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
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US-08-445-464C-3
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APPLICATION NUMBER: US/08/445,463B
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APPLICANT: LANG, Gunter
IITLE OF INVENTION: CLONING AND OVEREXPRESSION OF
IITLE OF INVENTION: GLUCOSE-6-PHOSPHATE DEHYDROGENASE FROM LEUCONOSTOC
IITLE OF INVENTION: DETTRANICUS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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APPLICATION NUMBER: DE P 40 24 158.0
FILING DATE: 30-JUL-1990
PRIOR APPLICATION NUMBER: US 07/737,071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/022,096
FILING DATE: 19930225
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                 TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
TELEX: 440142
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1696 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
NAME: MUITAY, Robert B. 890 REGISTRATION NUMBER: 22,891 REPERENCE/DOCKET NUMBER: 911 TELECOMMUNICATION INFORMATION:
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LOCATION: 123..1580
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20005-5701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Best Local Similarity 44.9%; Pred. No. 0.0072;
Matches 96; Conservative 0; Mismatches 118; Indels 0
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Glucose-6-Phosphate Dehydrogenases
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COMPUTER: IDM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230 ttgagccaccttngagnngnacntnnnnganna 263
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                                                                      REFERENCE/DOCKET NUMBER: P564-3005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caldwell, Robert M.
Bott, Richard R.
Barnett, Christopher C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Dade Behring Inc. STREET: 1717 Deerfield Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: GOODMAN, THOMAS C. APPLICANT: BECKEY, MARTIN APPLICANT: Ullman, Edwin F.
                  ATTORNEY/AGENT INFORMATION:
NAME: Chin, Monica F.
REGISTRATION NUMBER: 36,105
                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FILING DATE: 30-JUL-1991
                                                                                                                                                                                           TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: 123
US-08-022-096-1
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TELEFAX: (
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APPLICANT:
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tive 0; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Homogenous Immunoassays Using Mutant
TITLE OF INVENTION: Glucose-6-Phosphate Dehydrogenases
                                              APPLICATION NUMBER: US 08/044,857
FILING DATE: 08-APR-1993
ATORNEY/AGENT INFORMATION:
NAME: RUSZALA, LOIS K.
REGISTRATION NUMBER: 39,074
REFERENCE/DOCKET NUMBER: BEH-7261 DIV 2
TELEPOMMUNICATION INFORMATION:
TELEPHONE: (847) 267-5364
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         718 TTGATGCCGCTTGGAATAAGGACTATATCAAAA 751
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Levy, Mark J.
Goodman, Thomas C.
Becker, Martin
Ullman, Edwin F.
Caldwell, Robert M.
Bott, Richard R.
Barnett, Christopher C.
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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1717 Deerfield Road
                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FILING DATE: 22-MAY-1995
                                                                                                                                                                                                                                                LENGTH: 1696 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 44.98
Matches 96; Conservative
                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                      CLASSIFICATION:
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ZIP: 60015
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APPLICANT:
APPLICANT:
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APPLICANT:
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110 ataggctgacacaatatcttctttcaaactttcaggaaaagcaaatatatagaattganc 169
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14.1%; Score 37.2; DB 5; Length 1696;
Best Local Similarity 44.9%; Pred. No. 0.0072;
Matches 96; Conservative 0; Mismatches 118; Indels 0
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                    NAME: RUSZAIA, LOIS K.
REGIZRATION NUMBER: 39,074
REFERENCE/DOCKET NUMBER: BEH-7261 DIV 1
TELECOMMUNICATION INFORMATION:
TELEFACOR (847) 267-5364
TELEFACOR (847) 267-5376
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
ILENCTH: 1696 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230 ttgagccaccttngagnngnacntnnnnnganna 263
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              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,464C
FILING DATE: 22-MAY-1995
CLASSIFICATION: 435
                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/044,857
FILING DATE: 08-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16, Application US/08933821
Patent No. 5972338
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genentech, Inc.
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CITY: South San Francisco
STATE: California
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HYPOTHETICAL: NO
ANTI-SPMT
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US-08-445-464C-7
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CLASSIFICATION: 536

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Best Local Similarity 60.0%; Pred. No. 0.17;
Matches 51; Conservative 0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                       Query Match 12.5%; Score 33; DB 4; Length 2042; Best Local Similarity 60.0%; Pred. No. 0.17; Matches 51; Conservative 0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER REDDABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 19 C compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-981
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2042 base pairs
TYPE: NUCLEIC Acid
STRANBEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 aggaatchcagthaaaatccthcag 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
GAPLICANT: Gurney, Austin
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: P107(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEPHONE: 650/252-9811
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2042 base pairs
TYPE: Nucleic Acid
STRANDENNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08934494 Patent No. 6030831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genentech, Inc.
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STATE: California
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US-08-934-494-5
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US-08-934-494-5
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November 4, 2000, 11:51:59; Search time 4352.3 Seconds (without alignments) 373.614 Million cell updates/sec
                                                                                                                     1 gaagcacttttggatgttgc......agnngnacntnnnnnganna 263
                                                                                                                                                                                                 14379728
GenCore version 4,5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                       7189864 seqs, 3091403243 residues
                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                     OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                         IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
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em_esthum10:
em_esthum11:
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em_gss11: *
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gb_gss20:*
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1117:
1118:
1120:
121:
122:
122:
124:
126:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	0545 MtBA3	526947 M66J03ST	561737 AV5617	18140 AV548140	394720 EST26	91202 EST24191	5120 NF038D0	3861 MgA	95224 AU0952	3122 23661 3724 11212	1645 113122	AW/84451 ZD62911.9	100103 3000	0 6010/203	TEGOO COTON	DAA HVSME	9 4179410 r	AA432848 V1/JULU:1 AA671883 V107611.r	167 EST0510	62 601147	35 vq67c01.s	330 Tetrao	113 AV416113	16 EST3983	.54 EST34025	AA999427 MCCE3283.	σ.	C25654 C25654 DICT	CMU38	י כ	MS3H3STM	T74002 vc81c06.r1	BB246584 BB246584	5 EST33223	22 HS_	33	AW696807 NF109B12S	8	389 HS_314	1122 af19h06	202192 100230	
DB ID	14 AL37054	21 AW33383	19 AV56	19 AV54814	13 AI89472	11 AI49120	23 AW68612	20 AW18086	15 AU09522	22 AW4	23 AW66964	24 AW78445	34 BE26463	36 BE54802	36 BED4838	36 BE51582	33 BEU00/4	4 u	2021/004	34 BEZ169	5 AA645495	122 CF	18 A	35 BE4	35 BE44915	7 AA999427	35 BE4125	36 C25654		6 AA803355	115 AZ	30 BE32#13	28 RR24658	24 AW73624	89 AQ12422	23 AW68533	24 AW6968	91 AQ312198	112 AQ892	Ly AWUZI4Z	00	2 AM20213
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ALIGNMENTS

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Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O.,
Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Gianinazzi-Pearson
Medicago truncatula ESTs from nitrogen-starved roots
Unpublished (2000) 0; Gaps 10-JUL-2000 AL370545 443 bp mRNA EST 03-AUG-2000 MLBA38E01F1 MtBA Medicago truncatula cDNA clone MtBA3BE01F1 MtBA3BE01F197 121 caatatettettteaaaettteaggaaaageaaatatatagaattganeatetaet 176 320 CAATATCTTCTCTCGAAGTTTGAGGAAAAGCAACTATATAGGTATTCATACCTTCT 375 Ouery Match
Best Local Similarity 87.5%; Pred. No. 7.6e-31;
Matches 154; Conservative 0; Mismatches 22; Indels 0; AW335839 295 bp mRNA EST 21995 MARC 1BOV Bos taurus CDNA 5', mRNA sequence. AW335839 Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Location/Qualifiers AL370545.1 GI:9670298 barrel medic. DEFINITION BASE COUNT ORIGIN DEFINITION ORGANISM TITLE JOURNAL ACCESSION AW335839 ACCESSION REFERENCE AUTHORS KEYWORDS FEATURES COMMENT RESULT VERSION LOCUS SOURCE á δ

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BASE COUNT
ORIGIN
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SOURCE
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                                                                                                                             1 (bases 1 to 295)

Smith,TP-D., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,

Bennett,G.A., Fabrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid

W.W. and Keele,J.W.

Design and use of four pooled tissue normalized cDNA libraries for

Unpublished (2000)
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                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pCMV SPORT6; Site_1: Xbal; Site_2: Xhol; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary." 84 c 81 g 61 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 ttcccataggctgacacaatatcttcttcaaactttcaggaaaagcaaatatatagaat 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 CTCCAACCAGCTGTCCAACCACCACCACCAGAGACCAGATCTACCGCAT 125
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Best Local Similarity 51.0%; Pred. No. 0.00015;
Matches 104; Conservative 0; Mismatches 100; Indels 0
                                                                                                                                                                                                                                                                         USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                 Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACKWARD: GTTTTCCCAGTCACGACG
Plate: 15 row: B column: 17
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="MARC 1BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="pooled"
/lab_host="DH10B"
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AW335839.1 GI:6832460
                                                                                                            Bovidae; Bovinae; Bos.
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                   KEYWORDS
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 260)
White,J.A., Todd,J., Nowman,T., Focks,N., Girke,T., Martinez de Ilarduya,O., Jaworski,J.G., Ohlrogge,J. and Benning,C. An ew set of Arabidopsis ESTS from developing seeds: the metabolic pathway from carbohydrates to seed oil
                                                                                                                                                                                                                                                          Contact: Benning, C
Dept. of Blochemistry & Molecular Biology
Michigan State University
224 Biochemistry, Michigan State University, East Lansing, MI 48824
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Rosidae; eufosids II;
Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 624)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,§.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clones were originally prepared at Michigan State University. Arabidopsis Biological Resource Center, The Ohio State University, 309 Botany & Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX: 6142920603 TEL: 6142929371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AV561737 Arabidopsis thaliana green siliques Columbia Arabidopsis thaliana cDNA clone SQ156f07F 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 ATTCGTTGATGTGGTTAGGTGTGCAAGTCTTAGAGCCTCCTCAGAGAATGGCTGGACAAG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 cataatatttgagaagccatttggctttgatgcactttcttcccataggctgacacaata 125
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/db_xref="taxon:3702"
/clone="600035613R1"
/clone_lib="Arabidopsis developing seed"
/tissue_type="seed"
/dev_stage="5-13 days after flowering"
/lab_host="E.coli"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                              Plant Physiol. (2000) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: benning@msu.edu
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AV561737.1 GI:8733163
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Eukaryota; thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; endicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 583)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries

AL DNA Res. 7, 175-180 (2000)
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
COntact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
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                                                                                                                                                                          Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"
//strain="Columbia"
//bxref="taxon:3702"
/clone="SQ156f07F"
/clone="Lib="Arabidopsis thaliana green siliques Columbia"
/tissue_type="green siliques"
/note="Vercor: pBluescriptII SK-; Site_1: BcoRI; Site_2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 ctgacacaatatcttctttcaaactttcaggaaaagcaaatatatagaattgancatcta 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               538 CTIGGGAAGGAATTAGTICAAAACATGTIGGTCCTCCGGTTIGCAAATCGCTTTTTCTTG 597
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Pred. No. 0.00059;
0; Mismatches 105;
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AV548140 Arabidopsis thaliana roots Colı
CDNA clone RZL48a11F 3', mRNA sequence.
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Best Local Similarity 49.0%;
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/organism="Arabidopsis thaliana"

/strain="Columbia" /db_xref="taxon:3702"

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Enkaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids 1; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 382)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato callus tissue
Unpublished (1999)
Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; supplier: Giovannoni laboratory; cLEC - Cotyledons of seedlings 7-10 days post-germination were excised, cut at both ends and placed on MS medium with no selection. Mixed callus was harvested at 25 and 40 days and included undifferentiated masses. Tomato Callus EST Library"
                                                                                                                                                                                                                                                         ö
/clone="RZL4BallF"
/clone_llb="Arabidopsis thaliana roots Columbia"
/tissue_type="roots"
/note="Vector: pBluescriptII SK-; Site_1: BcoRI; Site_2:
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                                                                                                                                                                                                                                                                                                                             357 GGATGGACACGGATTGTTGTGTGTGGAGAGCCATTTGCCAGGACCTTGAATCTGCAGGGAA 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 ctaggaaggaatencagtnaaaateetneaggtttaagggttteaaannnagnttttgag 234
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Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
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Clemson University
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/dev_stage="25-40 days old"
/lab_host="XL1-Blue MRF'"
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/db_xref="taxon:4081"
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EST241911 tomato shoot, Cornell Lycopersicon esculentum cDNA clone
cLEB1G14 similar to glucose-6-phosphate dehydrogenase, mRNA
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-Tomato Shoot Meristem EST Library. Oligo-dr primed cDNA
library made from tomato vegetative shoots including
meristers and small expanding leaves."
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0
                                                                                                                                           Score 46.6; DB 13; Length 382; Pred. No. 0.0023;
                                                                                                                                                                                                             0; Mismatches 109; Indels
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/cultivar="TA496"
/db_xref="taxon:4081"
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
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/dev_stage="8 week old plants"
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47.88;
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17.7%; Score 46.6; DB 11; Length 649; 47.8%; Pred. No. 0.0026;

Query Match Best Local Similarity

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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Medicago.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula nodulated root library
                                                      55 ggatggaatcgcataatatttgagaagccatttggctttgatgcactttctcccatagg 114
                                                                                                         360 GGTIGGACACGAATCGTIGITGAGAAGCCCTICGGCAAGGATTAGCTTCATCTGAACAA 419
                                                                                                                                                                                                                        420 CTAAGTTCCCAGATCGGAGAACTATTTGACGAACCCCAAATTTATCGCATTGACCATTAT 479
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NF038D09NR1F1000 Nodulated root Medicago truncatula cDNA clone
                                                                                                                                                                  115 ctgacacaatatcttctttcaaactttcaggaaaagcaaatatatagaattgancatcta 174
                                                                                                                                                                                                                                                                                 175 ctaggaaggaatcncagtnaaaatcctncaggtttaagggtttcaaannnagnttttgag 234
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               0; Gaps
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47.8%; Pred. No. 0.0026;
tive 0; Mismatches 109; Indels 0;
      0; Mismatches 109; Indels
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
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/db_xref="taxon:3880"
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Insert Length: 661 Std Error: 0.00
Plate: 038 row: D column: 09
Seq primer: TCACACAGGAAACAGCTATGAC.
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/tissue_type="root"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         540 CCGCTCTGGAATCGTGACAACATTGATAA 568
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Matches 100; Conservative
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Fax: 580 221 7380
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                                                                                                                                                                                                                                                                                              MgA1030f MgA Library Mycosphaerella graminicola cDNA clone MgA1030
5' similar to GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 ataggetgacacaatatettettteaaaettteaggaaaagcaaatatatagaattgane 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Keon, J.P.R., Bailey, A.M. and Hargreaves, J.A. A group of expressed cDNA sequences from the wheat fungal leaf blotch pathogen, Mycosphaerella graminicola Unpublished (1999)
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                                                                                             157 ITGGGAAAGGAACTAGTGCAAAACATGTTAGTACTTCGTTTTGCAAATCGGTTCTTCTTG 216
  175 ctaggaaggaatcncagtnaaaatcctncaggtttaagggtttcaaannnagnttttgag 234
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                                                                                                                                                                                                                                                                                17-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Ascomycota incertae sedis;
Mycosphaerellaceae; Mycosphaerella.
1 (bases 1 to 735)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mycosphaerella graminicola"
                                                                                                                                                                                                                                                                                  EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: john.hargreaves@bbsrc.ac.uk
Insert Length: 1100 Std Error: 0.00
Seq primer: M13 reverse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Long Ashton, Bristol, BS41 9AF, UK
Tel: +44(0)1275 392181
Fax: +44(0)1275 394281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell Biology Department
IACR-Long Ashton Research Station
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/clone="MgAl030"
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Mycosphaerella graminicola
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Hargreaves JA
                                                                                                                                                                                                                                                                                                                                                             AW180861.1 GI:6448056
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RESULT 10

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/clone_lib="Rice cDNA from immature leaf including apical meristem (under short day condition)"
//dev_stage="immature leaf including apical meristem (under short day condition)"
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                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.
1 (bases 1 to 465)
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
                                                  (under short day condition) Oryza sativa cDNA clone E60680, mRNA
  AU095224 465 bp mRNA EST 30-JUN-2000
AU095224 Rice cDNA from immature leaf including apical meristem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 TIGGGAAAAGAGTIGGTCCAAAACCIGCTIGTGGTTTTGCCAACCGCTTGTTCTTG 214
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                                                                                                                                                                                                                                                                                                                       SasAXi,T. and Yammamoto,K.
Rice CDNA from immature leaf including apical meristem (2000) Unpublished (2000)
Contact: Tawkuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
30-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 ctaggaaggaatcncagtnaaaatcctncaggtttaaggggtttcaaannnagnttttgag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 0298-38-7441
Fax: 0298-38-7468
Email: tsasaki@abr.affrc.go.jp
PROJECT = 'KGP'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="Nipponbare"
/db_xref="taxon:4530"
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                                                                                                                                                                                            Oryza sativa.
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Email: smitheemail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
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McCombie,W.R., See,L.-H., Baker,J.P., Bahret,A., Dedhia,N.N., de la Bastide,M., Huang,E.N., King,L., Kirchoff,R.A., Miller,B., Nascimento,L.U., O'Shaughnessy,A.L., Preston,R.R., Kodriguez,M.A., Shah,R.S., Shekher,M., Spiegel,L.A., Toth,K., Vil,M.D. and Hannon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW784451 385 bp mRNA EST 19-MAY-2000
zb62g11.g1 Canis cDNAs from mdck cells Canis familiaris cDNA clone
zb62g11 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43.2; DB 23; Length 577;
Pred. No. 0.024;
0; Mismatches 59; Indels 0;
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                Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                              /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
                                                                                                                                                                                                                                                                                       Plate: 107 row: L column: 13
Seg primer: ATTTAGGTGACACTATAG.
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Plate: zb62 row: g column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="pooled"
                                                                                                                                                                                                                                            FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                             BACKWARD: GTTTTCCCAGTCACGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B"
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56.9%;
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AW784451.1 GI:7838827
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                                                                                                                                                                     Contact: Smith TPL,
USDA, ARS, US Meat Animal Research Center
USDA, ARS, US Meat Animal Research Center
PED Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4396
Fax: 402 762 4390
Fmail: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
and minmatch 12 options.
                1 (bases 1 to 360)
Smith,T.P., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid,
W.W. and Keele,J.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pCMV SPORT6; Site_1: Xba1; Site_2: Xho1; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."

123 c 84 g 67 t
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Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid,W.W. and Keele,J.W.
Design and use of four pooled tissue normalized cDNA libraries for EST discovery in cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
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Plate: 14 row: B column: 22
Seq primer: ATTTAGGTGACACTATAG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9913"
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/lab_host="DH10B"
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Unpublished (2000)
Bovidae; Bovinae; Bos.
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Matches 78; Conservative
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                                                                                                                                                              /note="Vector: Lambda Zap II, The library was provided by Greg Hannon (Cold Spring Harbor Laboratory). This library is oligo(dT) primed using stratagene Zap CDNA synthesis kit. It was made from exponentially growing mdck cells. Please contact Greg Hannon (hannon@cshl.org) with any library related inquiries."
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/tissue_type="small cell carcinoma"
/cell_line="MGC2"
/cell_line="MGC3"
/lab_host="MH10B (phage-resistant)"
/lab_host="lang; Vector: pOTB7; Site_1: XhoI; Site_2:
Focal; cDNA made by Oligo-df priming. Directionally
cloned into ECORI/And sites using the following 5'
adaptor: GGCACGAG(G), Size-selected >500bp for average
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I (bases 1 to 565)

INH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel. (301) 496-1550
Email: Robert Strausbergenih.gov
Plate: LLCM218 row: n column: 06
High quality sequence stop: 565.
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48.5%; Pred. No. 0.033;
tive 0; Mismatches 105; Indels 0.
                                                            1. .385
/organism="Canis familiaris"
/old_xref="taxon:9615"
/clone="taxon:9611"
/clone_lib="Canis cDNAs from mdck cells"
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/db_xref="taxon:9606"
/clone="IMAGE:3536453"
Seq primer: -40M13RevUniv
High quality sequence stop: 385.
Location/Qualifiers
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/note="Organ: placenta; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 782)

NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

National institutes of Health, Mammalian Gene Collection (MGC)
insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.W.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8448 row: j column: 13
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                                                                                                                                                                                                                     DB 34; Length 565;
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48.5%; Pred. No. 0.036;
tive 0; Mismatches 105;
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/lab_host="DH10B"
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AB029456 Trifticum	AB029455 Trition	AR029454 Trittoum	III 8238 Modicaco sa	X74421 S tuberosum	AR012863 Detrocel:	A.TO01770 Nicotiana	AF012862 Detroceli	ATOUTE FELLOSETT	A.TO10970 Arabidons	A.TO10971 Arabidons	AP000381 Arabidops
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Query	56.5	56.5	56.5	45.8	43.7	43.3	41.6	41.2	40.9	40.9	40.3	33.5
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AL35602 Homo sapi
AC041038 Homo sapi
AC007511 Homo sapi
AC009386 Homo sapi
AC018976 Homo sapi
AC18976 Homo sapi
AC5935974 Staphyloc
AF269329 Staphyloc
AC068066 Mus muscu
AC068066 Mus muscu
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Isolation of novel early salt-responding genes from wheat (Triticum aestivum L.) by differential display
Theor. Appl. Genet. 98, 673-678 (1999)
                                                                                                                                                                                                                 ALO96843 Human DNA
ACO24847 Caenorhab
ACO68750 Homo sapi
ACO36237 Homo sapi
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AC006889 Caenorhab
Z53503 H.sapiens (
AL132962 Arabidops
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Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.
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299110 Bacillus su
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AC016905 Homo sapi
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                                                                                                                                                                                                                                                                                                                 AP001989 Homo sapi
Mesembrya
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KKYYSGSYDSGESEKLAKEISDYEMSNSGSSFNLFYLALPESVYPSVCKMIFTYCM
SPTSRGWTRYVURKPFGRGLDSAEELSSQLGELFEEDQLYRIDHYLGKELVQNLLVL
RRANRLELPLWNRDNVDNIQIVFREDFGTDGRGGFFEDQYGIIRGIIQNHILLQVFCLVA
MERVSIKPEHTRDEKVKULQSVNPIRDEVVLGQYQGYREDPTVDDSNTPFFASIV
LRVHNERWEGGYPFILKAGKALNSRKAEIRVQFKDVPGDIFKCKRGGRREFVIRLQPSE
AMYMKLIVKRFQLEMAFEQSELDLSYGHRYQDVWIPEAYFRILLDTIRGDQHFVRRD
ELKAAMQIFTPLLHDIDAGKLKAVSYKPGSRGPKEADELSEKVGYMQTHGYIMIPPTL
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Triticum aestivum g6pdh mRNA for glucose-6-phosphate dehydrogenase,
complete cds, clone:Tagpd2.
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Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.
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Triticum aestivum (cultivar:Chinese spring, isolate:root) seedling
cDNA to mRNA, clone:Tagpd2.
Triticum aestivum
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Best Local Similarity 76.3%; Pred. No. 6.3e-29;
Matches 177; Conservative 0; Mismatches 49; Indels 6;
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Isolation of novel early salt-responding
aestivum L.) by differential display
Theor. Appl. Genet. 98, 673-678 (1999)
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/cultivar="Chinese spring"
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                                       /db_xref="taxon:4565"
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153. .1682
                                                                                                                                                                                                            /gene="g6pdh"
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162. 1691
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162, 1691
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Triticum aestivum aestivum culivar:Chinese Spring, isolate:root) seedling Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.
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Triticum aestivum g6pdh mRNA for glucose-6-phosphate dehydrogenase,
complete cds, clone:Tagpdl.
                                                      Submitted (01-JUL-1999) to the DDBJ/EMBL/GenBank databases. Yasue Nemoto, Yokohama City University, Kihara Institute for Biological Research; Maioka, Totsuka, Yokohama 244-0813, Japan (E-mail:nemoto@yokohama-cu.ac.jp, Tel:81-45-820-1902,
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glucose-6-phosphate dehydrogenase.
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161. .1702
     (bases 1 to 1924)
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Nemotorr, Kawakami, N. and Sasakuma, T. Isolation of novel early salt-responding genes from wheat (Triticum aestivum L.) by differential display Theor. Appl. Genet. 98, 673-678 (1999)
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ELKAAWQIFTPLLHDIDAGKLKAVSYKPGSRGPKEADELSEKVGYMOTHGYIMIPPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (01-JUL-1999) to the DDBJ/EWBL/GenBank databases. Yasue Nemoto, Yokohama City University, Kihara Institute for Biological Research; Maloka, Totsuka, Yokohama 244-0813, Japan (E-mail:nemotodgyokohama-cu.ac.jp, Tel:81-45-820-1902, Fax:81-45-820-1901)
                                                                                                                                                                                                                            Molecular characterization of glucose-6-phosphate dehydrogenase
                                                                                                                                                                                                                                                           (G6PDH) from wheat (Triticum aestivum L.): gene expression in response to salt stress
Unpublished (1999)
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OHFVRRDELKASWQIFTPLLHKIDRGELKPVPYNPGSRGPAEADELLEKAGYVQTPGY
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                                                                                                                                                                         Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Medicago.
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                  Medicago sativa glucose-6-phosphate dehydrogenase mRNA, complete
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Submitted (06-DEC-1994) Theo Fahrendorf, Samuel Roberts Noble
Foundation, Plant Biology Division, 2510 Sam Noble Parkway,
Ardmore, OK 73402, USA
30-JAN-1997
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/protein_id="AAB41552.1"
/db_xref="G1:603219"
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/cultivar="Apollo"
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38. .1585
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/db_xref="taxon:56147"
                                                                                                                                                              Medicago sativa subsp. sativa
      mRNA
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Best Local Similarity 66.1%;
Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="G10"
                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 1785)
Fahrendorf,T.
      1785 bp
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YCMNKBDLGGWTRIVEKPFGKDLASSEQLSSGJGELFDEPQIYRIDHYLGKELVQNL
LVLRFANRFLPLWNRDNIDNIQIVFREDFGTEGRGGYFDSYGJIRDIJQUHLQVIC
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TMVLRIHNERWEGYPPIMKAGKALNSRKAEIRVQFKDVPGDIFRCQKGGRNEFVIRLO
PSEAMYMKLTVKKPGLEMSTVQSELDLSYGQRYQGVVIPEAYERLILDTIRGDQQHFV
RRDELKAAWEIFTPLLHRIDNGEVKPIPYKRGSRGPAEADELLQNAGYVQTHGYIWIP
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                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
Asteridae; Solananae; Solanales; Solanaceae; Solanum; Potatoe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Purification, characterization, and cDNA sequence of glucose-6-phosphate dehydrogenase from potato (Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                               Submitted (30-JUL-1993) A. von Schaewen, Universitaet Osnabrueck Pflanzenphys., Barbarastr 11, 49069 Osnabrueck, FRG (bases 1 to 1689)
                                                                                                                              cytosolic enzyme; g6pdh gene; glucose-6-phosphate dehydrogenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 342 GITICIGCAACTGATIAAATACGICAGTGGTTCTTAIGAITCTGCTGAGGGAITTACGTC 401
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                                   21-SEP-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="glucose-6-phosphate 1-dehydrogenase"
/protein_id="CAA52442.1"
                                                         S.tuberosum mRNA for glucose-6-phosphate dehydrogenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_line="S.tuberosum L. Desiree" /clone_lib="lambda ZAPII"
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64.8%; Pred. No. 4.9e-20;
Live 0; Mismatches 82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Solanum tuberosum"
/cultivar="Desiree"
/db_xref="taxon:4113"
/haplotype="diploid"
/dev_stage="vegetative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="green leaves"
/cell_type="mesophyll"
                                                                                                                                                      oxidative pentose phosphate pathway.
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/EC_number="1.1.1.49"
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94236152
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                                          mRNA
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                                          1689 bp
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Matches 151; Conservative
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61 attgaatgaggcaatctctgagtatgagacttcagaaaacaatgactcgggaagctaccg 120

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Eukaryota; Viridipiantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids if, Apiales; Apiaceae; Petroselinum.
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EDGCLSTVVLGASGDLAKKKTFPALFNLYRQGFLQSHEVYIFGYARTKISDDDLRDRI
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VIIPEAVERLLIDTIRGDQQHFVRRDELKAAMEIFTPLLHRIDKSELKSVSKGRYG
PERADELLKKVGYVQTHGYTWIPPTL"
                                                                                                                                                                                                                                                                                                                Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 2 (CGGPDH2) mRNA, complete cds.
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Extensive reprogramming of cellular metabolism by fungal elicitor
or infection in parsley suggests a new perception of
'defense-related' genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Batz,O., Logemann,E. and Hahlbrock,K.
Direct Submission
Submitted (08-JUL-1997) Biochemistry, MPI f. Zuechtungsforschung,
Carl-von-Linne-Weg 10, Cologne, NRW 50829, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="cytosolic glucose-6-phosphate dehydrogenase 2"
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121 cagattattttatttggcattgcctccatcagtctacccatcagtatgcgagatgataag 180
                                                                                    440 TITCIGCAACTGATCAAATACGTCTGTGGTTCTTATGACGCAGCGAGGGTTTTCAGTGT 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 100.8; DB 7
Pred. No. 9.7e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:4043"
/cell_type="cultured cells"
1. .1957
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Location/Qualifiers
1. .1957
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AF012863.1 GI:2352922
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KTFPALFULYRQGFLQSNEVHIFGYARTKISDDDLRGRIRGYLSQGKENEEEVSEFLQ
LIKYVSGSYDSGEGFSLLDKAIAEHEIAKNSTEGSSRRLFYFALPPSYYPSVCRMIKN
YCMNKSDLGGWTRIVVEKPFGKDLASAEQLSSQIGELFDEPQIYRIDHYLGKELVQNL
LVLRFANRFFLPLWNRDNIDNIQIVFREDFGTEGRCGYFDEYGIIRDIIQNGLLQVLC
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TMVLRIHNERWEGVPFIMKAGKALNSRKAEIRVQFKDVFGDIFRCKKQGRNEFVIRLQ
PSEAMYMKLTVKKPGLEMSTVQSELDLSYRQRYQGVVIPEAYERLILDTIRGDQOHFV
RRDELKAAWEIFTPLLHRIDDGEVKPIPYKPGSRGPAEADELLQNVGYVQTHGYICIP
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/translation="MAASWCIEKRGSIRLDSFRDNDNIPETGCLSIIVLGASGDLAKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (18-SEP-1997) von Schaewen A., Plant Physiology,
University Osnabrueck, Barbarastr. 11, D-49069 Osnabrueck, GERWANY
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   von Schaewen, A.

Buidence for functional convergence of redox regulation in G6PDH isoforms of cyanobacteria and higher plants
Plant Wol. Biol. 40 (3), 487-494 (1999)
                                                                  500 TIGGATAAGGAAATATCTGAGCATGAAATATCAAGAAACAGTATTGAAGGATGGTCGG 559
                                         122 agattattttatttggcattgcctccatcagtctacccatcagtatgcgagatgataaga 181
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Nicotiana tabacum mRNA for cytosolic glucose-6-phosphate
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                                                                                                                                                          620 ACTTACTGCATGAATAAATCTGATGTGGTGGATGGACTGGTATTGTTGTTG 671
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/protein_id="CAA04993.1"
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/db_xref="taxon:4097"
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LOVLCLVAMER PVSIKPEHIRDEKVRVLQSVVPIKOBEVVLGGYDGYLEDPTVPDGSY
TYPTATMVLTRINBRIMGSVPFILKAGKALNSRKAEIRVQFKDVPGDIFKSKKQGRNEF
VIRLQPSEAMYMKLIVKQPGIKMSTVQSEMDLSYGQRYQDVIIPEAYERLILDTIRGD
QQHFVRRDELKAAWEIFTPLLHRIDKGEFKSLPYKFGSRGPEESG"
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/protein_id="AaB69318.1"
/db_xref-"GI:2352921"
/translation="WTSDKWSIEKRAPLRNDSVLKEENVPEIGCLSIVVLGASGDLAK
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Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
II; Apiales; Apiaceae; Petroselinum.
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TNFLQLIKYVCGSYDTEEGYQLLDKEISEHEIYRNCTEGSSRRLFYLALPPSVYFPVC
                                                                                                                                                                                                                                                                                                           Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6ppH1) mRNA, complete cds.
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Extensive reprogramming of cellular metabolism by fungal elicitor
or infection in parsley suggests a new perception of
'defense-related' genes
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      attgaatgaggcaatctctgagtatgagacttcagaaaacaatgactcgggaagctaccg 120
                                          144 ACTGGACAAGGCTATAGCTGAGCACGAAATTGCAAAAATAGCACAGAAGGATCATCCAG 503
                                                                                   cagattattttatttggcattgcctccatcagtctacccatcagtatgcgagatgataag 180
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Best Local Similarity 63.4%; Pred. No. 2.6e-18;
Matches 147; Conservative 0; Mismatches 85; Indels
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/db_xref="taxon:4043"
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1. .1848
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41. .1528
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Direct Submission
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/db_xref="SPTREMEL:065854" | https://db.xref="SPTREMEL:065854" | https://db.xref="SPTREMEL:065854" | https://db.xref="SPTREMEL:06585RELEAR" | https://db.xref="SPTREME" | https://db.xref="SPTREME" | https://db.xref="SPTREME" | https://db.xref="SPTREME" | https://dr.xref="SPTREME" | 
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MYLRHIBERWEGYPFIMKAGKALNSKRAEIRVGFKDVPGDIFRCKKGGENEFVTRLOP
SEAMYMKLTVKRPGLEMSTVOSELDLSYGQRYGGVU IPEAYERLIDTIRGDOGHFVR
RDELKAAWEIETPLLHRIDDGEIKPIPYRFGSRGPAEADELLQUNGYVQTHGYIWIPP
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Submitted (18-SEP-1997) von Schaewen A., Plant Physiology,
University Osnabrueck, Barbarastr. 11, D-49069 Osnabrueck, GERWANY
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Nicotiana tabacum mRNA cytosolic glucose-6-phosphate dehydrogenase
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Wendt,U.K., Hauschild,R., Lange,C., Pietersma,M., Wenderoth,I. and
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Evidence for functional convergence of redox regulation in G6PDH
isoforms of cyanobacteria and higher plants
Plant Mol. Biol. 40 (3), 487-494 (1999)
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ive 0; Mismatches 86; Indels 0;
                                                                                                                                                                                                                                                                                            182 tcatattgcatgagtccatcttcacacccggttggacaagggttattgttg 233
                                                                                                                                                                                                                                                                                                                                                      /product="glucose-6-phosphate dehydrogenase"
/protein_id="CAA04992.1"
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102. 1634
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/cultivar="Samsun NN"
/db_xref="taxon:4097"
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LUVOMLVLRFANRLFLPLMNRDNIANVQIVFREDFGTEGRGGYFDEYGIIRDIIQNHL
LOVLCLVAMEKPISLKPBHTREKKVKTAĞSVIPIKDESVVLGQYEGYBDPTVPNDSN
TPTFATTILRINNERESVPFILKAGKAMSSKRADIRIQFKDVFGDIFKCQNGGRNEF
VIRLQPSEAMYMKLTVKQPGLEMQTVQSELDLSYKQPYQDVSIPEAYERLILDTIRGD
QQHFVRRDELKAAMEIFTPLLHRIDKGEVKSVPYKQGSRGPAEADQLLKKAGYMQTHG
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KKKTFPALFNLFHQGFLNPDEVHIFGYARSKITDEELRDKIRGYLVDEKNASKKTEAL
SKFLKLIKYYSGPYDSEEGFKRLDKAILEHBISKKTABGSSRRLFYLALPPSVYPPVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          von Schaewen,A.
Evidence for functional convergence of redox regulation in G6PDH isoforms of cyanobacteria and higher plants
Plant Mol. B101, 40 (3), 487-494 (1999)
61 attgaatgaggcaatctctgagtatgagacttcagaaaacaatgactcgggaagctaccg 120
                                                                                           121 cagattattttatttggcattgcctccatcagtctacccatcagtatgcgagatgataag 180
                                                                                                                          515 AAGACTCTTCTACTTGCTCTTCCTCCATCAGTATATCCCTCTGTTTGCAGGATGATAAA 574
                                             455 ACTGGACAAGGCGATAGCTGAGCACGAATTCGCAAAAATAGCACGGAAGGATCATCCAG 514
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Submitted (04-SEP-1998) von Schaewen A., Plant Physiology,
University Osnabrueck, Barbarastrasse 11, D-49069 Osnabrueck,
GERMANY
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Arabidopsis thaliana mRNA for cytosolic glucose-6-phosphate
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/protein_id="CAB52674.1"
/db_xref="G1:5732195"
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40.9%; Score 95.4; DB 8; Length 1862;
Best Local Similarity 63.1%; Pred. No. 4e-18;
Matches 147; Conservative 0; Mismatches 86; Indels 0;
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/db_xref="taxon:3702"
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von Schaewen, A.
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KRYPELLENLYROGFINPDEWHIFOTARTKISDEELRDRIRGYLUDEKUREDGEALS.
MIKTCCMNKSDLGGWTRIVVEKPFGKDLESARDGELDESQUIYRDBYLGKEL
VONMLVLRFARNFFFFIDBYLGKURLDRINGYLESAGIGELDESQUIYRDBYLGKEL
VONMLVLRFARNFFFILEDWINDNI BNYQIVFREDFGTBCGRGYFDEYGIIRDIIGNHLL
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PTFATTILIRHNERWEGVPFILKAGKSLNSRNEREIRRQFROFGDIRGYGGYGREPV
IRLQPBSRAMYMKLIYRQPGLDMNTVQSELDLSYGQRYQGYAIPROFGIIRCGQGGREPV
GHFVRRDELKVAMFEFTPLLHRIDKGEVKSIPYRFGSRGFREADQLLEKAGYLQTHGY
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Von Schaewen, A.

Evidence for functional convergence of redox regulation in G6PDH isoforms of cyanobacteria and higher plants
Plant Mol. Biol. 40 (3), 487-494 (1999)
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                                              61 attgaatgaggcaatctctgagtatgagacttcagaaaacaatgactcgggaagctaccg 120
                                                                                    414 ATTAGACAAGGCGATTTTGGAGCACGAGATATCTAAAAAGACTGCTGAAGGATCTTCGAG 473
                                                                                                                                     121 cagattattttatttggcattgcctccatcagtctacccatcagtatgcgagatgataag 180
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University Osnabrueck, Barbarastrasse 11, D-49069 Osnabrueck,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Arabidopsis thaliana mRNA for cytosolic glucose-6-phosphate
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                                                                                                                                                                                                                                                            /product="glucose-6-phosphate 1-dehydrogenase"
/protein_id="CAB52675.1"
/db_xref="G1:5732197"
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thale cress.
Arabidopsis thaliana

    1690 "Arabidopsis thaliana"
/db_xref="taxon:3702"

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Best Local Similarity 62.79
Matches 146; Conservative
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Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cg1-bin/agd_graph.cgj?czk17E12
Genes with similarity to proteins in the databases are described
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CR-081.mit.edu/GENSCAN.html),
GENSCAN (Chris Burge, MIT, http://CR-081.mit.edu/GENSCAN.html),
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremlini.zool.lastate.edu/cgi-bin/sp.cgi).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence may not be the entire insert of this clone. It may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       shorter because we remove overlaps between neighboring submissions.
The 5' clone is MYF5 and the 3' clone is K1G2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (28-JUL-1999) to the DDBJ/EMBL/GenBank databases. Yasukatu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Structural analysis of Arabidopsis thallana chromosome 3. II. Sequence features of the regions of 4,251,695 bp covered by ninety P1, TAC and BAC clones
DNA Res 7, 217-221 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaneko,T., Kato,T., Sato,S., Nakamura,Y., Asamizu,E. and Tabata,S.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AP000381 63604 bp DNA PLN 19-JUL-2000
Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:K17E12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui TAC
                                                        375 GITICIGCAGCIGATIAAGIATGIGAGIGGCCCTIAIGAIGCIGAGGAGGGGIICCAGAG 434
                                                                                                             attgaatgaggcaatctctgagtatgagacttcagaaaacaatgactcgggaagctaccg 120
                                                                                                                                                                                                                                        121 cagattattttatttggcattgcctccatcagtctacccatcagtatgcgagatgataag 180
                                                                                                                                                                                                                                                                       complement(join(3373. .3519,3594. .3676,3763. .3835,
435 ATTAGACAAGGCAATTTCAGAGCACGAAATCTCCAAAAATAGTACTGAAGGGTCTTCTAG
                                                                                                                                                                                                                                                                                                                                                            181 atcatattgcatgagtccatcttcacacccggttggacaagggttattgttg 233
                                                                                                                                                                                                                                                                                                                                                                                           /organism="Arabidopsis thaliana"
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/clone_lib="Mitsui TAC"
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Nakamura,Y
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VPERKLFLOPHQLPLGKDSRFGITEWYSSVGHSGRSTDLGSYMSYKPERCPDDMS
LGQKLILRACEPLPRRCLAKTVQKQDLSKSPDSLWRSVSNKSVNWSGLGGKSFDCLK
GKKLSRECVGCFDLGYFKDRRFVKKGKNDFLIDDVLGGLGSGRIRIGFDISGGSGTFAA
RMARKNYVITNTLNNGAPFSEFIAARGLFPLFLSLDHRFPFLIDNVFDLIHASSGLDV
3921. .4014,4236. .4296,4481. .4541,4626. .4709,4797. .4991,
5261. .5340,5669. .5765,5900. .6018,6097. .6166,6238. .6329,
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LLVIGGQEGPEMAKPNSPIFKCSRRREIFNGEVYMMDEEMKWKMLPPWPKNNSHIESA
WIIVNNSIVIVGGTTDWHPVTKRLVLVGEIFRFQLDTLTWSVIGRLPYRVKTAMAGFW
NGYLYFTSGQRDRGPDNPQPGKVIGEWWRTKLKF"
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sysavfsiwvpvnrpbigipiidskivQkrskQsndTkDHVRFLSaifaDiPapELKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEMESAPVPRLDGYSVQINNLLYVESGYGSLDYVHSHVDVFNFTDNKWCDRFHTPKEM
ANSHLGIVTDGRYVYVVSGQLGPQCRGPTSRSFVLDSFTKTWLEFPSLPAPRYAPATQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YSGYDFCKKLCGVSYIRSGESMENALRACCKGIKICKTLIHRDGDNGMQLIYERLPSD
ISERHVLLLDPVLGTGNSANQAIELLIQKGYPEAHIIFLNLISAPEGIHCVCKRFPKL
KTYSEIDGCLNEEFRYIPGLGEFGDRYFGTDE"

complement(join,7607. 7950,8044. 8209))
//note="gene_id:K17E12.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="wkmgavlvilvfsgllsvktalaarhviggsogweosydfdsws
sdosfrygdolelhsvvelgsetaykscdlgtsvnslssgndvyklsktgtryfacgy
vghceogmrikvnvyssdsksasspsgsgsgsbsgsgsgsgsgsghglrastgymfvygs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MGSSSSSLNNSPIRADSMYTPESQMTVNDNKNDNVSILSPSVK
KSFESPRKSTSIPANNNLTPVKSRWSFSSSKKSFGSKDETFFDSQPWLQSDSDDDFHS
                                                                                                                                                                                                                                                                                                                     /translation="MPEDSTAIDYVMEKASGPHFSGLRLDGLLSSPSKSSVSSPSHFR
LSNSSFSATDDPAAPHQPFVIGVTGGTASGKTTVCDMIIQQLHDHRIVLVNQDSFYRG
LSTSELEHVOPGENFDHPDAFDTBQLLHCVDLIKSGPPVQIPTVDFFTHQRKVDAFRQV
LATSELLIVPEDGENFYDLMMMKIFVDTDADVRLARRIREDTYCRGRDVDSVLED
YAKFVKPAFDDFVLFSKRADVIIPRGGDNHYAVDLIVQHIHTKLGQHDLCKIYPNVF
VIETTFQIRGMHTLIREKDISKHDFVESDRLIRLVVEHGLGHLPFFRSVVTTFSV
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REERESGSSSAISTPYLSGANSREFNDTAIEKEEKKKSNWHHRRCLPGFSSCGGSFM
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/note="gene_1d:K17E12.4
unknown protein"
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/note="contains similarity to unknown protein
                                                                                                                                                                                      /evidence=not_experimental
/product="uridine kinase-11ke protein"
/protein id="BABO2114.1"
/db_xref="GI:9294212"
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/db_xref="G1:9294213"
                                                                                                                /note="gene_id:K17E12.1"
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34134. .34241,34515. .34595,34685. .34794,35165. .35234,
35378. .35520,35718. .36272)
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20791. .20862,20950. .21229,21627. .21838,22180. .22239))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISGEYSPLDODSLDPSVKSIIGEETOETUTWGMFNGSVTAEMETWYTVESVTSVCEGS
LSSHAVGIIDVEIVDNLGKDTCPAFVSDGSNRVWWYNEAYRRNYGDDSTASYSPEVY
VMLVAEEATAAMHCNYQAFTCRVRWQYTWKETKYTKTVPCDVWKMEFGGFAMRLDTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CEASE A LIOR - "MYDEAAFPGGYYRNTFEAPEESEGGSGSSAQIDTEVTASENSSTPARKCIMLANNBEDPYGYQRQVISSRVSWRSTPANSGSERKDLIYELKLELBQTKIVLKNBELQRM
NPAAVSSTSDRYGFSTGQKISSRVSWRSKRSDFANGSGKKYRHQNGTSRGWRRGTSGK
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DLGTYRKNIAGGYYSSPHEFAADVRLFTTNAMTYNPPGHDVHIMGDILSKLEFARWKT
KKLPPGSMQTLAFATISVPPARKRKASRYRESVPEPVRELEFERRWKT
RHRCGROLESLLDELFAHIIDPLKKHNSNGGEIAEDBIEIDJULSDEVLYTIKNLLD
EYIQNKEAKQTNVEPCEIELINGSRPSNSSLORGNERADEYYGGNEPPISRSSDSDS
SSEDQGSDARRHYGGDSKLVNLQWPETANSGGEIAEDBIEIDJUNGSPPISRSSDSDS
SSEDQGSDARRHYGGDSKLVNLQWPETANSEAQDENTRIDDEFYGSOGTGALEQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DICSQUALSSDESDOQHEGNILETPASSEKRYRAALIKNRRADI ILKAREKDI.DONG
KGAPPERLEKEELVLQKKKEKARLQAERAABARRQAEAAABAAABAAABAARRKELE
REAARQALLKMEKTVEINENSKYLEDLEMLSSSASPEQLPSSAEETSPERPLDALGSFN
LIKGSNELEQUGLIYMGODDEEEPRAPAYPKDETSTERPLDALGSSKLGEONFLEGUG
LYMKQDDGEEEPRAPVVVRPNETSLERPVDARGSFNLKGSNPLEQUGLIYMKQDDDEE
                                                                                                                                                                                                                                                                                                                           LALLGAGVTGLLSFSTVASADEÄEHGLESPEYPWPHDGILSSYDHASIRRGHQVYQQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADNNNNSSYGMSKRTKRKYVRVSKNNKGTCRGKSRSDLSDDREQTDVVTLQLLPEKSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MEPITYSKOLPLEFSIFIEVYLLGYLFIFKKWTPETRPLASSCL
ISLLHGVSAVVLATNALLSDPNRGFSSVNTQSQNSILDFSSAYFLADLVHLAVFPSPA
GGDSLFAAHHLAVLEVFLTCRYMVAHGACALLALLVVAEATSACQNTWTLADARGKDA
PLAVSLHRFVTVPFYASYSVCRCVLAPLLIVKMTWFYVSGGADDVIPRWVWVSWTVVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(40773. .41084,41393. .41920)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VTAVTVSILWIWNLWVLFFQERYSKFTKKVR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene_id:KI7E12.7
similar to unknown protein"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similar to unknown protein"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental
/protein_id="BAB02121.1"
/db_xref="G1:9294219"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
/protein_id="BAB02122.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="gene_id:K17E12.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                            25502. .26350
/note="emb|CAB62340.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPEAPAVPNLANDVEEGEID"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="GI:9294220"
                               KADAQVYLSAVLQKPVRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene_id:K17E12.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene_id:K17E12.8
                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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Mesembryanthemum crystallinum
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae;
Caryophyllates; Alzoaceae; Mesembryanthemum.
I (bases 1 to 1777)
Michalowski, C.B. and Bohnert, H.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAKKKTEPALFNUT KROGELPPEGYHIEGYARGKMTDDDLRDRIRGHLIPRNYTAEISE
LAWKKTEPALFNUT KROGELPPEGYHIEGYARGKMTDDDLRDRIRGHLIPRNYTAEISE
CRAIT KLCCMNKSDLGATRI YVEKPERFREILESABGLSADIGEBDESGY TRIDHYLGKE
LVQNLLYMRFANRLE-PLWMRNIANVOIVPERBFGTOGRGGYFDOYGI IRDIIONH
LQYLCLYMARRPONSI KPEHIRDRYKYLOAVNI IKDEEVVLGGY EGYKDDPTVPEDSN
TPTATWLKIHNERWIGV PFILKAGKALNSKRAEIRVOFKOPTOFKORNOGNEF
VIRLOPSEALYMKLTINNERWIGV PFILKAGKALNSKRAEIRVOFKOPTOFKORNOGNEF
VIRLOPSEALYMKLTINDRYGRGY TOGSELDLSYGGRYGOYUPBAYERLILDTIKG
OOHFVRRDELKAAWEIFTPLLHRIDKGEFKPISY KPGTRGPARABALLILDTIKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="cytoplasmic glucose-6-phosphate 1-dehydrogenase"
/protein_id="AAD11426.1"
/db_xref="G1:4206114"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MGSGEWHVERRSSLKSELSKDIGESESSQECGSLSIIVLGASGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glucose-6-phosphate 1-dehydrogenase mRNA from the common ice plant
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2. (bases 1 to 1777)
Michalowski.C.B. and Bohnert, H.J.
Direct Submission
Submitted (09-OGT-1998) Biochemistry, University of Arizona, Bio
Sciences West 513, Tucson, AZ 85721, USA
                                                                                                                                                                                                                                                       49536 TTAGACAAGGCGATTTTGGAGCACGAGATATCTAAAAAGACTGCTGAAGGATCTTCGAGG 49477
                                                                                                                                                                                                                                                                                                                                       62 ttgaatgaggcaatctctgagtatgagacttcagaaaacaatgactcgggaagctaccgc 121
                                                                                                                                                                                                                                                                                                           122 agattattttatttggcattgcctccatcagtctacccatcagtatgcgagatgataaga 181
                                                            Gaps
                                                                                                2 tttttgcagttagtagaatatgttagtggctcctatgatagggtggaaggatttgagtta 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF097663 1777 bp mRNA PLN 01-FEB-1999 Mesembryanthemum crystallinum cytoplasmic glucose-6-phosphate 1-0ehygrogenase (G6PD) mRNA, complete cds.
                                                               ö
        Length 63604;
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mesembryanthemum crystallinum"
Score 78; DB 8; Le
Pred. No. 6.7e-13;
0; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="6 hours NaCl treatment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:3544"
/tissue_type="root"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /EC_number="1.1.1.49"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          б
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
33.5%;
63.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="RR26"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="G6PD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1777 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="G6PD"
                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                 182 tcatattgca 191
                        Similarity
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Fax:81-438-52-3934)
Address for correspondence: kaos@kazusa.or.jp
Fax:81-438-52-3934)
Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=KlB16
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/),
CENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremlinl.zool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
The 5' clone is MNR13 and the 3' clone is MHK7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Tabata,S.
Structural analysis of Arabidopsis thaliana chromosome 5. VII.
Structural analysis of Arabidopsis thaliana chromosome 5. VII.
Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned P1 and TAC clones
DNA Res. 5 (5), 297-308 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                            ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (17-JUN-1998) to the DDBJ/EMBL/GenBank databases. Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakamura,Y., Sato,S., Asamizu,E., Kaneko,T., Kotani,H., Miyajima,N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AB015470 14323 bp DNA PLN 09-AUG-2000 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:KlBl6.
                                                                                                                                                                                                                                                                                                                                                            417 ITAGATGATGAAATATCAAAGTATGAG---TGTCAAAAGAACAGCCAGGAACATTCTAAG 473
                                                                                                                                                                                                                                          62 ttgaatgaggcaatctctgagtatgagacttcagaaaaacaatgactcgggaagctaccgc 121
                                                               Gaps
                                                                                                                     2 tttttgcagttagtagaatatgttagtggctcctatgatagggtggaaggatttgagtta 61
                                                            3;
33.4%; Score 77.8; DB 7; Length 1777; 65.2%; Pred. No. 7e-13;
                                                               Indels
                               Pred. No. 7e-13;
0; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   534 CTTTGCTGTATGAATAAATCT 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 tcatattgcatgagtccatct 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:3241918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 14323)
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Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .14323
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                                                                  Matches 131; Conservative
                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AB015470.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AB015470
         Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
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/clone_llb="Mitsui TAC"
join(53. .226,319. .404,482. .542,632. .818,989. .1146,
1233. .130,1,386. .1444,1545. .1581,1712. .1783,1998. .2145,
2348. .2443,2550. .2620,2721. .2836,2951. .2996,3158. .3325)
/note="gene_id:Klb16.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DRFRGYMDOTYGEGTHELIPILGRPHIFDIRTKPHTFSSISGTKDLQMVNLTLRVLSR
PEVSRLPYIRGTLGLEYDEKVLPSIGNEVLKAVVAQFNADQLLTERPHVSALVRESLI
TRAKDFNIVLDDVAITHLSYGVEFSRAVEQKOVAQQEAERSKEVYMKADQERRAAVIR
AEGESEAAQLISDATAKAGMGLIELRRIEASREIASTLARSPNVAYLPGGQSMLFALN
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                                                                                                                                                                                                                                                                                                                                                                                       KKKTFPALFNLYRQGFLNPDBYHIFGYARTKISDEELRDRIRGYLVDEKNAEQAEALS
KFLOIIKYVSGPYDAEEGFQRLDKAISEHEISKNSTEGSSRRLFYLALPPSVYPSVCK
MIKTCCMNKSDLGGWTRIVVEKPFGKDLESAEQLSSQIGELFDESQIYRIDHYLGKEL
VQNMLVLRFANRFFLPLMNRDNIENVQIVFREDFGTEGRGGYFDEYGIIRDIIQNHLL
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OHFVRRDELKVAWEIFTPLLHRIDKGEVKSIPYKPGSRGPKEADOLLEKAGYLQTHGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MGSQQAAVSFLSNLAKAAFGLGTAATVLNTSLFTVDGGERAVIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OVLCLVAMEKPISLKPEHIRDEKVKVTOSVVPISDDEVVLGGYEGYRDDDTVPNDSNT
PTFATTILRIHNERWEGVPFILKAGKALNSRKAEIRIOFKDVPGDIFRCOKOGRNEFV
                                                                                                                                                                                                                                                                                                                                                                     /translation="MGSGQWHVEKRSTFRNDSFVREYGIVPETGCLSIIVLGASGDLA
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14150. .14323
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2456 c 2257 g 4789 t
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IMPORTANT: This sequence is not the entire insert of clone upon. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone U9D4 is at 1 in this sequence. The true left end of clone U2JD1 is at 37084.
USD4 is from the human chromosome X-specific cosmid library.
                                                                                                                                                                                              HSU9D4 37184 bp DNA PRI 23-NOV-1999
Human DNA sequence from cosmid U9D4, between markers DXS366 and
DXS87 on chromosome X.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 37184)
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9335. 9535

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                                                                                                                                                                                                                                                                                  KEYWORDS
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//OCLE="25 Copies of 4 mer 82 % conserved"

//OCLE="25 Copies of 4 mer 82 % conserved"

//OCLE="MSTC element fragment"

//OCLE="MSTC element fragment"
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20699. 20864
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Best Local Similarity 50.3%; Pred. No. 0.28;
Matches 96; Conservative 0; Mismatches 95; Indels 0.
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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V52279 V62392 X7925 X79412 T39622 X82749 X92304 V31303 V31303 T79660 T79668 V52310 X30255 X30255	X30259 X30255 X30255 X30201 X30201 X30201 X30201 X3120 X31320 X31320 X17320 X17320 X17320 X17320 X17320 X17320 X17320 X17320 X17320 X17320 X17320 X17320	ALIGNMENT	polynu diagno tate; ptor-p	MA,
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
                                                                                                                                                                                                                                                                                   A00010 to A02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                               Polynucleotide library used to determine cancerous states of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 ctacagtaagatgtcattatttaatttattgattgtggaaagacaaaagtaccagatgat 107
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Jones LW, Stache-Crain B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 278 BP; 73 A; 49 C; 49 G; 78 T; 29 other;
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                                                                                                                                                                                                                                     Claim 1; Page 426; 1097pp; English.
   Garcia V,
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       Kita D,
                                                               WPI; 2000-126369/11.
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       Leshkowitz D,
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V74765
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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access medium, preferably selected from a floppy or hard disk, random access the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, coalded skin syndrome, tot. Organisms transformed with the DNA sequences can be used for the complaint production of the polypeptides. The new DNA sequences contained on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of
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Pred. No. 0.89;
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Local Similarity 53.2%;
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misc_feature
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
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                                                                                                                         Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
                                                                   Staphylococcus aureus contig SEQ ID #544.
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16-MAR-1999 (first entry)
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EP786519-A2

30-JUL-1997

97EP-0100117. 07-JAN-1997;

96US-0009861. 05-JAN-1996;

(HUMA-) HUMAN GENOME SCI INC.

Kunsch CA; Fannon MR, Barash SC, Choi GH, Dillon PJ, Rosen CA;

WPI; 1997-374922/35.

Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of anti-S.aureus vaccines

Claim 1; Page 1479-1482; 3271pp; English.

of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (RAM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelld infections, food poisoning, osteomyelitis, syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences C homologues of any of the S.aureus DNA sequences contained on the This sequence represents one of 5191 Staphylococcus aureus DNA sequences computer readable medium.

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73 aatctctgagtatgagacttcagaaacaatgactcgggaagctacgcagat 125

13 agtagaatatgttagtggctcctatgatagggtggaaggatttgagttattgaatgaggc 72

Query Match 12.8%; Score 29.8; DB 20; Length 5631; Best Local Similarity 54.0%; Pred. No. 2.9; Matches 61; Conservative 0; Mismatches 52; Indels 0;

Sequence 5280 BP; 2057 A; 744 C; 854 G; 1442 T; 183 other;

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                                                                    1470 getectataatatgggtgtatgattcaaattaegtaataaaacaatetaattataataga 1529
                                              30 gctcctatgatagggtggaaggatttgagttattgaatgaggcaatctctgagtatgaga 89
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The process systems exchinocandin (ECB) binding domain. ECB binding peptides are useful for screening for antifungal compounds. The method of the invention may be adapted to automated systems such as a PANDEX (RTM) system, allowing high-volume screening of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes a 1,3-beta-glucan synthase protein.
                             ö
   Length 5280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New ECB binding peptide useful for screening for antifungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5631 BP; 1574 A; 1058 C; 1145 G; 1854 T; 0 other;
                                                                                                                                                                                                                                                                                    1,3-beta-glucan synthase; echinocandin binding domain; ECB binding peptide; antifungal compound; ss.
  DB 18;
Score 29.8; DE
Pred. No. 2.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1..5631
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 9-17; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           such as a PANDEX (RTM) system, a potential antifungal compounds.
                                                                                                                                                                                  X85506 standard; DNA; 5631 BP.
12.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        98EP-0310497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0068658
                                                                                                                                                                                                                                       (first entry)
                         Conservative
                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae.
                                                                                                                       1530 ttggagcatacaa 1542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ELIL ) LILLY & CO ELI.
                                                                                               90 cttcagaaaacaa 102
          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-397162/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dixon CK, Ma D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; Y23162.
                                                                                                                                                                                                                                                              DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-DEC-1997;
                                                                                                                                                                                                                                     03-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                      EP931834-A2
                         46;
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Query Match
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                                                                                                                                                                                                             X85506:
                      Matches
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Smooth muscle alpha actin gene; SM alphaA; rat; smooth muscle cell; SMC; anticancer; antiproliferative; cardiant; cis regulatory element; cancer; treatment; proliferative disorder; coronary artery disease; stroke; hypertension; asthma; multiple gastrointestinal disorder; gene therapy; urogenital disorder; reproductive disorder; CARG; ds.
                        Rat smooth muscle-alpha actin (SM alphaA) gene regulatory sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYVI-) UNIV VIRGINIA PATENT FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Owens GK, Mack C, Blank R;
09-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-350519/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200024254-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-MAY-2000
                                                                                                                                       Rattus sp
                                                                                                                                                                                  promoter
                                                                                                                                                                                                           enhancer
                                                                                                                                                                                                                                                                                                                                                                                                                                     enhancer
                                                                                                                                                                                                                                                                               enhancer
                                                                                                                                                                                                                                                                                                                                                                                            intron
                                                                                                                                                                                                                                                                                                                                                      exon
                                                                                                                                                                     Kev
 FK506; antifungal; fungicide; cell wall biosynthesis; fksl gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S. cerevisiae YSK132 (hypersensitive to FK506 at 0.1 ug/ml) was crossed to wild-type YFK005 and a meiotic segregant was backcrossed to YFK007 (sensitive to 50 ug/ml FK560) to generate strain YFK532-10B. The FK506-sensitivity gene FKS1 was then cloned by complementation of the FK506 hypersensitive phenotype of YFK532-10B. Microbial hosts contg. the DNA are used to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding FR506 sensitivity genes – used in in vitro assays to screen for antifungal cpds., including cpds. that affect cell wall biosynthesis
  3090 AATTTGTAAGTCTGGGTAAGCTCTCAACAAAACTCAGCATTTTCCAGTTCAT 3038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 29.8; DB 16; Length 7655; Pred. No. 3.3; 0; Mismatches 52; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cpds that modulate glucan-synthase activity or that affect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7655 BP; 2188 A; 1440 C; 1511 G; 2516 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                            El-Sheerbeini M;
                                                                                                                                                                                                                                                                                                                                                                                                            Douglas CM, El-Sheerbeini
3, Marrinan JA, Morin NR;
Ramadannm, Shei G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig.6; 130pp; English.
                                                                         ΗB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.8%;
54.0%;
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93US-0135149.
93US-0135150.
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                                                                         Q86896 standard; DNA; 7655
                                                                                                                                19-DEC-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                            Clemas J, Do
nj, Kelly R,
                                                                                                                                                                                                                 Saccharomyces cerevisiae.
                                                                                                                                                         S. cerevisiae fksl gene.
                                                                                                                                                                                                                                                                                                                                                                                   (MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Onishi JC, Parent SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-161809/21
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                                                                                                                                                                                                                                                                                                                                                                                                                            Kahnj,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; R72853
                                                                                                                                                                                                                                                                                                 11-OCT-1994;
                                                                                                                                                                                                                                                                                                                                          12-0CT-1993;
12-0CT-1993;
                                                                                                                                                                                                                                                                                                                           .2-OCT-1993;
                                                                                                                                                                                                                                           WO9510625-A1
                                                                                                                                                                                                                                                                     20-APR-1995.
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                                                                                                                                                                                                                                                                                                                                                                                                               Chrebet GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                    086896;
                                             5
                                                           /968980
                                              RESULT
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/label= Intronic_CArg
/note= "Highly conserved cis acting element essential to
direct SMC-specific transcription in vivo"

99WO-US24972.

7.238..247 2438..247 /*tag= b //abbl= CArg_B //note= "Highly conserved cis acting element essential to direct SMC-specific transcription in vivo"

Location/Qualifiers

.2558

/note= "HighIy conserved cis acting element essential to direct SMC-specific transcription in vivo"

/*tag= c /label= CArg_A

2488..2495

/number= 1 3331..3656

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/*tag=

2559..3330

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/*tag=

3559..3568

/*tag=

/numper=

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The present DNA sequence is the rat smooth muscle alpha actin (SM alphaA) gene 5' regulatory sequence, comprising the promoter and first intron. It corresponds to bases -2558 to 4-784 of the SM alphaA gene. An intronic fragment from 4-73 to -1098 bp relative to the start of transcription is bighly conserved and contains cis-acting elements required to direct antiproliferative and cardiant activity. The SM alphaA regulatory sequence is useful to inhibit and treat smooth muscle cell (SMC)-related cancers or other proliferative disorders. It is also used for the treatment of SMC-related disorders, like coronary artery disease, stroke, hypertension, asthma and multiple gastrointestinal, urogenital and reproductive disorders. It is also used in gene therapy.
Isolated polynucleotide is used for inhibiting or treating smooth muscle cell-related cancer or other proliferative disorders and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5342 BP; 1533 A; 1178 C; 1127 G; 1504 T; 0 other;
                                                                                                                                                                                                                      Claim la; Page 84-85; 94pp; English.
                                                                                                              preventing or delaying heart attack
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0; Gaps

4310 AGCGGAATAGATTCTTGGCTCCTCACCTTCAGTCAAAGGTGGCTCTTCATCCAAGTAGGC 4251

4250 AATTGTAAGGTCGGGTAAGCTCTGAAGAAACTCAGGATTTTCCAGTTCAT 1198

74/c D00374 standard; DNA; 5342 BP.

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D00374/ RESULT

D00374;

73 aatetetgagtatgagaetteagaaaacaatgaetegggaagetaeegeagat 125

13 agtagaatatgttagtggctcctatgatagggtggaaggatttgagttattgaatgaggc 72

61; Conservative

Matches

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57 agttattgaatgaggcaatctctgagtatgagacttcagaaaacaatgactcgggaagct 116
                                                                                                            117 accgcagattattttattttggcattgcctccatcagtctacccatcagtatgcgagatga 176
                                                                                                                                       837 TACTTATATTTATTTATTATGAGCACAGTGTAACTGTCTTCAGATACACCAGAAGA 778
                                   Gaps
                                                                                ö
   DB 21; Length 5342;
                                 Indels
                              68;
Score 29.2; DB Pred. No. 4.5; 0; Mismatches
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X13263 standard; DNA; 5354 BP.
12.5%;
50.7%;
                                                                                                                                                                    177 taagatcatattgcatga 194
                                                                                                                                                                                               777 GGGTATCAAATATCATTA 760
                                                                                                                                                                                                                                                                                                                                  (first entry)
          Best_Local Similarity 50.7
Matches 70; Conservative
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                                                                                                                                                                                                                                                                                                    X13263;
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Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds. (HUMA-) HUMAN GENOME SCI INC. 97US-0066009. 97US-0044031. 97US-0046655. 98WO-US08985. Enterococcus faecalis. WO9850555-A2 04-MAY-1998; 14-NOV-1997; 06-MAY-1997; 12-NOV-1998

Enterococcus faecalis genome contig SEQ ID NO:326.

New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus

Kunsch CA;

Barash SC, Dillon PJ,

WPI; 1999-045171/04.

Claim 1; Page 1421-1424; 2084pp; English.

982 nucleotide sequences isolated from the Enterococus faecalis genome. X12938 to X13919 represent these nucleotide sequences which are primary can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence diagnosang faecalis in samples. They can also be used for progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivor or in vitro. In particular the products encoded by the Enterococcus faecalis, or polypeptides encoded by the Enterococcus faecalis nucleotide sequences and be used in very modulate the grown or in vitro. In particular the grown or in vitro. In particular the grown or in vitro is the procession of an be used to mother related organism, in vivor or in vitro. In particular the grown or in vitro is the procession of an be used in vaccines to prevent or attenuate an Enterococcal computer readable medium has been developed which has recorded on it

Sequence 5354 BP; 1424 A; 1146 C; 1020 G; 1759 T; 5 other;

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//note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note- "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
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/note= "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
are included to maintain the nucleotide numbering
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                           Gaps
                                                                                                                                                                                             370 TICATATTTAATAGTATCACTTTGTCGCACGACAGATATAATGCGCCTTTTGCACTTGTT 311
                                                                                                                                       tttgcagttagtagaatatgttagtggctcctatgatagggtggaaggatttgagttatt 63
                                                                                        ö
                            Length 5354;
                                                                                        Indels
                                                                                                                                                                                                                                                         64 gaatgaggcaatctctgagtatgagacttcagaaaacaatgact 107
                                                                                                                                                                                                                                                                                                               310 GCATTAGCCACAGCAAGGCAAAAGGTGTAAAAAAAAACAACGACT 267
                                                                                  47;
                            Score 28.8; DB 20;
                                                        Pred. No. 6.1;
                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus contig SEQ ID #112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                      12.4%;
54.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V74423 standard; DNA; 18613
Query Match
Best Local Similarity 54.8%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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/note=
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V74423/c
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DD 18209 TAAATATTTTTGTTAATACTGAACTTAGTCCTAGGTTGGCAATGGGT 18162

BP

V29268 standard; cDNA; 7313

V29268

178 aagatcatattgcatgagtccatcttcacacaccggttggacaagggt

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of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or required trained from sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
                                                            /note "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence" 15301..15360
                                                                                                                                                                                                                                                                                                                 the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents one of 5191 Staphylococcus aureus DNA sequences
                                                                                                                                                                                                                                                                                       "these bases represent a line of missing text in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of anti-S.aureus vaccines
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       misc_feature
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/transl_except= (pos: 1861..1863, aa: Gly) /transl_except= (pos: 1603..1605, aa: Gly)

/product= "PLAG1 protein"

/*tag= b

/*tag=

Location/Qualifiers

HOMO sapiens.

..1983 /*tag=

Human PLAG1 gene; PLAG1; tumourigenesis gene; T-gene; PLAG2; CTNNB1; antibody; benign tumour; malignant tumour; leukaemia; lymphoma; cancer; inhibition; ss.

Nucleotide sequence of human PLAG1.

21-AUG-1998 (first entry)

V29268;

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This is the nucleotide sequence of the human PLAGI gene. It is a tumourigenesis gene (T-gene), which is isolated in the form of PLAGI, tumourigenesis gene (T-gene), which is isolated in the form of PLAGI, point Grankly genes. Their proteins can be used as a starting point for preparing antibodies for clinically/medically diagnosing cells having a non-physiological proliferative capacity as compared to wild type cells, where the former cells are selected from both chenign and malignant tumours, as well as leukaemia and lymphomas. Derivatives of the T-gene are also used in the diagnosis and preparation of therapeutical compositions for the treatment of cancers, such as nucleic acid derivatives, and antibodies. The T-gene may be uses as a starting point for designing suitable expression-modulating compounds or techniques for the treatment of non-physiological compounds in humans or animals. Expression inhibitors of the T-gene can be used in the treatment of diseases involving
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SXXCCCCCCCCCCCCCXXX B B B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X
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Gaps

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87; Indels

Mismatches Score 28.8; 1 Pred. No. 10;

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12.4%; nilarity 48.2%; Conservative (

Local Similarity

Query Match

81;

Best Loca Matches

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DB 18; Length 18613;

Db 18269 CCGTAAATGATTATACCTTTCGTCGTTTTCATAAGTTCTTCCGTTAAAATTTAGGTATG 18210

118 ccgcagattattttatttggcattgcctccatcagtctacccatcagtatgcgagatgat 177

Db 18329 GTTAACGGTAGAGTAAATATTAATTTAAAATTTAATATAAATACAGCAATCATAAAGGTA 18270

58 gttattgaatgaggcaatctctgagtatgagacttcagaaaacaatgactcgggaagcta 117

New tumourigenesis T-genes and proteins - useful for, e.g. preparing antibodies for clinically diagnosing cells having non-physiological proliferative capacity such as lipoblastomas

M.;

(KULE-) KU LEUVEN RES & DEV. (UYGO-) UNIV GOETEBORGS HOLDINGBOLAGET AB. (LEUV-) LEUVEN RES & DEV.

97EP-0200130.

17-JAN-1997; 22-AUG-1996;

EP825198-A1. 25-FEB-1998 96EP-0202339

Kas KP, Stenman KGD, Van De Ven WJM,

WPI; 1998-132252/13. P-PSDB; W37948. Sequence 7313 BP; 2287 A; 1327 C; 1356 G; 2342 T; 1 other;

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Query Match

V74481/c

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20 tatgitagiggctcctatgatagggiggaaggatttgagitatigaatgaggcaatctct 79
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 attattttatttggcattgcctccatcagtctacccatcagtatgcgagatgataagatc 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q86693 encodes R72576 Candida tropicalis pK233 isocitrate lyase (ICL). By isolating the expression controlling region of Q86693, the claimed promoter sequences Q86694-Q86705 were prepd. These promoter sequences can be used in the prepn. of heterologous proteins, in eukaryotic and prokaryotic host cells.
Score 28.6; DB 19; Length 7313;
Pred. No. 8.1;
0; Mismatches 34; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 28.4; DB 16; Length 3508;
Pred. No. 7.1;
0; Mismatches 26; Indels 0;
                                                                                                                                                                                                                                                                                                   Candida tropicalis pK233; isocitrate lyase; ICL; promoter; eukaryotic; prokaryotic; exprssion controling DNA; ds.
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                                                                                                                              2106 cattaagccagtataaaatagaa 2128
                                                                                                     80 gagtatgagacttcagaaaacaa 102
                                                                                                                                                                                            Q86693 standard; DNA; 3508 BP
 12.3%;
59.0%;
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62.9%;
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                        49; Conservative
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            Local Similarity
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             Best Loca
Matches
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Q86693/c
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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can also be used in a varcine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyalitis, skin and surgical wound infections, food poisoning, costeomyalitis, syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
                                                                                                                                                                                                                                                                          Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of anti-S.aureus vaccines
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                                                                                                                                                                                                          Staphylococcus aureus contig SEQ ID #170.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
V74481 standard; DNA; 5333 BP.
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RESULT 11

Sequence 17710 BP; 4342 A; 4712 C; 4675 G; 3967 T; 14 other;

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This sequence represents a E. coli strain 196 contig containing pathogenicity island (PAI) sequences, and represents a nucleic acid molecule of the invention. PAIS are large fragments of DNA which comprise pathogenicity determinants. The sequences of the invention are taken from PAI IV and PAI IV is located at approximately 64 min (near pheV) on the E. coli crimomosome and is greater than 170 kb. PAI V is located at approximately 94 min (at pheR) on the E. coli chromosome and is approximately 160 kb in size. Antibodies specific to the proteins encoded by the PAI open reading frames of the invention can be used in kits to detect uropathogenic E. coli. The proteins are used in vaccines to elicit a protective immune response in an animal to the uropathogenic E. coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAI; pathogenicity island; uropathogenic E. coli detection; PAI IV; pheR; PAI V; pheV; vaccine; protective immune response; ds.
                                                                                                                                                                                                                                                                                                                       3787 TATGCGCGTGGCAGAAGCAGCAACACAAGCAGGCGGAATAACCTTCGTTACAATTTTATT 3728
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                             15 tagaatatgttagtggctcctatgatagggtggaaggatttgagttattgaatgaggcaa 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated uropathogenic E. coli nucleotide sequences - used to develop products for the detection of pathogenic E. coli and to elicit an immune response to pathogenic E. coli
homologues of any of the S.aureus DNA sequences contained on the
                                                                                                                                                                                                                           ö
                                                                                                                                                                      Length 5333;
                                                                                Sequence 5333 BP; 1830 A; 921 C; 782 G; 1620 T; 180 other;
                                                                                                                                                                                                                           Indels
                                                                                                                                                                12.2%; Score 28.4; DB 18; 50.0%; Pred. No. 8.4; tive 0; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E. coli J96 pathogenicity island contig #70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 21; Page 171-181; 250pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3727 TGGCATATTGTACATCATTTA 3706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 tggcattgcctccatcagtcta 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Welch RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56/c
V31256 standard; DNA; 17710 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-US21347.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0061953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1998 (first entry)
                                                                                                                                              Query Match
Best Local Similarity 50.vv
T; Conservative
                             computer readable medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UNIV WISCONSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Choi GH, Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-312461/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L4-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09822575-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (OXMI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V31256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
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strain J96

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The present invention describes a computer readable medium which has
the nucleotide sequences SEQ ID NO:1 to 391 (V52134 to V52524) recorded
the nucleotide sequences SEQ ID NO:1 to 391 (V52134 to V52524) recorded
to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEO ID NO:1
to 391 (V52134 to V52524) are genomic fragments from Streptococcus
to 391 (V52134 to V52524) are genomic fragments from Streptococcus
condecule encoding a homologue of any of the fragments of the S. pneumoniae
complexity and the member of any of the fragments of the S. produced
by a process comprising: (a) screening a genomic DNA library using as a
complexity sequence defined by any of the sequences in SEQ ID NO:1
to 391, identifying members of the library which contain sequences
that hybridise to the target sequence and isolating the nucleic acid
molecules from the members; or (b) isolating the nucleic acid
from an organism, amplifying nucleic acid molecules whose nucleotide
sequence is homologous to amplification primers derived from the
fragment of the S. pneumoniae genome to prime the amplification and
                                     ö
                                                                                                     Db 12723 GACCATCTGACGCTGGACACATTTTCAGACTCCGGACCACCTTCTGCACGGTGTTGAC 12664
                                                                                                                                                  160 atcagtatgcgagatgataagatcatattgcatgagtccatcttcacacaccggttggac 219
                                                                           100 caatgactcgggaagctaccgcagattattttatttggcattgcctccatcagtctaccc 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Computer-readable medium with recorded Streptococcus pneumoniae polynuclectide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus
                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay; computer readable medium; vaccine; pharmaceutical composition; ds.
Length 17710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dougherty BA, Fannon M;
                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae genome fragment SEQ ID NO:146.
   DB 19;
 Score 28.4; DB; Pred. No. 14; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 978-985; 1409pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                   V52279 standard; DNA; 11887 BP.
     12.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-0029960.
                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                     12663 GATGGTTCCGGTTG 12650
                                             68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae.
                                                                                                                                                                                                                                220 aagggttattgttg 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-272225/24.
                         Best Local Similarity
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Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pneumoniae
       Query Match
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                                                                                                                                                                                                                                                                                                                               RESULT 13
                                               Matches
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isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome of commercial importance, or expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines for S. pneumoniae.
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Sequence 11887 BP; 3478 A; 2714 C; 2103 G; 3592 T; 0 other;

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                                                                                                                            9025 TITITIAATICAGIAIGGAAIGIAIGGAGAICATIAIAAAACAIAGAAGGIICIAAGACI 8966
                                                                                                                                                                                              8965 TIAGAATAGGCAAATAAAGCATATGCAATTCCACAATATCCATGAGCAAAGGTATAGTCT 8906
                                                                                                                                                                62 ttgaatgaggcaatctctgagtatgagacttcagaaaacaatgactcgggaagctaccgc 121
                                                                                           2 tttttgcagttagtagaatatgttagtggctcctatgatagggtggaaggatttgagtta 61
                              Length 11887;
                          DB 19;
                        12.1%; Score 28.2; D 49.7%; Pred. No. 13; tive 0; Mismatches
                                                                                                                                                                                                                                                        8905 AAATGCTTTCTTTGGCTGTATCTC 8881
                                                                                                                                                                                                                                        agattattttatttggcattgcctc 146
Query Match
Best Local Similarity 49.78;
....hes 72; Conservative
                                                                                                                                                                                                                                        122
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Human; interleukin-1 receptor antagonist gene; IL-1; polymorphism; Human interleukin-1 receptor antagonist gene. V62392 standard; DNA; 12565 diagnosis; osteoporosis; ds (first entry) 19-JAN-1999 V62392; RESULT 14

Homo sapiens

08-OCT-1998.

98WO-GB00944 27-MAR-1998;

97GB-0006359 27-MAR-1997;

(GEMI+) GEMINI RES LTD.

Keen RW, Spector TD;

present invention describes genotyping a nucleic acid sample from a

WPI; 1998-557135/47.

Diagnosis of osteoporosis by determining genotype of interleukin-1 receptor antagonist gene - useful for diagnosing patient pre-disposition or susceptibility to osteoporosis and for therapeutic intervention

Disclosure; Page 21-27; 36pp; English.

A method has been developed for the diagnosis of osteoporosis comprising determining the genotype of an interleukin-1 (IL-1) receptor antagonist gene (IL-1RN). The present sequence represents the human interleukin-1 receptor antagonist gene. The method can be used for the diagnosis of disease, including diagnosis of osteoporosis and predisposition or susceptibility to osteoporosis and for therapy.

Sequence 12565 BP; 3217 A; 2980 C; 3072 G; 3294 T; 2 other;

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                                                            12129 tgctccttgacattgtagagcttctggcacttggagacttgtatgaaagatggctgtgcc 12188
                                        85 tgagacttcagaaaacaatgactcgggaagctaccgcagattattttatttggcattgcc 144
                         0; Gaps
                                                                                                                                                                                                                                               Human; interleukin 1; IL-1B; IL-1A; IL-1RN; diagnosis; detection; chronic obstructive airway disease; chronic bronchitis; emphysema; asthma; chronic bronchiolitis; proinflammatory haplotype; ss.
                                                                                                  12189 tetgeetgteteeceaccaggetgggagetetgeagaggaaacatgaete 12241
   Length 12565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genotyping nucleic acid samples for interleukin-1 (IL-1) proinflammatory haplotype alleles, useful for predicting susceptibility to developing chronic obstructive airway disease
                                                                                 145 tccatcagtctacccatcagtatgcgagatgataagatcatattgcatgagtc 197
                         Indels
  Score 28.2; DB 19;
Pred. No. 14;
                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      Lim S;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Giovine M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Fig 3; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                             (MEDI-) MEDICAL SCI SYSTEMS INC
 12.1%;
                                                                                                                                                                                                                                                                                                                                                           98WO-US23721.
                                                                                                                                                            X75925 standard; DNA; 12565
                                                                                                                                                                                                                                                                                                                                                                                          97GB-0023553
                                                                                                                                                                                                                           Human interleukin 1RN gene.
                                                                                                                                                                                                                                                                                                                                                                                98US-0005923
                                                                                                                                                                                                     29-JUL-1999 (first entry)
                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    Barnes PJ, Duff GW,
          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-327420/27
                                                                                                                                                                                                                                                                                                               W09924615-A2.
                                                                                                                                                                                                                                                                                                                                                          09-NOV-1998;
                   60;
                                                                                                                                                                                                                                                                                                                                                                                           07-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                             12-JAN-1998;
                                                                                                                                                                                                                                                                                                                                     20-MAY-1999
Query Match
Best Local 3
                                                                                                                                        RESULT 15
                    Matches
                                                                                                                                                X75925
                                                            g
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bright to determine at least one allele of an interleukin-1 (IL-1)

proinfilammatory haplotype. A method has also bee described for

proinfilammatory haplotype. A method has also bee described for

determining a subject; susceptibility to developing chronic obstructive

alway disease (COAD) or for predicting the rapidity or ultimate

progression of a COAD in the subject by: (a) obtaining a nucleic acid

IL-1 proinfilammatory haplotype in the sample, where detection of at

least one of these alleles indicates that the patient has an increased

the susceptibility to developing COAD. The method is useful for determining

the susceptibility of subjects to developing chronic obstructive airway

chronic obstructive airway disease (COAD). COAD can be astima, emphysema,

chronic bostructive airway disease (COAD). COAD can be astima, emphysema,

chronic bostructive airway disease (COAD). COAD can be astima, emphysema,

carly identification of chronic obstructive airway disease (COAD).

facilitating administration of appropriate treatment at the earliest

stage, thereby increasing the probability of a positive outcome. The

present sequence represents the human IL-IRN gene. Sequence 12565 BP; 3217 A; 2980 C; 3072 G; 3294 T; 2 other;

.; 0 0; Gaps Best Local Similarity 53.1%; Pred. No. 14; Matches 60; Conservative 0; Mismatches 53; Indels

Search completed: November 4, 2000, 13:40:19 Job time: 16146 sec

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

November 4, 2000, 08:56:04; Search time 189.35 Seconds

(without alignments)
186.106 Million cell updates/sec

Title:
233
Sequence:
1 gttttgcagttagtagaat.....ttggacaagggttattgttg 233
Sequence:
235
Sequence:
262060 seqs, 75620727 residues

Total number of hits satisfying chosen parameters:
524120

Minimum DB seq length: 2000000000

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Listing first 45 summaries
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1: /cgn2_6/ptodata/2/lna/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/lna/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/lna/5B_COMB.seq:*
4: /cgn2_6/ptodata/2/lna/5D_COMB.seq:*
5: /cgn2_6/ptodata/2/lna/5D_COMB.seq:*
6: /cgn2_6/ptodata/2/lna/6COMB.seq:*
7: /cgn2_6/ptodata/2/lna/5D_COMB.seq:*
7: /cgn2_6/ptodata/2/lna/backfiles1.seq:*

Issued_Patents_NA:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	# 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	, ,	1,5	, r	Sequence 13, Appl	ò -	ì	Seguence 1, Appli	- '		-`1	Sequence /, Appli	À (Sequence 3, Appl1	ກີ	77		4	13,	13,	'n	3,	Sequence 3. Appli	,	ì -	ì ,-	Sequence 5, Appli
SUMMARIES	ID	US-08-619-554-1	US-08-464-402-1	US-08-755-587-27	US-08-755-587-15	US-08-603-753D-3	US-08-639-501-1	US-09-044-946-1	US-08-245-294-7	US-08-474-499-7	US-08-307-279A-7	PCT-US95-06211-7	US-08-755-587-1	US-08-986-485-3	US-08-464-523B-3	IIS-08-404-0250	IIS-08-402-409-21	TZ - ZC / CZ + CO CC	#1570 #0# 00 GO	US-00-492-459-13	US-U8-423-752-13	05-08-0/0-30	05-08-6/6-9/4-3	US-09-098-487-3	US-08-485-569-1	US-08-480-993-1	US-07-903-079B-1	US-07-718-535-5
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ALIGNMENTS

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RESULT

1 Sequence 1. Application US/08619554

1 Sequence 1. Application US/08619554

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2 Sequence 1. Application US/08619554

2 Sequence 1. Application US/08619554

3 Septicant 1. DOUGLAS, Cameron M. APPLICANT: CLRREET, Gary L. APPLICANT: FOOR, Forrest APPLICANT: FOOR, Forrest APPLICANT: FOOR, Forrest APPLICANT: MARNINAN, Jennifer, APPLICANT: MARNINAN, Jennifer, APPLICANT: MARNINAN, Jennifer, APPLICANT: MARNINAN, Jennifer, SHELI, Gan-Ju TITLE OF INVENTION: SYNTHASE SUBUNITS GIUCAN INTELE OF INVENTION: SYNTHASE SUBUNITS SUBUNITS ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES OF SEQUENCES GIVEN APPLICANTION DAY ENCODIA - MERCK & CO., INC. STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000 STAPE: NJ

COUNTRY: USA

ZIP: 077065

COMPUTER: IDM COMPATIDE - P.O. BOX 2000 STAPE: NJ

COURREN APPLICATION DAYA:

MEDIUM TYPE: DISKRETCH DOS

SOFTWARE: FASTEM: DOS

COMPUTER: IDM COMPATION: 536

FILING DATE: MAGGINER: US/08/619,554

FILING DATE: TABLEATION NUMBER: US/08/619,554

FILING DATE: TABLEATION NUMBER: US/08/619,554

FILING DATE: TELECANINICATION NUMBER: 19104PI

TELECOMNINICATION NUMBER: 19104PI

TELECOMNINICATION NUMBER: 18104PI

TELECOMNINICATION NUMBER: 18104PI

TELECOMNINICATION NUMBER: 18104PI

TELEPHONE: 772-594-6730

TELEFAX: 772-594-6730

INFORMATION FOR SEO ID NO: 1: SEQUENCE CHARACTERISTICS: LEMEGR: TABLE CALL
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 gactogggaagctaccgcagattattttattttggcattgcctccatcagtctacccatca 163
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                              13 agtagaatatgttagtggctcctatgatagggtggaaggatttgagttattgaatgaggc 72
                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                 4250 AATTIGTAAGTCTGGGTAAGCTCTCAACAAAAACTCAGCATTTTCCAGTTCAT 4198
                                                                                                                                                                                                                                                                                   73 aattitgagtatgagacttoagaaaacaatgactogggaagctacogoagat 125
                                                                                                                12.8%; Score 29.8; DB 2; Length 7655; 54.0%; Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 12.0%; Score 28; DB 3; Length 3417; Best Local Similarity 53.7%; Pred. No. 2.9; Matches 58; Conservative 0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 gtatgcgagatgataagatcatattgcatgagtccatcttcacacacc 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD
                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WEIL ET AL.
TITLE OF INVENTION: Human DNA Ligase III
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRICE APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03939
FILING DATE: 31 MAR 95
ATTONNEY/AGENT INFORMATION:
NAME: FERRARG, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-388
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36,134
36,134
------325800-388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,402
FILING DATE: June 5, 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08464402
Patent No. 5858705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 3417 BASE PAIRS TYPE: NUCLEIC ACID STRANDEDNESS: SINGLE
                                                                                                                                                              61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: CDNA US-08-464-402-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEW JERSEY
: USA
               TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-619-554-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: LINEAR
                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ROSELAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07068
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                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
US-08-464-402-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                       Query Match
                                                                                                                                                                  Matches
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GENERAL INFORMATION:
APPLICANT: Futreal, Phillip A
APPLICANT: Ashworth, Alan
APPLICANT: Astracton, Michael R
TITLE OF INVENTION: Materials and methods relating to the
TITLE OF INVENTION: identification and sequencing of the BRCA2 cancer
TITLE OF INVENTION: susceptibility gene and uses thereof.
                                                                                                                                                                                                                                                                                                                                                                                       3: Bell Seltzer Park & Gibson
310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.8%; Score 27.4; DB 5; Length 5892; 65.6%; Pred. No. 6;
2351 GGTTGAAGGTCAACAAGATCTACTAGACTTCATCGTCCCAGACC 2398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADPLICATION NUMBER: US/08/755,587
FILING DATE: 25-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9523959.6
FILING DATE: 23-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 952555.0
FILING DATE: 14-DEC-1995
PRIOR APPLICATION NUMBER: GB 952555.0
FILING DATE: 14-DEC-1995
FILING DATE: 28-NOG-1995
APPLICATION NUMBER: GB 9617961.9
FILING DATE: 28-NOG-1996
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5405-135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                           Sequence 27, Application US/08755587 Patent No. 6045997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Kenneth D Sibley
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 544
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 5892 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Raleigh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
US-08-755-587-27
                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5014 C 5014
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                                                                                                                US-08-755-587-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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LIBRARY: CDNA library derived from human CLONE: obtained using published sequence POSITION IN GENOME: CHROMOSOME/SEGMENT: unknown NAP POSITION: unknown UNITS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens sapiens INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: CDNA tO MRNA
HYPOTHETICAL: no
                                                                                                                                                                                                            STREET: BOULEVALLE
CITY: DURHAM
STATE: NORTH CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 11283
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: BRCA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: no
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
                  Sequence 15, Application US/0875587

Sequence 15, Application US/0875587

GENERAL INFORMATION:

APPLICANT: Futreal, Phillip A

APPLICANT: Ashworth, Alan

APPLICANT: Stratton, Michael R

TITLE OF INVENTION: Identification and sequencing of the BRCA2 cancer;

TITLE OF INVENTION: Succeptibility gene and uses thereof.

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

ADDRESSER: Bell Settzer Park & Gibson

STREET: 310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107

CTTY: Realeigh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 aaggattigagttattgaatgaggcaatctctgagtatgagacttcagaaaacaatgact 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
11.8%; Score 27.4; DB 5; Length 7240;
Best Local Similarity 65.6%; Pred. No. 6.6;
Matches 40; Conservative 0; Mismatches 21; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING ALM COMPACTALLE
OPERATING SYSTEM: POC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/755,587
FILING DATE: 25-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9523959.6
FILING DATE: 23-NOV-1995
PRIOR APPLICATION NUMBER: GB 952555.0
FILING DATE: 14-DEC-1995
PRIOR APPLICATION NUMBER: GB 9617961.9
FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INVORBER: GB 9617961.9
FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5405-135
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Batent No. 5891857
GENERAL INFORMATION:
APPLICANT: HOLT, JEFFREY T.
APPLICANT: JENSEN, ROY A.
APPLICANT: PAGE, DAVID L.
APPLICANT: RING, MARY-CLAIRE
APPLICANT: SZABO, CSILLA I.
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Kenneth D Sibley
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 540
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 7240 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: CDNA
US-08-755-587-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                      USA
US-08-755-587-15
                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-603-753D-3
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 kB storage COMPUTER: IBM PC/XT/AT compatible OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORD PERRECT 6.1 and ASCII CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/603,753D
FILING DATE: 20 FEB 1996
CLASSIFICATION S14
PRIOR APPLICATION DATE: 17 JAN 1995
ATTORET/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/2
FELECOMMUNICATION INFORMATION:
RESTRENCE/DOCKET NUMBER: 1242/2
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                       ADDRESSEE: ARLES A. TAYLOR, JR.
STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER
STREET: BOULEVARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: gene encoding BRCA2 protein PUBLICATION INFORMATION: AUTHORS: Wooster, R. et al.
AUTHORS: Wooster, R. et al.
TITLE: Identification of the breast cancer TITLE: susceptability gene BRCA2
JOGRNAL: Nature
VOLUME: 379
PAGES: 789-792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEVELOPMENTAL STAGE: adult
TISSUE TYPE: female breast
CELL TYPE: normal and cancerous breast cells
ORGANELLE: no
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RESULT
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                                                                                                                                           0; Gaps
                                                                            Score 27.4; DB 3; Length 11283; Pred. No. 8; 0; Mismatches 21; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Simard, Jacques
APPLICANT: Couch, Fergus
APPLICANT: Couch, Fergus
APPLICANT: Couch, Fergus
APPLICANT: Weber, Barbara
APPLICANT: Weber, Barbara
TITLE OF INVENTION: Chromosome 13-Linked Breast Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 124
CORRESPEDNDENCE ADDRESS:
ADDRESSE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TIPE: FLORY GENERALINE
COMPUTER: TENDRY GENERALINE
COMPOTER: TENDRY GENERALINE
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/639,501
FILING DATE: 29-APR-1996
CLASSIFICATION TOWARE: US 08/585,391
FILING DATE: 11-JAN-1996
PRIOR APPLICATION NUMBER: US 08/585,391
FILING DATE: 11-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/576,559
FILING DATE: 21-DEC-1995
FILING DATE: 20-DEC-1995
FILING DATE: 18-DEC-1995
FILING DATE: 18-DEC-1995
FILING DATE: 18-DEC-1995
ATTONING NUMBER: US 08/573,779
FILING DATE: 18-DEC-1995
ATTONING NUMBER: 18-DEC-1995
ATTONING NUMBER: 18-DEC-1995
ATTONING NUMBER: 18-DEC-1995
ATTONING NUMBER: 18-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08639501 Patent No. 5837492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRRACTERISTICS:
LENGTH: 11385 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Tavtigian, Sean V.
APPLICANT: Kamb, Alexander
                                                                                     11.8%;
65.6%;
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                                                                                        Query Match 11.89
Best Local Similarity 65.69
Matches 40; Conservative
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US-08-603-753D-3
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US-08-639-501-1
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6611 AAGAATTTAAATTATCAAATAATTAAAAGTGGTGGTTCTTCAGAAAATAATCACT 6670
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                                                                                                                                                                                 Length 11385;
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Best Local Similarity 65.6%; Pred. No. 8;
Matches 40; Conservative 0; Mismatches 21; Indels
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APPLICANT: Kamb, Alexander
APPLICANT: Simard, Jacques
APPLICANT: Couch, Fergus
APPLICANT: Rommens, Johanna
APPLICANT: Weber, Barbara
TITLE OF INVENTION: Chromosome 13-Linked Breast Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Venable, Baetjer, Howard & Civiletti
1201 New York Avenue N.W., Suite 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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PRICATION LALE:
APPLICATION NUMBER: US 08/576,559
FILING DATE: 21-DEC-1995
PRICATION NUMBER: US 08/575,359
FILING DATE: 20-DEC-1995
FILING DATE: 20-DEC-1995
FILING DATE: 18-DEC-1995
ATPLICATION NUMBER: US 08/573,779
FILING DATE: 18-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REGISTRATION NUMBER: 28,957
REJECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/639,501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09044946
Patent No. 6033857
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TELEFAX: 202-962-8300
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMO sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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229..10482
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                                                                                   ; NAME/KEY:
; LOCATION:
US-08-639-501-1
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GENERAL INFORMATION:
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                    US-08-245-294-7
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APPLICANT: Anderson, Burt E.
APPLICANT: Requery, Russell L.
TITLE OF INVENTION: DIAGNOSING
TITLE OF INVENTION: DIAGNOSING
TITLE OF INVENTION: NOCHALIMAEA HENSELAE AND ROCHALIMAEA QUINTANA
TITLE OF INVENTION: INFECTION
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                 11.8%; Score 27.4; DB 5; Length 11385; 65.6%; Pred. No. 8; tive 0; Mismatches 21; Indels 0;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/245,294
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127 Peachtree Street, Suite 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 1414.612
TELECOMUNICATION INFORMATION:
TELEPHONE: 404/688-980
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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LENGTH: 11385 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 65.6%
Matches 40; Conservative
                                                                                                                                  ORGANISM: Homo sapiens
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STRANDEDNESS: double
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                                                  TOPOLOGY: linear
MOLECULE TYPE: CDNA
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                                                                                    HYPOTHETICAL: NO
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                                                                                                  ANTI-SENSE: NO
ORIGINAL SOURCE:
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US-09-044-946-1
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128 ttttatttggcattgcctccatcagtctacccatcagtatgcgagatgataagatcatat 187
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Query Match
Best Local Similarity 59.2%; Pred. No. 7.9;
Matches 45; Conservative 0; Mismatches 31; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Anderson, Burt E.
APPLICANT: Regnery, Russell L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: DIAGNOSING ROCHALIMAEA HENSELAE
TITLE OF INVENTION: AND ROCHALIMAEA QUINTANA INFECTION
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,499
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
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127 Peachtree Street, Suite 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/245,294
FILING DATE: 18 MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFENENCE/CDOCKET NUMBER: 1414.612
TELEPHONE: 404/688-0770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                    US-08-474-499-7/c; Sequence 7, Application US/08474499; Patent No. 5693776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
FRNGTH: 1791 base pairs
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                                                                                                                                                                                                      1165 GCCTTGATACCAGCTT 1150
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Best Local Similarity 59.28
Matches 45; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & P
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STRANDEDNESS: double
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NUMBER OF SEQUENCES:
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ROCHALIMAEA HENSELAE AND ROCHALIMAEA QUINTANA INFECTION
                                                                                                                                                                                                                                              APPLICANT: Anderson, Burt E.
APPLICANT: Regnery, Russell L
TITLE OF INVENTION: Nucleic Acids of Rochalimaea Henselae
TITLE OF INVENTION: and Methods and Compositions for Diagnosing Rochalimaea
TITLE OF INVENTION: Henselae and Rochalimaea Quintana Infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 ttttatttggcattgcctccatcagtctacccatcagtatgcgagatgataagatcatat 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: NEEDLE & ROSENBERG, P.C. STREET: 127 Peachtree Street, N.E., Suite 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/307,279A FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIF: 50500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                          US-08-307-279A-7/c
; Sequence 7, Application US/08307279A
; Patent No. 5736347
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Spratt, Gwendolyn D.
REGISTATION UNBER: 36,016
REFERENCE/DOCKET WUMBER: 1414.
TELECOMMUNICATION INFORMATION:
TELEFAX: (404) 688-9780
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1791 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                          1165 GCCTTGATACCAGCTT 1150
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                               188 tgcatgagtccatctt 203
                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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COUNTRY: USA
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PCT-US95-06211-7/C
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APPLICANT: Stratton, Michael R
TITLE OF INVENTION: Materials and methods relating to the
TITLE OF INVENTION: identification and sequencing of the BRCA2 cancer
TITLE OF INVENTION: susceptibility gene and uses thereof.
NUMBER OF SEQUENCES: 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1225 TITGCTAGATCACGGACATCATTAATCTTCTCACCATTTACCGAAATAATAACATCACCT 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 ttttatttggcattgcctccatcagtctacccatcagtatgcgagatgataagatcatat 187
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ADDRESSEE: Bell Seltzer Park & Gibson
STREET: Bell July UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
CITY: Raleigh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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Pred. No. 7.9;
0; Mismatches 31; Indels 0
                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TSM PC COMPATIBLE
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US95/06211
PRIOR APPLICATION NUMBER: WS 08/245,294
FILING DATE: 18 MAY 1994
CLASSIFICATION NUMBER: WS 08/245,294
FILING DATE: 18 MAY 1994
CLASSIFICATION:
NAME: Sprat, Weendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 1414.6121
TELECHONE: 404/688-0770
TELECHONE: 404/688-0780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              %3-08-755-587-1
; Sequence 1, Application US/08755587
; Patent No. 6045997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ashworth, Alan
APPLICANT: Stratton, Michael R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Futreal, Phillip A APPLICANT: Wooster, Richard F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.3%;
59.2%;
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MEDIUM TYPE: Floppy disk
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TYPE: nucleic acid
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Best Local Similarity 59.29
Matches 45; Conservative
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PCT-US95-06211-7
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                                                                                                          Georgia
: USA
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Best Local Similarity 63.9%; Pred. No. 8.1;
Matches 39; Conservative 0; Mismatches 22; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22; Indels
                                         SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/755,587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-986-485-3/c

Sequence 3, Application US/08986485

Fatent No. 6046030

GENERAL INFORMATION:
APPLICANT: WU, SHUJIAN
APPLICANT: TRUNEH, ALEMSGED
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAINER & PRESTIA
STREET: P.O. BOX 980
CORREST: P.O. BOX 980
CORREST: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast5ED for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            NAME: Kenneth D Sibley
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405-135
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1917 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                 FILING DATE: 25-NOV-1996

PRIOR APPLICATION DATA;

APPLICATION NUMBER: GB 9523959.6

FILING DATE: 23-NOV-1995

PRIOR APPLICATION DATA;

APPLICATION NUMBER: GB 952555.0

FILING DATE: 14-DEC-1995

PRIOR APPLICATION DATA;

APPLICATION NUMBER: GB 9617961.9

FILING DATE: 28-NOC-1996

ATTORNEY AGENT INFORMATION:
                                                                                  JMBER: US/08/755,587
25-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/986,485
FILING DATE: 08-DEC-1997
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 60/059,448
FILING DATE: 22-SEP-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRESTIA, PAUL F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 08 CLASSIFICATION:
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83 tatgagacttcagaaaacaatgactcgggaagctaccgcagattattttatttggcattg 142
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                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                        11.2%; Score 26.2; DB 5; Length 3159;
49.6%; Pred. No. 12;
tive 0; Mismatches 68; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Toni A. Voelker
APPLICANT: Ling Yuan
APPLICANT: Jean Kridi
APPLICANT: Jean Kridi
APPLICANT: Jeborah Hawkins
APPLICANT: Aubrey Jones
TITLE OF INVENTION: Plant Acyl ACP Thioesterase
VUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/464,523B
FILING DATE: 02-JUN-1995
CLASSIFICATION NUMBER: US/08/464,523B
FRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/13131
FILING DATE: 10-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/152,004
FILING DATE: 10-NOV-1993
PRIOR APPLICATION DATA:
FILING DATE: 16-JUN-1994
APPLICATION NUMBER: 08/261,695
FILING DATE: 16-JUN-1994
ATTORNEY/AGENT INPORMATION:
NAME: Donna E. SCHAFET
                    REFERENCE/DOCKET NUMBER: GH-70264
TELECOMMUNICATION INFORMATION:
TELEFHONE: 610-407-0700
TELEFAX: 610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Microsoft Word 5.1(a) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 3, Application US/08464523B
; Patent No. 5723761
REGISTRATION NUMBER: 23,031
                                                                              TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3159 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                      Query Match 11.29
Best Local Similarity 49.69
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 tcacacaccggttgg 217
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                 ; TOPOLOGY: linear;
; MOLECULE TYPE: CDNA
US-08-986-485-3
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STATE: CA
COUNTRY: USA
95616
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US-08-464-523B-3/C
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HERCISTRATION WINDING NUMBER: 34.719
HAMEZ CALI J. Schwedler 36.924
RESISTENCYOCKER NUMBER: CORE 100-1MO
TELECOMMUNICATION HUMBER: CORE 100-1MO
TOPOLOGY: 110-1MO
TATLE 100-1MO
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TELEDAMINI HUMBER: 33-67
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TELEDAMINI HUMBER: 30-311-80-30
TELEDAMINI HUMBER: 30-311
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November 4, 2000, 06:48:03; Search time 4352.3 Seconds (without alignments) 330.996 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                              7189864 seqs, 3091403243 residues
                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                   OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                   IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                               Sequence:
                                                       Run on:
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44: em_esthum2:*
45: em_esthum3:*
46: em_esthum3:*
48: em_esthum6:*
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117: gb_gss18:*
118: gb_gss19:*
119: em_gss13:*
120: gb_gss20:*
121: gb_gss21:*
122: gb_gss21:*
123: gb_gss21:*
124: gb_gss24:*
125: em_gss14:*
126: em_gss16:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	316967 FRUM	W565200 LG1 '		412330 MCG0	CEDE STORES	31640 6513	3144 / EST2	16550 ESTZ	5585 EST3	19154 EST3	91202 EST2	41197 sb85	4410 N210	36245 EST3	548140 AV54	561737 AV56	15829 WHE0	131906 EST3	55246 EST3	30010 EST3	54552 AV56	49133 NF03	AW689492 NF019H04S	23696 M40E8STM	73149 EST4	41181 EST34528	7079 EST33850	9284 EST34029	50103 EST40099	7104 EST33853	54983 ML1164 p	55222 ML216 pe	34970 NF023F11	26520 M65J22ST	17385 EST32379	17091 EST32350	35333 NF027C04	94720 EST26416	342388 EST39523	223852 EST30066	774199 EST33335	980083 EST34159	621290 EST3	03098 EST40312	26794 AV52	0271530 nhxh
	3031000	BEZIO30	AWDODZO	BE4123	AWOYUSI	BE43184	AWU3144	AW21655	AW61658	BE44915	AI49120	AI94119	AW58441	AW73624	AV54814	AV56173	BE51582	BE43190	AW45524	AW98001	AV56455	BE24913	AW6	BE52369	BE47314	BE34118	AW73707	BE44928	BE45010	AW73710	AW25498	AW25522	AW68497	BE52652	AW61738	AW61709	AW68533	AI8947	BE34238	AW22385	AW77419	AW98008	AW62129	BE2030	AV5267	A02715
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ALIGNMENTS

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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Sorghum.
1 (bases 1 to 621)
Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C. and Pratt, L.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                       Triticum aestivum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.
1 (bases 1 to 881)
Anderson, J.M., Williams, C.E. and Goodwin, S.B.
Analysis of an EST database reveals a probable CF2 resistance gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW565200 621 bp mRNA EST 19-JUL-2000 LG1_328_D07.b1_A002 Light Grown 1 (LG1) Sorghum bicolor cDNA, mRNA
         ESTOSIO Triticum aestivum Lambda Zap Triticum aestivum CDNA Clone
JAI_SC_E06_T3 5' similar to Putative glucose-6-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
03-JUL-2000
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70.7%; Score 164.8; DB 34; Length 881;
Best Local Similarity 81.9%; Pred. No. 1.4e-40;
Matches 190; Conservative 0; Mismatches 42; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="JA1_5C_E06_T3"
/clone_lib="Triticum aestivum Lambda Zap"
//tissue_type="leaf"
                                                                                                                                                                                                                                                                         Crop Production & Pest Control Research Unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="9 day old seedlings"
175 c 196 g 256 t
                                                                                                                                                                                                                                                                                                                                                                                                               /organism-"Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:4565"
                                         dehydrogenase, mRNA sequence.
BE216967
 mRNA
                                                                                                                                                                                                                 homolog in wheat
Unpublished (2000)
Contact: Anderson, J.M.
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AW565200.1 GI:7219078
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                                                                            BE216967.1 GI:8904653
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Sorghum bicolor
                                                                                                            bread wheat.
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                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Light Grown (LG1)"
/clone_lib="Light Grown (1G1)"
/note="Organ: 10- to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site_1: XhoI; Site_2: EcoRI
: The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
a 147 c 133 g 175 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ï
                                                                                                                                                                                         Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hordeum vulgare
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.
1 (bases 1 to 850)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Larman, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., International Triticeae EST Cooperative (TTEC): Production of Expressed Sequence Tags for Species of the Triticeae Contact: Graner A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59.2%; Score 138; DB 23; Length 621; 78.0%; Pred. No. 2.5e-32; Live 0; Mismatches 45; Indels
  An EST database from Sorghum: light-grown seedlings Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                              /organism="Sorghum bicolor"
/db_xref="taxon:4558"
                                                                                                                                                                                                                                                                           High quality sequence stop: 591 POLYA=No.
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                     Email: mmpratt@uga.edu
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                                                                                                                                                                                                                                                       Seq primer: JEN REV
                                                                                                                             Tel: 706 542 1860
Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                        .621
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Best Local Similarity
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Medicago.
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He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula stem library Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW690515 616 bp mRNA EST 15-JUN-2000
NF030E099ST1F1000 Developing stem Medicago truncatula cDNA clone
NF030E09ST 5', mRNA sequence.
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9
                                                                                                                                                                                            /organism="Hordeum vulgare"
/db_xref="taxon:4513"
/clone="McG002.B10"
/clone=lib="ITEC MCG Barley Leaf/Culm Library"
/tissue_type="leaf/culm"
/dev_stage="etiolated"
a 214 c 198 g 213 t 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                             DB 35; Length 850;
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Institute for Plant Genetics & Crop Plant Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                  Email: a_graner@ipk-gatersleben.de
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2510 Sam Noble Parkway, Ardmore, OK 73402, USA
                Corrensstr. 3, D-06466 Gatersleben GERMANY
Tel: 49 39482 5521
Fax: 49 39482 5137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50;
                                                                                                                                                                                                                                                                                                                                                                                                                        56.3%; Score 131.2; DB 3
75.9%; Pred. No. 3.3e-30;
iive 0; Mismatches 50
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Insert Length: 616 Std Error: 0.00
Plate: 030 row: E column: 09
Seq primer: TCACACAGGAAACACCTATGAC.
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The Samuel Roberts Noble Foundation
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AW690515.1 GI:7565251
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Matches 176; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 580 221 7302
Fax: 580 221 7380
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/lab_host="SOLR"
long="Weedror: paluescriptsKmCUadapt; Site_1: EcoRl;
site_2: XhoI; Fruit were harvested at the breaker stage
(first sign of lycopene accumulation on the blossom end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eŭkaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
I; Solanales; Solanaceae; Solanum; Lycopersicon.
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Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Glovannoni,J.J. and Tanksley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 cagattattttatttggcattgctccatcagtctacccatcagtatgcgagatgataag 180
                                                                                                                                                                                                                                                                                                                                                                                                                                         61 attgaatgaggcaatctctgagtatgagacttcagaaaacaatgactcgggaagctaccg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 gittitgcagitagtagaataigttagtggcicciatgatagggitggaaggatitgagit 60
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                                                                                                                                                                                                                                                                                               Gaps
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/tissue_type="stem"
/dev_stage="fem"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of internodal stem segments"
105 c 140 g 180 t 3 others
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                                                                                                                                                                                                                                                 42.8%; Score 99.8; DB 24; Length 616; 63.9%; Pred. No. 1.6e-20; tive 0; Mismatches 84; Indels 0
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/cultivar="TA496"
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Clemson University
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/dev_stage="breaker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone cLEG4I11, mRNA sequence.
/db_xref="taxon:3880"
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Location/Qualifiers
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Contact: David Frisch
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Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                    Matches 149; Conservative
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JOURNAL
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Lycopersicon esculentum Eukaryota; Tracheophyta; Spermatophyta; Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Bagnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
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the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp." 98\ c 108\ g 150\ t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 attgaatgaggcaatctctgagtatgagacttcagaaaacaatgactcgggaagctaccg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 ACTGGACAAGGCAATACTGAGCACGAATTCTCAAAAAATAGCACAGAAGGATCATCCAG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 GITTCTGCAACTGATTAAATACGTCAGTGGCTCTTATGATTCTGGTGAGGGCTTTACGTT 225
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                                                                                                                                                                                                                                                                                                                                      0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 97; DB 35; Length 502;
Pred. No. 1.1e-19;
0; Mismatches 85; Indels
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/cultivar="TA496"
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Fax: 864 656 4293
Email: dfrisch@cLEMSON.EDU
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Clemson University Genomics Institute
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Best Local Similarity 63.5%;
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//tissue_type="callus"
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//dev_stage="15-40 days old"
//dev_stage="15-40 days old"
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//note="vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
//note: Site_1: Site_1: EcoR1; Site_2:
//note: Site_1: Site_1: CoR1; Site_2:
//note: Site_1: EcoR1; Site_2: Site_2:
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
1; Solanales; Solanaceae; Solanum; Lycopersicon.
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Alcala, J. Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Tankaley, S.D. and Giovannoni, J. Generation of ESTs from tomato callus tissue
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EST295264 tomato callus, TAMU Lycopersicon esculentum cDNA clone
                                                                                                                                                                                                                                                                                                                                 61 attgaatgaagcaatctctgagtatgagacttcagaaaacaatgactcgggaagctaccg 120
                                                                                                                                                                                                                384 ACTGGACAAGGCAATATCTGAGCACGAATTCTCAAAAAATAGCACAGAAGGATCATCCAG 443
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Query Match

Query Match

41.6%; Score 97; DB 19; Length 560;
Best Local Similarity 63.5%; Pred. No. 1.1e-19;
Matches 148; Conservative 0; Mismatches 85; Indels
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/cultivar="TA496"
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
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Email: dfrisch@CLEMSON.EDU
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/clone="cLEC86B9"
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Lycopersicon hirsutum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
I; Solanales; Solanaceae; Solanum; Lycopersicon.
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van der Hoeven, R.S., Bezzeredes, J.L., Matern, A.L., Holt, I.E., Liang
'F., Hansen, T., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W.,
Fraser, C.M., Martin, G.B., Glovannoni, J.J. and Tanksley, S.D.
Generation of ESTs from wild tomato (Lycopersicon hirsutum)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW616585 602 bp mRNA EST 24-FRAN 2000
EST322996 L. hirsutum trichome, Cornell University Lycopersicon
hirsutum cDNA clone cLHT11D22 5', mRNA sequence.
                                           326 GTTTCTGCAACTGATTAAATACGTCAGTGGCTCTTATGATTCTGGTCAGGGCTTTACGTT 385
                                                                                              61 attgaatgaggcaatctctgagtatgagacttcagaaaacaatgactcgggaagctaccg 120
                                                                                                                                    386 ACTGGACAAGGCAATATCTGAGCACGAATTCTCAAAAAATAGCACAGAAGATCATCCAG 445
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/tissue_type="trichome"
/dev_stage="mixed stages"
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1 gtttttgcagttagtagaatatgttagtggctcctatgatagggtggaaggatttgagtt
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/db_xref="taxon:62890"
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Fax: 864 656 4293
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Contact: David Frisch
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Query Match 41.6%; Score 97; DB 20; Length 595; Best Local Similarity 63.5%; Pred. No. 1.1e-19; Matches 148; Conservative 0; Mismatches 85; Indels

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/tissue_type="trichome"
/dev_stage="mixed stages"
/note="Leaves of various stages were shaken in liquid
/note="teaves of various stages were shaken in liquid
/nitrogen, shearing off trichomes. This procedure yielded a
mixture of cells which is highly enriched for trichome
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van der Hoeven, R.S., Bezzeredes, J.L., Matern, A.L., Holt, I.E., Liang
van der Hoeven, R.S., Bezzeredes, J.L., Ronning, C.M., Nierman, W.,
F., Hansen, T., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W.,
Fraser, C.M., Martin, G.B., Giovannoni, J.J., and Tanksley, S.D.
Generation of ESTs from wild tomato (Lycopersicon hirsutum)
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Eukaryota, Viridiplantae, Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
I; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 608)
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                                                                                                                                                     Query Match
41.6%; Score 97; DB 35; Length 608;
Best Local Similarity 63.5%; Pred. No. 1.1e-19;
Matches 148; Conservative 0; Mismatches 85; Indels
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/db_xref="taxon:62890"
/clone="cLHT28E8"
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Clemson University Genomics Institute
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Fax: 864 656 4293
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Lycopersicon esculentum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
I; Solanales; Solanaceae; Solanum; Lycopersicon.
I (bases 1 to 649)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: DBK_CMV; Site_1: EcoR1; Site_2: Xhol; cLEB
- Tomato Shoot Meristem EST Library. Oligo-dr primed cDNA
library made from tomato vegetative shoots including
meristems and expanding leaves."
                                                                                                                                                                                                                                                                                                                                                                                                                                                           van der Hoeven, R.S., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D. Generation of ESTs from tomato shoot meristem Unpublished (1999)
Contact: David Frisch
Clemson University Genomics Institute
                                                                                                                                               A1491202 649 bp mRNA EST 29-JUN-1999 EST241911 tomato shoot, Cornell Lycopersicon esculentum cDNA clone cLEB1G14 similar to glucose-6-phosphate dehydrogenase, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 cagattattttatttggcattgcctccatcagtctacccatcagtatgcgagatgataag 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 AAGACITITCTACITIGCICITCCICCGICAGIAIATCCCICIGITIGCAGAAIGAIAAA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 ACTGGACAAGGCAATATCTGAGCACGAATTCTCAAAAAATAGCACAGAAGGATCATCCAG 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 GITTCTGCAACTGATTAAATACGTCAGTGGCTCTTATGATTCTGGTGAGGGCTTTACGTT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 gtttttgcagttagtagaatatgttagtggctcctatgatagggtggaaggatttgagtt 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="CLEB1G14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="tomato shoot, Cornell"
/tissue_type="shoot meristem"
/dev_stage="8 week old plants"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: dfrisch@CLEMSON.EDU.
                                                                                                                                                                                                                                                                             AI491202.1 GI:4386512
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181 atcatattgcatgagtccatcttcacacaccggttggacaagggttattgttg 233

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A1941197 287 bp mRNA EST 13-DEC-1999 sb85911.yl Gm-c1010 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1010-1821 5' similar to SW:G6PD_MEDSA Q42919 GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM ;, MRNA
                                                                                                                                                                                                                                                                                                               1 (bases 1 to 287)
Shoemaker, R. Kehm, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna
A., Bolla, B., Marra, M., Hiller, L., Kucaba, T., Martin, J., Beck, C.,
Wylie, T., Underwood, K., Steptce, M., Theising, B., Allen, M., Bowers
Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R. Kitter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
Public Soybean EST project
Unpublished (1999)
                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudlcotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="young cotyledons of greenhouse grown plants"
/dev_stage="2cm long 12 week old"
/lab_host="XL10-Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1010-1821"
/clone_lib="Gm-c1010"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        info@genomesystems.com web site: www.genomesystems.com
Possible reversed clone: similarity on wrong strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 106.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
                                                                                                                       AI941197
AI941197.1 GI:5688182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     314 286 1800
314 286 1810
                                                                                                                                                                                                                        Glycine max
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KEYWORDS
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/tissue_inp_mnAm.
/tissue_inp_mnAm.
/tissue_inp_mnAm.
/tissue_inp_mnAm.
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days post-inculation with Glomus versiforme. The library was made from a mixture of RNA from each of these stages."
/lab_host="E. coli strain SOLR"
/hote="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: Khoi; cDNA was prepared from polyA+ enriched RNA from roots harvested at 10, 17, 22, 31 and 38 days post-incoulation with Glomus versiforme. The cDNA was directionally ligated into the Unizap RN vector from extracts. Plasanids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in SOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Medicago truncatula/Glomus versiforme mixed EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mjharrison@noble.org
Other name: MHAM-2a-F08; Date: 3/14/00; Updated to the Database of
Expressed Sequence Tags (dbEST) on 04/27/00; More information is
available at http://chrysie.tamu.edu/medicago'.
                                                                                                                                                                                                                                                                                                 Medicago truncatula/Glomus versiforme mixed EST library.
Medicago truncatula/Glomus versiforme mixed EST library
Eukaryota; mixed EST libraries.
1 (bases 1 to 697)
Harrison,M.J., Liu,J., Peng,H., Gonzales,M., Ellis,L., Town,C.D.,
ESTS from roots of Medicago truncatula after colonization with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 attgaatgaagcaatctctgagtatgagacttcagaaaacaatgactcgggaagctaccg 120
                                                                                                                                                               28-APR-2000
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                                                                                                                                                                             N210452e MHAM Medicago truncatula/Glomus versiforme mixed EST
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218 GAACTTGTGCATGAATAAATCTGATGTGTGGATGGACGTGTNGTTGTCG 270
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Live 0; Mismatches 81; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cultivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
/clone="MHAM-2K15"
                                                                                                                                                                                                     library cDNA clone MHAM-2K15, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2510 Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-223-5810
Fax: 580-221-7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: Harrison M.J.
Plant Biology Division
The Samuel Roberts Noble Foundation
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                                                                                                                                                                                                                                                      AW584410.1 GI:7261464
                                                                                                                                                       697 bp
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                                                                                                                                                                                                                                                                                                                                                                                                Medicago truncatula
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotylodons; core eudicots; Rosidae; eurosids I;
Fabales; Pabaceae; Papilionoideae; Medicago.
I (bases 1 to 489)
VandenBosch,K., Hurt,J., Moore,J., Beremand,P., Peng,H., Ellis,L.,
Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESTs from roots of Medicago truncatula after Rhizobium inoculation Unpublished (1999)
Contact: VandenBosch K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="pkV3-1213"
/clone_lib="kV3"
/tisue_type="Seedling roots"
/dev_stage="3 days post-inoculation with Sinorhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 gtttttgcagttagtagaatatgttagtggctcctatgatagggtggaaggatttgagtt 60
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cagattattttatttggcattgcctccatcagtctacccatcagtatgcgagatgataag 180
                                                                         24-APR-2000
                                                                                                                                                                                                                                                                                  EST332231 KV3 Medicago truncatula cDNA clone pKV3-1213, mRNA
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                                                                                                                                  181 atcatattgcatgagtccatcttcacacaccggttggacaaggg 224
                                                                                                                                                       'http://chrysie.tamu.edu/medicago'
Seg primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. coli strain SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         College Station, TX 77843-3258, USA Tel: 409 845 7707
Fax: 409 845 2891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: kate@mail.bio.tamu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Texas A&M EST name:T255752e
TIGR sequence name:MTEAE50TK
                                                                                                                                                                                                                                                                                                                                           AW736245.1 GI:7643094
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Texas A&M University
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Asamizu.E., Nakamura,Y., Sato,S. and Tabata,S. hallana: Generation along acale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA inbraries
DNA Res. 7, 175-180 (2000)
Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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61 attgaatgaggcaatctctgagtatgagacttcagaaaacaatgactcgggaagctaccg 120
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                                                                                                                                                                                                                                                                    262 GACTGCTTGCATGAATAAATCTGATGATGGAGGGGGGGGACACGTATTGTTGTTG 314
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/clone_lib="Arabidopsis thaliana green siligues Columbia"
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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/clone="SQ156f07F"
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